

Fri Nov 7 08:48:20 2003

us-10-081-817a-19-plus-1-12-of-seq3.rge

Page 1

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 6, 2003, 10:03:01 ; Search time 1999 Seconds  
(without alignments)  
11521.821 Million cell updates/sec

Title: US-10-081-817A-19-PLUS-1-12-OF-SEQ3  
Sequence: 1 CGGCGG999G9GCGGCGG9.....CCGCGCGCATGAGCTCGCC 563

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues  
Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: gb\_bac:\*  
2: gb\_hvg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pac:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pt:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_hvg\_hum:\*  
31: em\_hvg\_hiv:\*  
32: em\_hvg\_ocher:\*  
33: em\_hvg\_mus:\*  
34: em\_hvg\_pln:\*  
35: em\_hvg\_rtd:\*  
36: em\_hvg\_mam:\*  
37: em\_hvg\_vtc:\*  
38: em\_sy:\*  
39: em\_hvg\_hum:\*  
40: em\_hvg\_mus:\*  
41: em\_hvg\_ocher:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
C 1	500.6	88.9	137488	2	AC022095	AC022095 Homo sapi
C 2	498	88.5	168347	2	AC025336	AC025336 Homo sapi
C 3	487	88.5	190024	2	AC122714	AC122714 Homo sapi
C 4	487	86.5	166777	2	AC106813	AC106813 Homo sapi
C 5	481.8	85.6	130129	2	AC108083	AC108083 Homo sapi
C 6	132	23.4	562	2	BD082141	BD082141 Reagents
C 7	129	12.0	190	6	BD082137	BD082137 Reagents
C 8	90	12.0	519	6	BD082142	BD082142 Reagents
C 9	90	12.0	570	6	AR252648	AR252648 Sequence
C 10	90	12.0	570	6	AX403520	AX403520 Sequence
C 11	89	15.8	244	6	BD082138	BD082138 Reagents
C 12	89	15.8	135020	2	AF429315	AF429315 Homo sapi
C 13	74	13.1	172550	2	AP005772	AP005772 Oryza sat
C 14	71	12.6	172729	11	PM2H12G	PM2H12G Homo sapi
C 15	68.2	12.1	215852	2	AC084804	AC084804 Mus muscu
C 16	66.8	11.9	63082	2	AC022663	AC022663 Homo sapi
C 17	64.8	11.5	63082	2	PM12H12B	PM12H12B Homo sapi
C 18	64.4	11.2	1007	11	PM3H11G	PM3H11G Homo sapi
C 19	63.2	11.2	167624	2	AC143386	AC143386 Macaca mu
C 20	63.2	11.0	1082	11	PM2H12B	PM2H12B Homo sapi
C 21	62.2	11.0	63082	2	AC022663	AC022663 Homo sapi
C 22	62.2	11.0	63082	2	AC139773	AC139773 Homo sapi
C 23	62	11.0	65351	2	AC112672	AC112672 Mus muscu
C 24	61.8	11.0	72645	2	AC027353	AC027353 Homo sapi
C 25	61.8	11.0	101509	2	AC141871	AC141871 Mus muscu
C 26	61.8	11.0	187413	10	AF411253	AF411253 Mus muscu
C 27	61.6	10.9	125020	9	AF429315	AF429315 Homo sapi
C 28	61.6	10.9	125020	2	AC031610	AC031610 Rattus no
C 29	61.6	10.9	125020	2	AC031610	AC031610 Rattus no
C 30	61.6	10.9	167077	2	AC031610	AC031610 Rattus no
C 31	61	10.8	2685	6	HUMBA10	HUMBA10 Homo sapi
C 32	61	10.8	43058	6	AX332817	AX332817 Sequence
C 33	61	10.8	43058	6	AX333047	AX333047 Sequence
C 34	61	10.8	43058	6	AX411306	AX411306 Sequence
C 35	61	10.8	43058	9	HS6G1	HS6G1 Human DNA s
C 36	61	10.8	258002	2	AC014149	AC014149 Homo sapi
C 37	60.8	10.7	159980	2	AF005743	AF005743 Oryza sat
C 38	60.4	10.6	1065	11	PM2H12B	PM2H12B Homo sapi
C 39	59.6	10.6	1094	11	PM7G11B	PM7G11B Homo sapi
C 40	59.6	10.6	240957	9	AC011407	AC011407 Homo sapi
C 41	58.8	10.4	85268	2	AC022648	AC022648 Homo sapi
C 42	58.8	10.4	85434	2	AC066610	AC066610 Homo sapi
C 43	58.8	10.4	85434	2	AC138109	AC138109 Mus muscu
C 44	58.8	10.4	224777	2	AC138109	AC138109 Mus muscu
C 45	58.8	10.4	224777	2	AC138109	AC138109 Mus muscu

## ALIGNMENTS

RESULT 1  
AC022095/c 127488 bp DNA linear HTG 20-APR-2001  
LOCUS Homo sapiens chromosome 5 clone CTB-36B8, WORKING DRAFT SEQUENCE,  
DEFINITION 13 unordered pieces.  
ACCESSION AC022095  
VERSION AC022095.5 GI:13699618  
KEYWORDS HTG; HTGS PHASE1; HTGS\_DRAFT; HTGS\_ACTIVEFIN.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 DOE Joint Genome Institute.  
Sequencing of Human Chromosome 5

JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 127488)  
 AUTHORS DOE Joint Genome Institute.  
 TITLE Direct Submission  
 JOURNAL Submitted (26-JAN-2000) Production Sequencing Facility, DOE Joint  
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
 COMMENT On Apr 20, 2001 this sequence version replaced gi:7711676.  
 -----Genome Center  
 Center: Joint Genome Institute  
 Center Code: JGI  
 Web site: http://www.jgi.doe.gov

Project Information  
 Center Project Name: 78060  
 Center Clone Name: CIT978SKB\_3688

Summary Statistics  
 Consensus quality: 110477 bases at least Q40  
 Consensus quality: 117221 bases at least Q30  
 Consensus quality: 120225 bases at least Q20  
 Estimated insert size: 131000; pulse field gel estimation  
 Estimated insert size: 126288; sum-of-coverage estimation  
 Quality coverage: 7.48 in Q20 bases; pulse field gel estimation  
 Quality coverage: 7.76 in Q20 bases; sum-of-coverage estimation.  
 NOTE: This is a 'working draft' sequence. It currently  
 consists of 13 contigs. The true order of the pieces  
 is not known and their order in this sequence record is  
 arbitrary. Gaps between the contigs are represented as  
 runs of N, but the exact sizes of the gaps are unknown.  
 This record will be updated with the finished sequence  
 as soon as it is available and the accession number will  
 be preserved.

1 1116: contig of 1116 bp in length  
 1117 1216: gap of unknown length  
 1217 1254: contig of 1038 bp in length  
 2255 2354: gap of unknown length  
 2355 3412: contig of 1058 bp in length  
 3413 5005: contig of 1493 bp in length  
 5006 5105: gap of unknown length  
 5106 7647: contig of 2542 bp in length  
 7648 7747: gap of unknown length  
 7748 10237: contig of 2490 bp in length  
 10238 10337: gap of unknown length  
 10338 12440: contig of 2103 bp in length  
 12441 12540: gap of unknown length  
 12541 15935: contig of 3395 bp in length  
 15936 16035: gap of unknown length  
 16036 24396: contig of 8361 bp in length  
 24397 24496: gap of unknown length  
 24497 39085: contig of 14589 bp in length  
 39086 39185: gap of unknown length  
 39186 60545: contig of 21360 bp in length  
 60546 79490: gap of unknown length  
 79491 79590: contig of 18445 bp in length  
 79591 127488: contig of 47898 bp in length.  
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 /mol\_type="Genomic DNA"  
 /db\_xref="taxon:9606"  
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BASE COUNT 31643 a 32392 c 31616 g 30626 t 1211 others

Query Match 88.9%; Score 500.6; DB 2; Length 127488;  
 Best Local Similarity 95.9%; Pred. No. 2.2e-74;  
 Matches 541; Conservative 0; Mismatches 5; Indels 18; Gaps 2;

1 CGCGCGGAGCGCGCGGAGTAGGCTGATGCTCCCTGCGCCCTCCACCTCCCGAGG 60

|||||  
 Db 84291 CGCGCGGAGCGCGCGGAGTAGGCTGATGCTCCCTGCGCCCTCCACCTCCCGAGG 84232  
 Qy 61 CGCGAGAGCGCGCCCAAGAGACCCCAAGTGCCTGACGAGTGTGGATCAGAG 120  
 Db 84231 CGCGAGAGCGCGCCCAAGAGACCCCAAGTGCCTGACGAGTGTGGATCAGAG 84172  
 Qy 121 CAGGAGCAAGAGAGCGAGAACTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180  
 Db 84171 CAGGAGCAAGAGAGCGAGAACTGGCGCGCGCGCGCGCGCGCGCGCGCGCG 84112  
 Qy 181 CCTCAGCAGAGAGAACTCCCTCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240  
 Db 84111 CCTCAGCAGAGAGAACTCCCTCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 84069  
 Qy 241 AGACCGCAAGAGAGAGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300  
 Db 84068 AGACCGCAAGAGAGAGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 84009  
 Qy 301 CT-CTCGAGAGAGCG 359  
 Db 84008 CTCTCTCAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 83949  
 Qy 360 GGGGCGAGCGCGCTTCCAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 419  
 Db 83948 GGGGCGAGCGCGCTTCCAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 83889  
 Qy 420 GAGCGGAGCGCGCGAGCGCGCTTCTCAGAGCGCGCGCGCGCGCGCGCGCGCGCG 479  
 Db 83888 GAGCGGAGCGCGCGAGCGCGCTTCTCAGAGCGCGCGCGCGCGCGCGCGCGCG 83829  
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 Db 83828 ACCGGGTATPAGAGCGCTGAGCGCTTCCCGGCGAGCGCGCGCGCGCGCGCGCG 83769  
 Qy 540 AGCG 563  
 Db 83768 AGCG 83745

RESULT 2  
 AC025336/c 168347 bp DNA linear HTG 25-MAR-2000  
 LOCUS Homo sapiens chromosome 5 clone RP11-451H23 map 5, WORKING DRAFT  
 DEFINITION  
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 VERSION AC025336.2 GI:7328761  
 KEYWORDS HTG; PHASE1; HTGS\_DRAFT.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1. (bases 1 to 168347)  
 Birren, B., Linton, L., Nusbaum, C. and Lander, E.  
 Unpublished  
 2. (bases 1 to 168347)  
 Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,  
 Anderson, S., Baldwin, J., Barna, N., Bastien, V., Bedalov, G.,  
 Boguski, L., Boulikas, B., Brown, A., Burkett, G.,  
 Campione, A., Cooke, P., DeRubeis, R., Dewar, K., Diaz, J.S.,  
 Dodge, S., Domino, M., Doyle, W., Ferris, P., Fitzhugh, W., Gage, D.,  
 Galagan, J., Gargyala, S., Ginde, S., Goyette, M., Graham, L.,  
 Grand-Pierre, N., Grant, G., Hagos, B., Heatford, A., Horton, L.,  
 Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karas, A.,  
 Klein, J., LaRoque, K., Lamazares, R., Landers, T., Lebeck, J.,  
 Levine, R., Liu, C., Liu, G., Locke, K., MacDonald, P., Marquis, N.,  
 McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPeck, R.,  
 Murphy, J., Naylor, J., Norman, C.H., O'Connor, T., Olenda, V., Morrow, J.,  
 O'Neill, D., Oltar, T.M., Oliver, J., Peterson, K., Pierre, N.,  
 Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,



TITLE  
JOURNAL  
COMMENT

Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, R.,  
Strange-Rhoman, N., Stojanovic, N., Subramanian, A., Taimae, J.,  
Tastay, S., Theodore, J., Tirrell, A., Travers, M., Triggillo, J.,  
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, K., Wynn, D., Ye, W.,  
Young, G., Zannon, J., Zimmer, A. and Zody, W.  
Direct Submission  
Submitted 108-MAR-2000 Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Mar 25, 2000 this sequence version replaced g1:7210017.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WITB  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence\_submissions@genome.wi.mit.edu  
Project information  
Project name: L6686

Center project name: 451 H.23  
Summary Statistics  
Sequencing Vector: Min: M7815; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.960731  
Consensus quality: 150422 bases at least Q40  
Consensus quality: 159524 bases at least Q30  
Consensus quality: 161013 bases at least Q20  
Insert size: 165247; sum-of-contigs  
Quality coverage: 3.6 in Q20 bases; sum-of-contigs

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 32 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

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1 1389: contig of 1389 bp in length
* 1390 1489: gap of 100 bp
* 1490 3130: contig of 1641 bp in length
* 3131 3230: gap of 100 bp
* 3231 4942: contig of 1712 bp in length
* 4943 5042: gap of 100 bp
* 5043 6981: contig of 1939 bp in length
* 6982 7081: gap of 100 bp
* 7082 8708: contig of 1627 bp in length
* 8709 8808: gap of 100 bp
* 8809 10286: contig of 1478 bp in length
* 10287 10386: gap of 100 bp
* 10387 12212: contig of 1826 bp in length
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* 12313 14658: contig of 2346 bp in length
* 14659 14758: gap of 100 bp
* 14759 17941: contig of 3133 bp in length
* 17942 18041: gap of 100 bp
* 18042 21297: contig of 3256 bp in length
* 21298 21397: gap of 100 bp
* 21398 24992: contig of 3595 bp in length
* 24993 25092: gap of 100 bp
* 25093 27768: contig of 2676 bp in length
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* 27869 31288: contig of 3320 bp in length
* 31289 31889: gap of 100 bp
* 31890 33814: contig of 2426 bp in length
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# FEATURES

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* 66825 71568: contig of 4744 bp in length
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* 90054 90154: gap of 100 bp
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* 108116 118144: contig of 10029 bp in length
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* 130569 142339: gap of 100 bp
* 142340 142339: contig of 11671 bp in length
* 142340 157135: gap of 100 bp
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* 169347 169347: contig of 1112 bp in length
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Best Local Similarity 95.7%; Pred. No. 5,5e-74;  
Matches 540; Conservative 0; Mismatches 5; Indels 19; Gaps 2;

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DB 145202 CGGCGGAGGCGGCGGCGGAGTGGTCTGATCGTCCCTGAGCGCTTCACTCCAGG 145143  
QY 61 CGGAGAGGCGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120  
DB 145142 CGGAGAGGCGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 145083  
QY 121 CAGGAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180  
DB 145082 CAGGAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 145023  
QY 181 CCTCACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240  
DB 145022 C-----CCTCACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 144981  
QY 241 AGACCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300  
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QY 301 CT-CTCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 359  
DB 144920 CTGCTCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 144861  
QY 360 GGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 419  
DB 144860 GGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 144801  
QY 420 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 479  
DB 144800 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 144741  
QY 480 ACCGGGATTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 539  
DB 144740 ACCGGGATTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 144681  
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RESULT 3  
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LOCUS  
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VERSION AC122714.2 GI:28827858  
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ORGANISM Homo sapiens  
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AUTHORS 1 (bases 1 to 190024)  
TITLE DOE Joint Genome Institute and Stanford Human Genome Center.  
JOURNAL Direct Submission  
REFERENCE 2 (bases 1 to 190024)  
AUTHORS DOE Joint Genome Institute.  
TITLE Direct Submission  
JOURNAL Direct Submission  
REFERENCE 3 (bases 1 to 190024)  
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.  
TITLE Submitted (04-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
JOURNAL On Mar 4, 2003 this sequence version replaced gi:21206277.  
COMMENT Draft Sequence Produced by DOE Joint Genome Institute  
www.jgi.doe.gov  
Finishing Completed at Stanford Human Genome Center  
www.shgc.stanford.edu  
Quality: Phrap Quality >=40 99.8% of Sequence;  
Estimated Total Number of Errors is 0.9.  
NOTE: Shatter libraries failed to verify the dinucleotide repeat region 124370-125308. Unsure number of repeat copies 124370-125308. Forced join 124996.  
124370-125308. Forced join 124996.

## FEATURES

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BASE COUNT 45607 a 46028 c 46121 g 52268 t  
ORIGIN

Query Match 88.5%; Score 498; DB 9; Length 190024;  
Best Local Similarity 95.7%; Pred. No. 5,3e-74;  
Matches 540; Conservative 0; Mismatches 5; Indels 19; Gaps 2;

QY 1 CGGCGGAGGAGGCGGCGGAGTGGTCTGATCGTCCCTGAGCGCTTCACTCCAGG 60  
DB 81471 CGGCGGAGGAGGCGGCGGAGTGGTCTGATCGTCCCTGAGCGCTTCACTCCAGG 81412  
QY 61 CGGAGAGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120  
DB 81411 CGGAGAGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 81352  
QY 121 CAGGAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180  
DB 81351 CAGGAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 81292  
QY 181 CCTCACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240  
DB 81291 C-----CCTCACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 81250  
QY 241 AGACCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300  
DB 81249 AGACCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 81190  
QY 301 CT-CTCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 359  
DB 81189 CTGCTCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 81130

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QY 360 GGGGACCGGCTTCCAGAGGCGCCCGCCGACAGAGAGTGGCCAGGACGCGCT 419
Db 81129 GGGGACCGGCTTCCAGAGGCGCCCGCCGACAGAGAGTGGCCAGGACGCGCT 81070
QY 420 GAGCGAGCGGCGAGCGGCTTTCTCAGAGCGCGCGCCGCGCTGGAGGGCGAGG 479
Db 81069 GAGCGAGCGGCGAGCGGCTTTCTCAGAGCGCGCGCCGCGCTGGAGGGCGAGG 81010
QY 480 ACCGGGTATAGAGAGCGCTTCTGAGCGCTTCCGCGGCGAGCGCGAGTTCGCGCGCGCGCG 539
Db 81009 ACCGGGTATAGAGAGCGCTTCTGAGCGCTTCCGCGGCGAGCGCGAGTTCGCGCGCGCGCG 80950
QY 540 AGCCCCCGCGCATGAGCTCGCC 563
Db 80949 AGCCCCCGCGCATGAGCTCGCC 80926

RESULT 4
LOCUS AC108813 166777 bp DNA linear HTG 07-MAR-2002
DEFINITION Homo sapiens chromosome 5 clone RP11-586L9, WORKING DRAFT SEQUENCE,
3 ordered pieces.
AC108813
AC108813.3 GI:19224876
VERSION HTG PHASE2; HTGS_DRAFT; HTGS_ACTIVEFIN.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Eubacteria; Primates; Catarrhini; Homnidae; Homo.
Mammalia; 1 to 166777
1 (bases 1 to 166777)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 5
2 (bases 1 to 166777)
Unpublished.
DOE Joint Genome Institute.
Direct Submission
Submitted (12-JAN-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 166777)
DOE Joint Genome Institute.
Direct Submission
Submitted (07-MAR-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Mar 7, 2002 this sequence version replaced gi:18369924.
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
-----
Web site: http://www.jgi.doe.gov
Center Code: JGI
Project Information
Center Project Name: 1519801
Center clone name: RP11-586L9
-----
Summary Statistics
Consensus quality: 163497 bases at least Q40
Consensus quality: 166071 bases at least Q30
Consensus quality: 166432 bases at least Q20
Estimated insert size: 186250; agarose-ef estimation
Estimated insert size: 166577; sum-of-contigs estimation
Quality coverage: 9.4 in Q20 bases; sum-of-contigs estimation.
Quality coverage: 10.51 in Q20 bases; sum-of-contigs estimation.
NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* been provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 62237: contig of 62237 bp in length
* 62238 62337: gap of unknown length
* 62338 75837: contig of 13500 bp in length
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* 75938 166777: contig of 90840 bp in length.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="5"
/clone="RP11-586L9"
/clone_11b="RP11 human BAC library 11"
BASE COUNT 44627 a 39804 c 41258 g 40888 t 200 others
ORIGIN
Query Match 86.5%; Score 487; DB 2; Length 166777;
Best Local Similarity 95.6%; Pred. No. 3.7e-72;
Matches 540; Conservative 0; Mismatches 5; Indels 20; Gaps 3;
QY 1 CGGCGGGGAGAGCGCGCGGAGTGAAGCTGATCTCTCTGCGCGCTTCCACCTCCACAG 60
Db 119104 CGGCGGGGAGAGCGCGCGGAGTGAAGCTGATCTCTCTGCGCGCTTCCACCTCCACAG 119163
QY 61 CGCAGAGCGCGCCGACAGAGACCCCGAGTGCAGGTCGACAGGTCGAGGATCAGAG 120
Db 119164 CGCAGAGAGCGCCGACAGAGACCCCGAGTGCAGGTCGACAGGTCGAGGATCAGAG 119223
QY 121 CAGGACCAAGAGAGCGAGAACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
Db 119224 CAGGACCAAGAGAGCGAGAACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 119283
QY 181 CCCTACACAGAGAGAGCTCCCTTCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
Db 119284 C-----CCTACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 119325
QY 241 AGACCGCAAGAGAGAGTGTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
Db 119326 AGACCGCAAGAGAGAGTGTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 119385
QY 301 CT-CTCTCAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 359
Db 119386 CTGCTCTCAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 119445
QY 360 GGGGACAGGCGCTTCCAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 419
Db 119446 GGGGACAGGCGCTTCCAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 119505
QY 420 GAGCGAGCGGCGAGGCGCTTCTCAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 478
Db 119506 GAGCGAGCGGCGAGGCGCTTCTCAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 119565
QY 479 GAGCGGTATAGAGAGCGCTGAGCGCTTCCGCGGCGAGCGCGCGCGCGCGCGCGCGCG 538
Db 119566 GAGCGGTATAGAGAGCGCTGAGCGCTTCCGCGGCGAGCGCGCGCGCGCGCGCGCGCG 119625
QY 539 GAGCGCGCGCGCGCATGAGCTCGCC 563
Db 119626 GAGCGCGCGCGCGCATGAGCTCGCC 119650

RESULT 5
LOCUS AC108083/c 130129 bp DNA linear HTG 25-JAN-2002
DEFINITION Homo sapiens chromosome 5 clone CTD-2031L15, WORKING DRAFT
SEQUENCE. 4 unordered pieces.
AC108083
AC108083.1 GI:18369929
VERSION HTG PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
KEYWORDS Homo sapiens
SOURCE Homo sapiens
ORGANISM Homo sapiens; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Eubacteria; Primates; Catarrhini; Homnidae; Homo.
Mammalia; 1 to 130129
1 (bases 1 to 130129)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 5
```

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JOURNAL REFERENCE AUTHORS TITLE JOURNAL	Unpublished 2 (bases 1 to 130129) DOE Joint Genome Institute. Direct Submission Submitted (25-JAN-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA -----Genome Center
COMMENT	

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Project Information
Center Project Name: 632820
Center clone name: CITB-H1_2013L15
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Summary Statistics

Consensus quality:	124488 bases at least Q40
Consensus quality:	128031 bases at least Q40
Consensus quality:	128842 bases at least Q20
Estimated insert size:	135000; agarose-fp estimation
Estimated insert size:	128829; sum-of-contigs estimation
Quality coverage:	7.66 in Q20 bases; sum-of-contigs estimation
Quality coverage:	7.97 in Q40 bases; sum-of-contigs estimation

NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

FEATURES	source
4321	1
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4420:	gap of unknown length
4422	1
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4422:	gap of unknown length
4424	1
4423:	contig of 24790 bp in length
4425	1
4424:	gap of unknown length
4426	1
4425:	contig of 81427 bp in length..
4427	1
4426:	contig of 81427 bp in length..
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4427:	contig of 81427 bp in length..
4429	1
4428:	contig of 81427 bp in length..
4430	1
4429:	contig of 81427 bp in length..
4431	1
4430:	contig of 81427 bp in length..
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4433:	contig of 81427 bp in length..
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ORIGIN

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Best Local Similarity	95.2%	Pred. No. 2.9e-71		
Matches 536	Conservative			

[illegible]

Qy	301	CT CTCTCAGAGGCGCCAGCGCTGCGCAAGAGAAAGTCTCTGAGAGCCCGGCGCAGGAG	359
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Qy	360	GGGCGACCGGCTCTCCAGAGGCGCGCGGCGCAGCAGAGAGATTGGCCAGGCGCAGTGGCTGT	419
Db	24427	GGGCGACCGGCTCTCCAGAGGCGCGCGGCGCAGCAGAGAGATTGGCCAGGCGCAGTGGCTGT	24168
Qy	420	GAGCGGAGCGGGCGAGGCTTCTCAGAGCGCGGGCGAGCGCGGCGTGTGAGAGGCGAGAG	479
Db	24167	GAGCGGAGCGGGCGAGGCTTCTCAGAGCGCGGGCGAGAGCGCGGCGTGTGAGAGGCGAGAG	24108
Qy	480	ACCGCGATTAAAGAGCTGTGTGCTTGTCCCGGCGAGCGGAGAGTGTCCCGCGCGCCCG	539
Db	24107	ACCGCGATTAAAGAGCTGTGTGCTTGTCCCGGCGAGCGGAGAGTGTCCCGCGCGCCCG	24048
Qy	540	AGCCCCCGGCGCATGAACTGCG	562
Db	24047	AG-CCCCGGGCGCATGAACTGCG	24026

RESULT 6	BD082141	BD082141	563 bp	DNA linear	PAT 27-AUG-2002
LOCUS					
DEFINITION					
REAGENT					
ACCESSION					
BD082141					
BD082141.1					
GI:22627751					
JP 2001522225-A/5.					
23a may					
23a may					
ORGANISM					

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD  
 1 (bases 1 to 562)  
 Model, P.A.B., Cohen, M., Colplitt, T.L., Friedman, P.N., Gordon, J.,  
 Grandos, E.N., Hodges, S.C., Krause, M.R., Kratochvill, J.D., Rapp, L.R.,  
 Russell, J.C. and Stroup, S.D.  
 Reagents and methods useful for detecting diseases of the lung  
 Patent: JP 200152225-A 5 13-NOV-2001;  
 ABSTRACT: 200152225-A 5 13-NOV-2001;  
 PM 11P 200152225-A 5 13-NOV-2001;  
 COMMENT

PD 13-NOV-1998 132622Z-4/5  
 PR 30-JAN-1998 JP 1998533078  
 PR 31-JAN-1997 US 08/793710  
 PI PATRICIA A BILLING MEDEL, MAURICE COHEN, TRACEY L COLPITTS, PAULA  
 PI  
 PI N FRIEDMAN,  
 PI JULIAN GORDON, EDWARD N GRANADOS, STEVEN C HODGES, MICHAEL R  
 PI KASS,  
 PI JON D KRATOCHVIL, LISA ROBERTS RAPP, JOHN C RUSSELL, STEPHEN D  
 PI STROUPE  
 PC C12N15/63, C12N15/10, C12Q1/68, C07K14/47//C07K16/30, G01N33/574 CC  
 Strandedness: Single;  
 CC Topology: Linear;  
 FH Key Location/Qualifiers.  
 Location/Qualifiers.

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1.562
/organism="Zea mays"
/mol_type="genomic DNA"
/db_xref="taxon:4579"
82 a -200 c 192 g 86 t
2 others
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Query Match	23.4%	Score 132;	DB 6;	length 562;
Best Local Similarity	99.2%			
Matches 132; Conservative		Pred. NO. 1.6e-12;		

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QY	431	0	1	0
Db	1	0	0	0
OY	491	0	0	0

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Db      61 GAAGCTTGCTGGCTTGGCCCGGCGAGCGGAGTTCCCGCGCGCCCGGAGCCCGCGCGC 120
QY      551 CATGAAGCTCGCC 563
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        |||
        |||
Db      121 CATGAAGCTCGCC 133

RESULT 7
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LOCUS      Reagents and methods useful for detecting diseases of the lung.
DEFINITION      BD082137.1 GI:22627747
ACCESSION      BD082137.1
VERSION      JP 2001522225-A/1.
KEYWORDS      Zea mays
SOURCE      Zea mays
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
              clade; Panicoideae; Andropogoneae; Zea.
REFERENCE      Medel,P.A.B., Cohen,M., Colpitts,T.L., Friedman,P.N., Gordon,J.,
AUTHORS      1 (bases 1 to 190)
              Granados,E.N., Hodges,S.C., Klass,M.R., Kratochvil,J.D., Rapp,L.R.,
              Russell,J.C. and Stroupe,S.D.
              Reagents and methods useful for detecting diseases of the lung
              Patent: JP 2001522225-A 1 13-NOV-2001;
              ABBOTT LABORATORIES
              PN JP 2001522225-A/1
COMMENT      PD 13-NOV-2001
              PF 30-JAN-1998 JP 1998533078
              PR 31-JAN-1997 US 08/791710
              PI PATRICIA A BILHNG MEDEL,MAURICE COHEN,TRACEY L COLPITTS,PAULA
              PI N FRIEDMAN,
              PI JULIAN GORDON,EDWARD N GRANADOS,STEVEN C HODGES,MICHAEL R PI
              PI KLASS,
              PI JON D KRATOCHVIL,LISA ROBERTS RAPP,JOHN C RUSSELL,STEPHEN D
              PI STROUPE
              PC C12N15/63,C12N5/10,C12Q1/68,C07K14/47//C07K16/30,G01N33/574 CC
              CC Strandedness: Single;
              CC Topology: Linear;
              CC Location/Qualifiers.
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Best Local Similarity 97.0%; Pred. No. 6,9e-12;
Matches 129; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      431 GCAGGGCTTTCTCAGAGCGCGGCGAGCGCGGCTGAGAGGCGAGAGCGGGGTATTA 490
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Db      1 GAGAGGCTTTCTCAGAGCGCGGCGAGCGCGGCTGAGAGGCGAGAGCGGGGTATTA 60
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        |||
        |||
QY      491 GAAGCTCGTGCGCTTGGCCCGGCGAGCGCGGCTGCCCGCGCGCCCGGAGCCCGCGCGC 550
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        |||
        |||
Db      61 GAGGCTCGTGCGCTTGGCCCGGCGAGCGCGGCTGCCCGCGCGCCCGGAGCCCGCGCGC 120
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        |||
QY      551 CATGAAGCTCGCC 563
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        |||
        |||
Db      121 CATGAAGCTCGCC 133

RESULT 8
BD082142      519 bp      DNA      linear      PAT 27-AUG-2002
LOCUS      Reagents and methods useful for detecting diseases of the lung.
DEFINITION      BD082142.1 GI:22627752
ACCESSION      BD082142.1
VERSION      JP 2001522225-A/6.
KEYWORDS

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SOURCE      Zea mays
ORGANISM      Zea mays
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
              clade; Panicoideae; Andropogoneae; Zea.
REFERENCE      Medel,P.A.B., Cohen,M., Colpitts,T.L., Friedman,P.N., Gordon,J.,
AUTHORS      1 (bases 1 to 519)
              Granados,E.N., Hodges,S.C., Klass,M.R., Kratochvil,J.D., Rapp,L.R.,
              Russell,J.C. and Stroupe,S.D.
              Reagents and methods useful for detecting diseases of the lung
              Patent: JP 2001522225-A 6 13-NOV-2001;
              ABBOTT LABORATORIES
              PN JP 2001522225-A/6
COMMENT      PD 13-NOV-2001
              PF 30-JAN-1998 JP 1998533078
              PR 31-JAN-1997 US 08/791710
              PI PATRICIA A BILHNG MEDEL,MAURICE COHEN,TRACEY L COLPITTS,PAULA
              PI N FRIEDMAN,
              PI JULIAN GORDON,EDWARD N GRANADOS,STEVEN C HODGES,MICHAEL R PI
              PI KLASS,
              PI JON D KRATOCHVIL,LISA ROBERTS RAPP,JOHN C RUSSELL,STEPHEN D
              PI STROUPE
              PC C12N15/63,C12N5/10,C12Q1/68,C07K14/47//C07K16/30,G01N33/574 CC
              CC Strandedness: Single;
              CC Topology: Linear;
              CC Location/Qualifiers.
              FH Key
              source      1..519
                        /organism="Zea mays"
                        /mol_type="genomic DNA"
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ORIGIN
Query Match      16.0%; Score 90; DB 6; Length 519;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      474 GCGAGACCGGGTATGAGAGCGCTCGGCTTGGCCCGGCGAGCGCGAGTTCCCGCGCGC 533
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Db      1 GCGAGACCGGGTATGAGAGCGCTCGGCTTGGCCCGGCGAGCGCGAGTTCCCGCGCGC 60
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QY      534 GCCCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 563
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        |||
        |||
Db      61 GCCCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 90
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        |||

RESULT 9
AX201348      569 bp      DNA      linear      PAT 30-AUG-2001
LOCUS      Sequence 27 from Patent WO0153486.
DEFINITION      AX201348
ACCESSION      AX201348
VERSION      AX201348.1 GI:15391167
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      Aghkenazi,A.J., Goddard,A., Godowski,P.J., Gurney,A.L.,
AUTHORS      Hillan,K.J., Marsters,S.A., Pan,J., Pitti,R.W., Roy,M.A., Smith,V.,
              Stone,D.M., Watanabe,C.K. and Wood,W.I.
              Compositions and methods for the treatment of tumour
              Patent: WO 0153486-A 27 26-JUL-2001;
              Genentech, Inc. (US)
TITLE      JOURNAL
              location/Qualifiers
              source      1..569
                        /organism="Homo sapiens"
                        /mol_type="genomic DNA"
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BASE COUNT      128 a 190 c 170 g 81 t
ORIGIN

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	DEFINITION	Homo sapiens junctophilin 3 (JPH3) gene, partial cds.				
	ACCESSION	AF429315				
	VERSION	AF429315.1	GI:17646244			
	KEYWORDS					
	SOURCE					
	ORGANISM	Homo sapiens (human)				
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
	REFERENCE	1 (bases 1 to 125020)				
	AUTHORS	Holmes,S.E., O'Hearn,E., Rosenblatt,A., Callahan,C., Hwang,H.S., Ingersoll-Ashworth,R.G., Fleisher,A., Stevanin,G., Brice,A., Potter,N.T., Ross,C.A. and Margolis,R.L. A repeat expansion in the gene encoding junctophilin-3 is associated with Huntington disease-like 2 Nat. Genet. 29 (4), 377-378 (2001)				
	TITLE					
	JOURNAL					
	MEDLINE	2 (bases 1 to 125020) 11694876				
	PUBMED					
	REFERENCE	Holmes,S.E., Ingersoll-Ashworth,R.G., Ross,C.A. and Margolis,R.L. Direct Submission (05-OCT-2001) Psychiatry, Johns Hopkins Medical Institutions, 600 N. Wolfe St., Baltimore, MD 21287, USA				
	AUTHORS					
	TITLE					
	JOURNAL					
	FEATURES					
	source	1..125020 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /chromosome="16" /map="16q24.3; between D16S520 and WI-12410" /note="Isolated from a patient with Huntington's Disease-Like 2 (HDL2)" complement(35581..35746) /rpt_type=tandem /rpt_unit=ctg complement(<36507..>36887) /gene="JPH3" /note="synonym: JP3"				
	gene	complement(<36507..>36887) /gene="JPH3" /product="junctophilin 3" complement(<36507..36887) /gene="JPH3" /complement(<36507..36887) /gene="JPH3" /note="component of the junctional complex between plasma membrane and endoplasmic reticulum"				
	mRNA	/codon_start=1 /product="junctophilin 3" /protein_id="AA140941.1" /db_xref="GI:17646245" translation="MSSGGRRFDDGSGYCGGWENKRGKHGVCTGPKGGEYSMS HGFVLGYVTPWSGNLTGOTMGQRHGHLGLSKOKNIVYKEEMWTHGRGRGVRECAQ NGAKYEGTWNSGLDYGTEITSDG"				
	CDS	-				
	BASE COUNT	29056 a 32731 c 30696 g 28283 t	4254 others			
	ORIGIN					
	Query Match	13.1%; Score 74; DB 9; Length 125020; Best Local Similarity 13.2%; Pred. No. 0.0014; Matches 64; Conservative 224; Mismatches 197; Indels 1; Gaps 1;				
OY		45 CCTCACACTCCAGAGCGGAGAGGCCACCAGAGAGACCCCGAGTGCCTCCGACGTTGCCAC	104			
DB	17694	STSYISYSCCMKMWSMWGSCTCKMKYISGMVSATSMGYYSSTPSCKRYKRSWMTKRTIS	17635			
OY		105 GGTCGTGGATCAGAGCGAGGACGAGGACCGAGGAAGTCCGCCGCCGCCCTTGCCC	164			
DB	17634	KSYRKRSYYWWGGKRAKKKYCACAGRPRMSYWKCCAKWMMSYCCWASYCMTYYSKST	17575			
OY		165 TGGCGCGAGAAGCTCCTCAACNAGAGGAAGCTCCCTCCAGCCGCGCCAGCCTGCAG	224			
DB	17574	YKSTCYTKRGGYWGSKTCTYSAGGKSRSMYTCMMRSSKSSWSMSMARBSWCMGWAGVR	17515			
OY		225 GGGGCGCGTGGGTCAAGCCGCAAACGAAAGTGGCGGGGCTGGGCTCGCGAGAG	284			

	Db	17514	RKRSRGMGAGRRSSSKGKRSTGMKRACSKTKTGYSGTGRSMWKKKGYSKTSRGNKGKKT	17455
	Oy	285	CMAAGCCCGGGCTCCTCTCTCAAGAGAGGCCCCAGGCCTGTCCCAAGAAGATCCTTCGAG	344
	Db	17454	CYCMKYYKYXRTSMQWYYYMKMSWGFKRYKRCMKMKKCCTGYRMSSSKSGYSMRMRNG	17395
	Oy	345	GCCCCGACGGAAGAAGGGGACACGGCTTCCAGAGGCCCGCCGCGCGAGCAGAAGT-TG	403
	Db	17394	SSTSTSCWSMCWCYSMMKMCKMTWSYKKKRBSRMGSMSKSGRYAARGCVSSSWSTRKR	17335
	Oy	404	GCCAGGACGACGGCCCTGTAGCGGAGCGGAGGCGCTTTCTCAGAGACCGGCGGCGAGCGCGG	463
	Db	17334	RSKCYSTKSTKCRGKMGWKMGKMGKSXYWSSMCKMKXSMSKYSTKSYSGRRKSXGW	17275
	Oy	464	CGCTGAGAGGGCGGAGACCGGGTATTAAAGCCTGTGTGCTTGCCCGGAGCGCGCAGG	523
	Db	17274	GRSTRSKYAKSMSMRMAASCKLTGYSVSNRNRRNRNKKTCYCMYRRSAMNNQNAAAAGC	17215
	Oy	524	TTTTCCC 529	
	Db	17214	TTCCCC 17209	
	RESULT 14			
	AP005772	172650 bp	DNA	HYG 26-SEP-2002
	LOCUS	Oryza sativa (japonica cultivar-group)	chromosome 2 clone	
	DEFINITION	OSUNBA0073A21, *** SEQUENCING IN PROGRESS ***.		
	ACCESSION	AP005772		
	VERSION	AP005772.1 GI:23491624		
	KEYWORDS	HTG; HTGS; PHASE2.		
	SOURCE	Oryza sativa (japonica cultivar-group)		
	ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.		
	REFERENCE	1 Sasaki, T.; Matsumoto, T. and Katayose, Y. Oryza sativa nipponbare (GM3) genomic DNA, chromosome 2, BAC clone: OSUNBA0073A21 Published Only in Database (2002) 2 (bases 1 to 172650)		
	JOURNAL TITLE	Sasaki, T., Matsumoto, T. and Katayose, Y. Direct Submission Submitted (25-SEP-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail: tssasaki@nias.affrc.go.jp, URL: http://rjp.dna.affrc.go.jp/, Tel: 81-298-38-7441, Fax: 81-298-38-7468)		
	COMMENT	* NOTE: This currently consists of 1 contigs. NOTE: It is represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved. * NOTE: This is a 'working draft' sequence. * This sequence will be replaced * by the finished sequence as soon as it is available and * the accession number will be preserved. Location/Qualifiers 1..172650 /organism="Oryza sativa (japonica cultivar-group)" /mol_type="genomic DNA" /cultivar="Nipponbare" /db_xref="taxon:39947" /chromosome="2" /clone="OSUNBA0073A21"		
	BASE COUNT	52696 a 34714 c 35062 g 49796 t 382 others		
	ORIGIN			
	Query Match	12.6%	Score 71;	DB 2;
	Best Local Similarity	42.4%;	Pred. No. 0.0039;	Length 172650;







XX PT Diagnosing and/or determining a predisposition to a cellular  
 PT proliferative disorder of breast tissue, in particular breast cancer,  
 PT by determining the state of methylation of one or more nucleic acids  
 PT isolated from the subject -  
 XX  
 XX Disclosure: Fig 9A, 115pp; English.  
 XX  
 CC The present invention relates to a method of diagnosing a cellular  
 CC proliferative disorder of breast tissue, which involves determining the  
 CC state of methylation of one or more nucleic acids isolated from the  
 CC subject, where the state of methylation of the nucleic acids as compared  
 CC with a state of methylation from a subject not having the cellular  
 CC proliferative disorder of breast tissue is indicative of a cellular  
 CC proliferative disorder of breast tissue in the subject. The nucleic acids  
 CC may be TWIST, HMOX5, NES-1, retinoic acid receptor beta (RARbeta),  
 CC oestrogen receptor, cyclin D2, Wilm's tumour gene (WT-1), 14.3.3 sigma,  
 CC HIN-1 or RASSF1A. The method is useful for diagnosing and/or determining  
 CC a predisposition to a cellular proliferative disorder, in particular  
 CC breast cancer including ductal carcinoma in situ, lobular carcinoma,  
 CC colloid carcinoma, tubular carcinoma, medullary carcinoma, metaplastic  
 CC carcinoma, intraductal carcinoma in situ, lobular carcinoma in situ and  
 CC papillary carcinoma in situ. The present sequence is a gene fragment used  
 CC in the exemplification of the invention.  
 XX  
 SQ Sequence 1794 BP; 240 A; 646 C; 522 G; 318 T; 68 other;  
 XX  
 Query Match 55.1%; Score 310.4; DB 24; Length 1794;  
 Best Local Similarity 92.9%; Pred. No. 1.9e-51;  
 Matches 314; Conservative 0; Mismatches 24; Indels 0; Gaps 0;  
 QY 226 GGGGCGCGTGGGATCGAGCCGCAAGCGAGAGTGCGGGCCGGTCCGCGAGAC 285  
 Db 846 GGGGCGCGTGGGATCGAGCCGCAAGCGAGAGTGCGGGCCGGTCCGCGAGAC 905  
 QY 286 AAGGCGCGCGTGGGATCGAGCCGCAAGCGAGAGTGCGGGCCGGTCCGCGAGAC 345  
 Db 906 AAGGCGCGCGTGGGATCGAGCCGCAAGCGAGAGTGCGGGCCGGTCCGCGAGAC 965  
 QY 346 CCGGCGCGCGTGGGATCGAGCCGCAAGCGAGAGTGCGGGCCGGTCCGCGAGAC 405  
 Db 966 CCGGCGCGCGTGGGATCGAGCCGCAAGCGAGAGTGCGGGCCGGTCCGCGAGAC 1025  
 QY 406 CAGGCGCGCGTGGGATCGAGCCGCAAGCGAGAGTGCGGGCCGGTCCGCGAGAC 465  
 Db 1026 CAGGCGCGCGTGGGATCGAGCCGCAAGCGAGAGTGCGGGCCGGTCCGCGAGAC 1085  
 QY 466 CTGGAGGCGCGTGGGATCGAGCCGCAAGCGAGAGTGCGGGCCGGTCCGCGAGAC 525  
 Db 1086 CTGGAGGCGCGTGGGATCGAGCCGCAAGCGAGAGTGCGGGCCGGTCCGCGAGAC 1145  
 QY 526 CCGGCGCGCGTGGGATCGAGCCGCAAGCGAGAGTGCGGGCCGGTCCGCGAGAC 583  
 Db 1146 CCGGCGCGCGTGGGATCGAGCCGCAAGCGAGAGTGCGGGCCGGTCCGCGAGAC 1183  
 XX  
 RESULT 2  
 ID AAV54620 standard; cDNA; 562 BP.  
 XX AAV54620;  
 AC  
 XX 25-MAR-2003 (updated)  
 DT 30-OCT-1998 (first entry)  
 XX  
 XX LUI05 specific consensus polynucleotide sequence.  
 DE  
 XX LUI05; lung disease marker; immunoassay; lung disease; cancer;  
 KW blood; plasma; serum; ss.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 FH Key Location/Qualifiers

FT CDS 122..436  
 FT /tag= a  
 FT /transl\_except= (pos:176..178, aa:Val)  
 FT /product= "LUI05 polypeptide"  
 XX  
 XX W09833926-A1.  
 XX  
 XX 06-AUG-1998.  
 XX  
 XX 30-JAN-1998; 98WO-US01766.  
 XX  
 XX 31-JAN-1997; 97US-0791710.  
 XX  
 XX (ABBO ) ABBOTT LAB.  
 XX  
 XX Billing-medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;  
 PI Granados EN, Hodges SC, Klass MR, Kratochvil JD, Robertsrapp L;  
 PI Russell JC, Stroppe SD;  
 XX WPI: 1998-437479/37.  
 DR P-PSDB; AAW5868.  
 XX  
 PT New nucleic acid for the lung disease marker LUI05 - polypeptides,  
 PT antibodies and genes, used for diagnosis, prevention, treatment of  
 PT lung disease, specifically cancer  
 XX  
 XX Claim 11; Fig 1; 123pp; English.  
 XX  
 XX Sequences shown in AAV54616 to AAV54621 represent LUI05 specific  
 CC polynucleotide sequences. These are used in the method of the invention  
 CC for detecting target LUI05 nucleic acid. The method comprises treating a  
 CC sample with at least one LUI05 specific nucleic acid, or its complement  
 CC which is at least 50 percent identical with the LUI05 specific nucleic  
 CC acid sequences (AAV54616 to AAV54621). LUI05 is a lung disease marker.  
 CC Cells transformed with a recombinant expression system that contains  
 CC LUI05 specific nucleic acid fragments, are used to express recombinant  
 CC LUI05 polypeptides which are used to raise antibodies. The antibodies are  
 CC used to detect the LUI05 antigen, and correspondingly this antigen is  
 CC used to detect specific antibodies, in usual immunoassays. The LUI05  
 CC polypeptides and nucleic acid sequences are used for diagnosis, staging,  
 CC monitoring, prognosis, prevention, treatment and determination of  
 CC susceptibility to, lung disease, specifically cancer. The LUI05  
 CC polypeptides are also used to screen for specific binding agents, useful  
 CC therapeutically. LUI05 is a marker for lung disease (present at high  
 CC concentration, in altered form or in an unusual body compartment). LUI05  
 CC can be detected in blood, plasma or serum in an inexpensive, non-invasive  
 CC test.  
 CC  
 CC (updated on 25-MAR-2003 to correct PI field.)  
 CC  
 XX  
 XX Sequence 562 BP; 82 A; 200 C; 192 G; 86 T; 2 other;  
 SQ  
 XX  
 Query Match 23.4%; Score 132; DB 19; Length 562;  
 Best Local Similarity 99.2%; Pred. No. 6e-17;  
 Matches 132; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 431 GCAGGCGCTTCTCAGAGCGCGGCGCGGCTGAGGCGCGAGACCGGTATATA 490  
 Db 1 GCAGGCGCTTCTCAGAGCGCGGCGCGGCTGAGGCGCGAGACCGGTATATA 60  
 QY 491 GAGGCGCTTCTCAGAGCGCGGCGCGGCTGAGGCGCGAGACCGGTATATA 550  
 Db 61 GAGGCGCTTCTCAGAGCGCGGCGCGGCTGAGGCGCGAGACCGGTATATA 120  
 QY 551 CATGAAGCTCGCC 563  
 Db 121 CATGAAGCTCGCC 133  
 XX  
 RESULT 3  
 ID AAV54616 standard; cDNA; 190 BP.  
 XX AAV54616;  
 AC

XX 25-MAR-2003 (updated)  
 DT 30-OCT-1998 (first entry)  
 XX  
 DE LUI05 specific polynucleotide sequence from clone 3353867.  
 XX  
 KW LUI05; lung disease marker; immunoassay; lung disease; cancer;  
 KM blood; plasma; serum; ss.  
 OS  
 SS Homo sapiens.  
 XX MO9833926-A1.  
 XX 06-AUG-1998.  
 XX 30-JAN-1998; 98WO-US01766.  
 XX 31-JAN-1997; .97US-0791710.  
 XX  
 XX (ABBO ) ABBOTT LAB.  
 XX Billing-medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;  
 PI Granados EN, Hodges SC, Klaas MR, Kratochvil JD, Robertstrapp L;  
 PI Russell JC, Stroupe SD;  
 XX WPI; 1998-437479/37.  
 DR New nucleic acid for the lung disease marker LUI05 - polypeptides,  
 XX antibodies and genes, used for diagnosis, prevention, treatment of  
 PT lung disease, specifically cancer  
 XX  
 XX Claim 11; Fig 1; 123p; English.  
 XX  
 XX Sequences shown in AAV54616 to AAV54621 represent LUI05 specific  
 CC polynucleotide sequences. These are used in the method of the invention  
 CC for detecting target LUI05 nucleic acid. The method comprises treating a  
 CC sample with at least one LUI05 specific nucleic acid, or its complement  
 CC which is at least 50 percent identical with the LUI05 specific nucleic  
 CC acid sequences (AAV54616 to AAV54621). LUI05 is a lung disease marker.  
 CC Cells transformed with a recombinant expression system that contains  
 CC LUI05 specific nucleic acid fragments, are used to express recombinant  
 CC LUI05 polypeptides which are used to raise antibodies. The antibodies are  
 CC used to detect the LUI05 antigen, and correspondingly this antigen is  
 CC used to detect specific antibodies, in usual immunoassays. The LUI05  
 CC polypeptides and nucleic acid sequences are used for diagnosis, staging,  
 CC monitoring prognosis, prevention, treatment and determination of  
 CC susceptibility to, lung disease, specifically cancer. The LUI05  
 CC polypeptides are also used to screen for specific binding agents, useful  
 CC therapeutically. LUI05 is a marker for lung disease (present at high  
 CC concentration in altered form or in an unusual body compartment). LUI05  
 CC can be detected in blood, plasma or serum in an inexpensive, non-invasive  
 CC test.  
 CC (Updated on 25-MAR-2003 to correct PI field.)  
 CC  
 CC Sequence 190 BP; 18 A; 69 C; 67 G; 32 T; 4 other;  
 XX  
 SQ  
 Query Match 22.9%; Score 129; DB 19; Length 190;  
 Best Local Similarity 97.0%; Pred. No. 2,4e-16;  
 Matches 129; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 431 GAGAGCTTTCTCAGAGCGCGCGAGCGCGCTGAGGGGCGAGACCGGGTAA 490  
 DB 1 GAGAGCTTTCTCAGAGCGCGCGAGCGCGCTGAGGGGCGAGACCGGGTAA 60  
 QY 491 GAGAGCTTTCTCAGAGCGCGCGAGCGCGCTGAGGGGCGAGACCGGGTAA 550  
 DB 61 GAGAGCTTTCTCAGAGCGCGCGAGCGCGCTGAGGGGCGAGACCGGGTAA 120  
 QY 551 GAGAGCTTTCTCAGAGCGCGCGAGCGCGCTGAGGGGCGAGACCGGGTAA 563  
 DB 121 GAGAGCTTTCTCAGAGCGCGCGAGCGCGCTGAGGGGCGAGACCGGGTAA 133

RESULT 4  
 ID AAZ98173 standard; CDNA; 543 BP.  
 XX AAZ98173;  
 AC AAZ98173;  
 XX  
 DT 11-MAY-2000 (first entry)  
 XX  
 DE Human signal peptide containing protein HSP-65 CDNA SEQ ID NO:199.  
 XX  
 KW Human; signal peptide-containing protein; HSP; diagnosis; cancer;  
 KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;  
 KW antimicrobial; neuroprotective; cardiovascular; hepatocytic;  
 KW antiaesthetic; gene therapy; cell proliferation; neurological disorder;  
 KW reproductive disorder; developmental disorder; arteriosclerosis;  
 KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anemia;  
 KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;  
 KW Parkinson's disease; Huntington's disease; ovulatory defect;  
 KW muscular dystrophy; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200000610-A2.  
 XX  
 XX 06-JAN-2000.  
 XX  
 XX 25-JUN-1999; 99WO-US14484.  
 XX  
 XX 26-JUN-1998; 98US-0090762.  
 XX 31-JUL-1998; 98US-0094983.  
 XX 01-OCT-1998; 98US-0102686.  
 XX 11-DEC-1998; 98US-0112129.  
 XX  
 XX (INCY-) INCYTE PHARM INC.  
 XX Lal P, Tang YT, Gorgone GA, Corley NC, Guejler KJ, Baughn MR;  
 PI Akersblom IE, Au-Yang J, Yue H, Patterson C, Reddy R, Hillman JL;  
 PI Bandman O;  
 XX WPI; 2000-160673/14.  
 DR P-PsDB; AAY87288.  
 XX  
 XX New human signal peptide-containing proteins useful in treatment,  
 PT prevention and diagnosis of e.g. cancer, inflammation and  
 PT cardiovascular disease  
 PT  
 XX  
 XX Claim 9; Page 289; 327p; English.  
 XX  
 XX AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the  
 CC human signal peptide-containing proteins HSP-1 to HSP-134. HSPs have  
 CC anticancer, anti-inflammatory, antitumor, hepatocytic, and can  
 CC neuroprotective, cardiovascular and antiaesthetic activities, and can  
 CC be used in gene therapy. HSPs can be used to treat or prevent disorders  
 CC associated with decreased activity or function of HSP. Antagonists of  
 CC HSP are used to treat or prevent disorders associated with increased  
 CC activity or function of HSP. Such disorders include cell proliferation  
 CC (including cancer), inflammation, cardiovascular, neurological,  
 CC reproductive or developmental disorders, e.g. arteriosclerosis,  
 CC cirrhosis, psoriasis, acquired immune deficiency syndrome, congestive or  
 CC asthma, Crohn's disease, microbial or other infections, Huntington's  
 CC disease, schizophrenia, Alzheimer's, Parkinson's or Huntington's  
 CC disease, heart disease, ovulatory defects, muscular dystrophy). HSP  
 CC nucleic acids can be used for the recombinant amplification assays (for  
 CC detecting HSP in standard hybridisation and amplification assays (for  
 CC diagnosis and monitoring), in gene therapy, for detecting related sequences  
 CC triplex-forming or ribozyme therapeutics, for detecting related sequences  
 CC or genetic variations, and for chromosomal mapping. Antagonists and  
 CC raised specific antibodies (Ab) and to screen for HSP, as therapeutic  
 CC antagonists (potential therapeutic agents). Ab are used to diagnose, or  
 CC monitor HSP-related diseases (in usual immunoassays), as therapeutic  
 CC antagonists, in competitive drug screens, and for purification of HSP  
 CC from natural sources.  
 XX

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SQ      Sequence 543 BP; 89 A; 194 C; 178 G; 82 T; 0 other;
      Query Match      18.5%; Score 104; DB 21; Length 543;
      Best Local Similarity 100.0%; Pred. No. 1.6e-11;
      Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      460 CCGGCGCTGAGAGGCGAGACCGGATATAGAAAGCCTGCTGCTTCCCGGCGACGCG 519
      1 CCGGCGCTGAGAGGCGAGACCGGATATAGAAAGCCTGCTGCTTCCCGGCGACGCG 60
      61 CAGGTTCCCGCGCGCGCGAGCCCGCGCCCATGAAAGCTCGCC 104

Db      RESULT 5
      AA229723
      ID AA229723 standard; DNA; 543 BP.
      AC AA229723;
      XX
      DT 27-MAR-2000 (first entry)
      DE Human lung specific gene lng107.
      KW Lung Specific Gene; LSG; lng107; human; diagnostic marker;
      KW prognosticate; lung cancer; diagnosis; ds.
      OS Homo sapiens.
      FH Key Location/Qualifiers
      FT CDS 93..1407
      FT /tag= a
      FT /product= "LSG lng107 protein"
      PN WO9960160-A1.
      PD 25-NOV-1999.
      PF 12-MAY-1999; 99WO-US10344.
      PR 21-MAY-1998; 98US-0086212.
      PA (DIAD-) DIADEXUS LLC.
      PI Yang F, Macina RA, Sun Y;
      DR WPI: 2000-116320/10.
      DR P-PSDB; AAW44458.
      XX
      PT A new method for diagnosing, monitoring and staging lung cancer -
      PT lung disease, specifically cancer
      PS Claim 6, Page 36; 40pp; English.
      CC The present sequence is a lung specific gene (LSG) lng107 from human
      CC clone ID 586271. The LSG has high level of tissue specificity for lungs
      CC and is overexpressed in cancerous tissues. The sequence serves as a
      CC diagnostic marker for detecting, monitoring, staging and prognosticating
      CC lung cancer. The diagnosis involves comparing levels of LSG in samples
      CC obtained from patient and normal control.
      CC
      SQ Sequence 543 BP; 89 A; 194 C; 178 G; 82 T; 0 other;
      Query Match      18.5%; Score 104; DB 21; Length 543;
      Best Local Similarity 100.0%; Pred. No. 1.6e-11;
      Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      460 CCGGCGCTGAGAGGCGAGACCGGATATAGAAAGCCTGCTGCTTCCCGGCGACGCG 519
      1 CCGGCGCTGAGAGGCGAGACCGGATATAGAAAGCCTGCTGCTTCCCGGCGACGCG 60
      61 CAGGTTCCCGCGCGCGCGAGCCCGCGCCCATGAAAGCTCGCC 563

Db      RESULT 6
      AAV54621
      ID AAV54621 standard; cDNA; 519 BP.
      AC AAV54621;
      XX
      DT 25-MAR-2003 (updated)
      DT 30-OCT-1998 (first entry)
      DE LUI05 polypeptide encoding cDNA clone 13278361H.
      KW LUI05; lung disease marker; immunoassay; lung disease; cancer;
      KW blood; plasma; serum; ss.
      OS Homo sapiens.
      FH Key Location/Qualifiers
      FT CDS 79..393
      FT /tag= a
      FT /transl_except= (pos:136..138, aa:Val)
      FT /product= "LUI05 polypeptide"
      PN WO9833926-A1.
      PD 06-AUG-1998.
      PF 30-JAN-1998; 98WO-US01766.
      PR 31-JAN-1997; 97US-0791710.
      PA (ABBO) ABBOTT LAB.
      PI Billing-medel PA, Cohen M, Colpiter TL, Friedman PN, Gordon J;
      PI Granados EN, Hodges SC, Klass MR, Kratochvil JD, Robertrapp L;
      PI Russell JC, Stroupe SD;
      DR WPI: 1998-437479/37.
      DR P-PSDB; AAW5868.
      XX
      PT New nucleic acid for the lung disease marker LUI05 - polypeptides,
      PT antibodies and genes, used for diagnosis, prevention, treatment of
      PT lung disease, specifically cancer
      PS Claim 11; Fig 1, 123pp; English.
      CC Sequences shown in AAV54616 to AAV54621 represent LUI05 specific
      CC polynucleotide sequences. These are used in the method of the invention
      CC for detecting target LUI05 nucleic acid. The method comprises treating a
      CC sample with at least one LUI05 specific nucleic acid, or its complement
      CC which is at least 50 percent identical with the LUI05 specific nucleic
      CC acid sequences (AAV54616 to AAV54621). LUI05 is a lung disease marker.
      CC Cells transfected with a recombinant expression system that contains
      CC LUI05 specific nucleic acid fragments, are used to express recombinant
      CC LUI05 polypeptides which are used to raise antibodies. The antibodies are
      CC used to detect the LUI05 antigen, and correspondingly this antigen is
      CC used to detect specific antibodies, in usual immunoassays. The LUI05
      CC polypeptides and nucleic acid sequences are used for diagnosis, staging,
      CC monitoring, prognosis, prevention, treatment and determination of
      CC susceptibility to, lung disease, specifically cancer. The LUI05
      CC polypeptides are also used to screen for specific binding agents, useful
      CC therapeutically. LUI05 is a marker for lung disease (present at high
      CC concentration, in altered form or in an unusual body compartment); LUI05
      CC can be detected in blood, plasma or serum in an inexpensive, non-invasive
      CC test.
      CC (Updated on 25-MAR-2003 to correct PI field.)
      SQ Sequence 519 BP; 78 A; 190 C; 170 G; 81 T; 0 other;
      Query Match      16.0%; Score 90; DB 19; Length 519;
      Best Local Similarity 100.0%; Pred. No. 8e-09;
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Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 474 GCGAGAGCCGGGTATAGAAAGCTTGGCTTGGCGGAGCGGAGGTTCCCGCGC 533  
 DB 1 GCGAGAGCCGGGTATAGAAAGCTTGGCTTGGCGGAGCGGAGGTTCCCGCGC 60

OY 534 GCGCCGAGCCCGCGCCCATGAAAGCTCGCC 563  
 DB 61 GCGCCGAGCCCGCGCCCATGAAAGCTCGCC 90

RESULT 7  
 ID ABK40267 standard; cDNA; 569 BP.  
 AC ABK40267;  
 XX  
 DT 15-JUL-2002 (first entry)  
 XX  
 DE cDNA encoding human PRO1245 polypeptide.  
 XX  
 KW Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;  
 KW leukemia; neuronal disorder; stromal disorder; blastocoele disorder;  
 KW inflammatory disorder; immune disorder; angiogenic disorder;  
 KW gene therapy; cyostatic; neuroprotective; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200153486-A1.  
 PD 26-JUL-2001.  
 XX  
 PF 11-FEB-2000; 2000WO-US03565.  
 XX  
 PR 08-MAR-1999; 99WO-US05028.  
 PR 11-MAR-1999; 99US-123972P.  
 PR 11-MAY-1999; 99US-133459P.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 22-JUN-1999; 98US-140650P.  
 PR 22-JUN-1999; 98US-140653P.  
 PR 26-JUL-1999; 98US-144756P.  
 PR 26-JUL-1999; 99US-145698P.  
 PR 17-AUG-1999; 99US-146222P.  
 PR 17-AUG-1999; 99US-149389P.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 15-SEP-1999; 99WO-US21030.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 01-DEC-1999; 99WO-US28634.  
 PR 05-JAN-2000; 2000WO-US00219.  
 XX  
 PA (GENENTECH INC.  
 PI Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Hillan KJ;  
 PI Marsters SA, Pan J, Pizzi RM, Roy WA, Smith V, Stone DM;  
 PI Matanabe CK, Wood WI;  
 XX  
 DR WPI; 2002-205567/26.  
 XX  
 PT Thirty five nucleic acids encoding PRO polypeptides, useful for  
 PT treating benign or malignant tumours, leukemias and lymphoid  
 PT malignancies, inflammatory, angiogenic and immunologic disorders -  
 XX  
 PS Claim 50; Fig 27; 302PP; English.  
 XX  
 CC The present invention relates to the isolation of novel human PRO  
 CC polypeptides and the polynucleotide sequences encoding them. The  
 CC PRO polypeptides, agonists, antagonists or anti-PRO antibodies are  
 CC useful for treating benign or malignant tumours (e.g. renal, kidney,  
 CC bladder, breast, etc), leukemias and lymphoid malignancies, other  
 CC disorders such as neuronal, glial, astrocytal, hypothalamic, glandular,

CC macrophagal, stromal and blastocoele disorders, inflammatory, immune  
 CC and angiogenic disorders. The polynucleotide sequences are also  
 CC useful in gene therapy. ABK40267-ABK40288 encode for the human PRO  
 CC polypeptides of the invention.  
 XX

Sequence 569 BP; 128 A; 190 C; 170 G; 81 T; 0 other;

Query Match 16.0%; Score 90; DB 24; Length 569;  
 Best Local Similarity 100.0%; Pred. No. 7.9e-09;  
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 474 GCGAGAGCCGGGTATAGAAAGCTTGGCTTGGCGGAGCGGAGGTTCCCGCGC 533  
 DB 1 GCGAGAGCCGGGTATAGAAAGCTTGGCTTGGCGGAGCGGAGGTTCCCGCGC 60

OY 534 GCGCCGAGCCCGCGCCCATGAAAGCTCGCC 563  
 DB 61 GCGCCGAGCCCGCGCCCATGAAAGCTCGCC 90

RESULT 8  
 ID AAZ65103 standard; cDNA; 570 BP.  
 AC AAZ65103;  
 XX  
 DT 05-APR-2000 (first entry)  
 XX  
 DE Membrane-bound protein PRO1245 encoding cDNA.  
 DE Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;  
 KW pharmaceutical; receptor immunoadhesin; gene mapping; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9963088-A2.  
 PD 09-DEC-1999.  
 XX  
 PF 02-JUN-1999; 99WO-US12252.  
 XX  
 PR 02-JUN-1998; 98US-0087607.  
 PR 02-JUN-1998; 98US-0087609.  
 PR 03-JUN-1998; 98US-0087827.  
 PR 04-JUN-1998; 98US-0088021.  
 PR 04-JUN-1998; 98US-0088025.  
 PR 04-JUN-1998; 98US-0088028.  
 PR 04-JUN-1998; 98US-0088030.  
 PR 04-JUN-1998; 98US-0088033.  
 PR 04-JUN-1998; 98US-0088167.  
 PR 05-JUN-1998; 98US-0088167.  
 PR 05-JUN-1998; 98US-0088202.  
 PR 05-JUN-1998; 98US-0088217.  
 PR 09-JUN-1998; 98US-0088655.  
 PR 10-JUN-1998; 98US-0088722.  
 PR 10-JUN-1998; 98US-0088730.  
 PR 10-JUN-1998; 98US-0088734.  
 PR 10-JUN-1998; 98US-0088740.  
 PR 10-JUN-1998; 98US-0088741.  
 PR 10-JUN-1998; 98US-0088742.  
 PR 10-JUN-1998; 98US-0088810.  
 PR 10-JUN-1998; 98US-0088811.  
 PR 10-JUN-1998; 98US-0088824.  
 PR 10-JUN-1998; 98US-0088825.  
 PR 10-JUN-1998; 98US-0088826.  
 PR 11-JUN-1998; 98US-0088858.  
 PR 11-JUN-1998; 98US-0088861.  
 PR 11-JUN-1998; 98US-0088863.  
 PR 11-JUN-1998; 98US-0088876.

PR 12-JUN-1998; 98US-0089090.  
PR 12-JUN-1998; 98US-0089105.  
PR 16-JUN-1998; 98US-0089440.  
PR 16-JUN-1998; 98US-0089512.  
PR 16-JUN-1998; 98US-0089514.  
PR 17-JUN-1998; 98US-0089532.  
PR 17-JUN-1998; 98US-0089533.  
PR 17-JUN-1998; 98US-0089539.  
PR 17-JUN-1998; 98US-0089599.  
PR 17-JUN-1998; 98US-0089600.  
PR 17-JUN-1998; 98US-0089653.  
PR 18-JUN-1998; 98US-0089801.  
PR 18-JUN-1998; 98US-0089907.  
PR 18-JUN-1998; 98US-0089908.  
PR 19-JUN-1998; 98US-0089947.  
PR 19-JUN-1998; 98US-0089948.  
PR 19-JUN-1998; 98US-0089952.  
PR 22-JUN-1998; 98US-0090246.  
PR 22-JUN-1998; 98US-0090258.  
PR 22-JUN-1998; 98US-0090259.  
PR 23-JUN-1998; 98US-0090349.  
PR 23-JUN-1998; 98US-0090353.  
PR 23-JUN-1998; 98US-0090429.  
PR 24-JUN-1998; 98US-0090431.  
PR 24-JUN-1998; 98US-0090435.  
PR 24-JUN-1998; 98US-0090444.  
PR 24-JUN-1998; 98US-0090445.  
PR 24-JUN-1998; 98US-0090461.  
PR 24-JUN-1998; 98US-0090472.  
PR 24-JUN-1998; 98US-0090535.  
PR 24-JUN-1998; 98US-0090538.  
PR 24-JUN-1998; 98US-0090540.  
PR 24-JUN-1998; 98US-0090557.  
PR 25-JUN-1998; 98US-0090676.  
PR 25-JUN-1998; 98US-0090678.  
PR 25-JUN-1998; 98US-0090688.  
PR 25-JUN-1998; 98US-0090690.  
PR 25-JUN-1998; 98US-0090691.  
PR 25-JUN-1998; 98US-0090694.  
PR 25-JUN-1998; 98US-0090695.  
PR 25-JUN-1998; 98US-0090696.  
PR 26-JUN-1998; 98US-0090862.  
PR 26-JUN-1998; 98US-0090863.  
PR 01-JUL-1998; 98US-0091358.  
PR 01-JUL-1998; 98US-0091360.  
PR 01-JUL-1998; 98US-0091544.  
PR 02-JUL-1998; 98US-0091478.  
PR 02-JUL-1998; 98US-0091486.  
PR 02-JUL-1998; 98US-0091516.  
PR 02-JUL-1998; 98US-0091628.  
PR 02-JUL-1998; 98US-0091633.  
PR 02-JUL-1998; 98US-0091634.  
PR 02-JUL-1998; 98US-0091673.  
PR 07-JUL-1998; 98US-0091978.  
PR 07-JUL-1998; 98US-0091982.  
PR 09-JUL-1998; 98US-0092182.  
PR 10-JUL-1998; 98US-0092247.  
PR 30-JUL-1998; 98US-0093339.  
PR 04-AUG-1998; 98US-0094651.  
PR 04-AUG-1998; 98US-0095282.  
PR 04-AUG-1998; 98US-0095285.  
PR 04-AUG-1998; 98US-0095301.  
PR 04-AUG-1998; 98US-0095302.  
PR 04-AUG-1998; 98US-0095318.  
PR 04-AUG-1998; 98US-0095321.  
PR 04-AUG-1998; 98US-0095325.  
PR 10-AUG-1998; 98US-0095916.  
PR 10-AUG-1998; 98US-0095929.  
PR 10-AUG-1998; 98US-0096012.  
PR 11-AUG-1998; 98US-0096143.  
PR 11-AUG-1998; 98US-0096146.  
PR 12-AUG-1998; 98US-0096329.

PR 17-AUG-1998; 98US-0096757.  
PR 17-AUG-1998; 98US-0096766.  
PR 17-AUG-1998; 98US-0096768.  
PR 17-AUG-1998; 98US-0096773.  
PR 17-AUG-1998; 98US-0096791.  
PR 17-AUG-1998; 98US-0096867.  
PR 17-AUG-1998; 98US-0096891.  
PR 17-AUG-1998; 98US-0096894.  
PR 17-AUG-1998; 98US-0096895.  
PR 17-AUG-1998; 98US-0096897.  
PR 18-AUG-1998; 98US-0096949.  
PR 18-AUG-1998; 98US-0096950.  
PR 18-AUG-1998; 98US-0096959.  
PR 18-AUG-1998; 98US-0096960.  
PR 18-AUG-1998; 98US-0097022.  
PR 19-AUG-1998; 98US-0097141.  
PR 20-AUG-1998; 98US-0097218.  
PR 24-AUG-1998; 98US-0097651.  
PR 25-AUG-1998; 98US-0097951.  
PR 26-AUG-1998; 98US-0097952.  
PR 26-AUG-1998; 98US-0097954.  
PR 26-AUG-1998; 98US-0097955.  
PR 26-AUG-1998; 98US-0097971.  
PR 26-AUG-1998; 98US-0097974.  
PR 26-AUG-1998; 98US-0097978.  
PR 26-AUG-1998; 98US-0097979.  
PR 26-AUG-1998; 98US-0097986.  
PR 26-AUG-1998; 98US-0098014.  
PR 31-AUG-1998; 98US-0098525.  
PR 16-SEP-1998; 98US-0100634.  
PR 12-JUN-1999; 99US-0115565.  
PR (GENTECH ) GENTECH INC.  
PR Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;  
PR Wood WI, Yuan J;  
PR WPI; 2000-072883/06.  
PR P-PSDB; AAY66757.  
PR Membrane-bound proteins and related nucleotide sequences -  
PR Claim 2; Fig 289; 822bp; English.  
XX The invention provides membrane-bound PRO polypeptides and  
XX CC polynucleotides encoding them. The PRO sequences of the invention were  
XX CC identified based on extracellular domain homology screening. The PRO  
XX CC sequences have homology with proteins including LDL receptors, TIE  
XX CC ligands and various enzymes. The membrane-bound proteins and receptor  
XX CC molecules are useful as pharmaceutical and diagnostic agents. Receptor  
XX CC immunoadhesins, for instance, can be used as therapeutic agents to block  
XX CC receptor-ligand interactions. The membrane-bound proteins can also be  
XX CC employed for screening of potential peptide or small molecule inhibitors  
XX CC of the relevant receptor/ligand interaction. The PRO encoding sequences  
XX CC are useful as hybridization probes, in chromosome and gene mapping and in  
XX CC the generation of antisense RNA and DNA. PRO nucleic acid sequences  
XX CC by recombinant techniques.  
SQ Sequence 570 BP; 129 A; 190 C; 170 G; 81 T; 0 other;  
Query Match 16.0%; Score 90; DB 21; Length 570;  
Best Local Similarity 100.0%; Pred. No. 7.9e-09; Indels 0; Gaps 0;  
Matches 90; Conservative 0; Mismatches 0;  
QY 474 GCGAGACCGGATTAAGAACCTCTGCGCTTCCCGGACCGCCAGATTCCCGCCG 533  
Db 1 GCGAGACCGGATTAAGAACCTCTGCGCTTCCCGGACCGCCAGATTCCCGCCG 60  
QY 534 GCCCGAGCGCGCGCCATGAGCTCGCC 563  
Db 61 GCCCGAGCGCGCGCCATGAGCTCGCC 90

RESULT 9  
AAFA4249 standard; cDNA; 570 BP.  
XX  
XX AAF44249;  
AC  
XX 02-APR-2001 (first entry)  
XX  
XX Human PRO1245 (UNQ629) nucleotide sequence SEQ ID NO:407.  
XX  
XX Human, secreted and transmembrane protein; PRO; cytosolic;  
XX cell death; cancer; chromosomal mapping; gene mapping; tissue typing;  
XX diagnostic assay; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200073454-A1.  
XX  
XX 07-DEC-2000.  
XX  
XX 30-MAR-2000; 2000WO-US08439.  
XX  
XX 02-JUN-1999; 99WO-US12252.  
XX 23-JUN-1999; 99US-0141037.  
XX 07-JUL-1999; 99US-0143048.  
XX 20-JUL-1999; 99US-0144758.  
XX 26-JUL-1999; 99US-0145698.  
XX 28-JUL-1999; 99US-0146222.  
XX 17-AUG-1999; 99US-0149396.  
XX 15-SEP-1999; 99WO-US21547.  
XX 08-OCT-1999; 99US-0158663.  
XX 30-NOV-1999; 99WO-US28313.  
XX 01-DEC-1999; 99WO-US28301.  
XX 16-DEC-1999; 99WO-US30911.  
XX 20-DEC-1999; 99WO-US30911.  
XX 05-JAN-2000; 2000WO-US00219.  
XX 06-JAN-2000; 2000WO-US00376.  
XX 11-FEB-2000; 2000WO-US03565.  
XX 18-FEB-2000; 2000WO-US04341.  
XX 22-FEB-2000; 2000WO-US04414.  
XX 24-FEB-2000; 2000WO-US04914.  
XX 02-MAR-2000; 2000WO-US05841.  
XX 15-MAR-2000; 2000WO-US06884.  
XX 20-MAR-2000; 2000WO-US07377.  
XX  
XX (GENT) GENENTECH INC.  
XX  
XX Ashkenazi AJ, Baker KP, Bolstein D, Desnoyers LJ, Eaton DL;  
XX Fehrera N, Fong S, Geider H, Gerritsen ME, Goddard A, Godowski PJ;  
XX Grimaldi CJ, Gurney AL, Klievin RJ, Napier MA, Pan J, Paoni NF;  
XX Roy MA, Stewart TA, Tumas D, Watanabe CX, Williams PM, Wood WT;  
XX Zhang Z;  
XX  
XX WPI; 2001-032160/04.  
XX P-FSDB; AAB65280.  
XX  
XX PRO polynucleotides used to produce polypeptides used to target  
XX bioactive molecules such as toxins, radiolabels or antibodies, to  
XX specific cells, to cause targeted cell death -  
XX  
XX Claim 2; Fig 289; 935PP; English.  
XX  
XX The present invention describes human secreted and transmembrane PRO  
XX proteins. The PRO proteins have cytostatic activity. The PRO proteins  
XX can be used for targeted delivery of bioactive molecules, PRO nucleotides  
XX toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide  
XX sequences, and their fragments, can be used as hybridisation probes in  
XX chromosomal and gene mapping, and in the generation of anti-sense RNA  
XX and DNA. They may also be used to produce transgenic animals which are  
XX used to develop and screen therapeutically useful reagents. The PRO

CC nucleotide and protein sequence can be used for tissue typing and in  
CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.  
CC AAF4270 to AAF4470 represent PCR primers and hybridisation probes used  
CC in the isolation of human PRO sequences. AAF4087 to AAF4269 and  
CC AAB6154 to AAB65300 represent human PRO polynucleotide and protein  
CC sequences given in the exemplification of the present invention.  
XX  
XX Sequence 570 BP; 129 A; 190 C; 170 G; 81 T; 0 other;  
XX  
XX Query Match 16.0%; Score 90; DB 22; Length 570;  
XX Best Local Similarity 100.0%; Pred. No. 7.9e-09;  
XX Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX Db 474 GCGAGACCGGGTATATAGAGCCTCTGCGCTTGGCGGAGCGCGAGATTCCCGCGC 533  
XX 1 GCGAGACCGGGTATATAGAGCCTCTGCGCTTGGCGGAGCGCGAGATTCCCGCGC 60  
XX  
XX Qy 534 GCGCGAGCGCGCGCGCGCATGAGCTCGCC 563  
XX Db 61 GCGCGAGCGCGCGCGCGCATGAGCTCGCC 90  
XX  
XX RESULT 10  
XX AABX80386 standard; DNA; 570 BP.  
XX  
XX AABX80386;  
XX  
XX 28-APR-2003 (first entry)  
XX  
XX Novel human secreted or transmembrane protein PRO1358 DNA.  
XX  
XX Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
XX cardiac insufficiency disorder; cancer; tumour; immune response;  
XX adrenal cortical capillary growth factor inhibition; c-fos induction;  
XX vascular endothelial growth factor inhibition; VEGF inhibition;  
XX endothelial cell growth inhibitor; T-lymphocytes stimulation;  
XX retinal neurons cell survival; rod photoreceptor cell survival;  
XX retinal disorder; retinitis pigmentosa; kidney disease;  
XX mammalian kidney mesangial cell proliferation; Berger disease;  
XX dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
XX chondrocyte redifferentiation; sports injury; arthritis; gene; da..  
XX  
XX Homo sapiens.  
XX  
XX US2002132252-A1.  
XX  
XX 19-SEP-2002.  
XX  
XX 14-NOV-2001; 2001US-0990442.  
XX  
XX 05-NOV-1997; 97WO-US20069.  
XX 16-SEP-1998; 98WO-US19330.  
XX 17-SEP-1998; 98WO-US19437.  
XX 07-OCT-1998; 98WO-US21141.  
XX 01-DEC-1998; 98WO-US25108.  
XX 05-JAN-1999; 99WO-US02106.  
XX 08-MAR-1999; 99WO-US05028.  
XX 02-JUN-1999; 99WO-US12252.  
XX 15-SEP-1999; 99WO-US21090.  
XX 15-SEP-1999; 99WO-US21547.  
XX 30-NOV-1999; 99WO-US28313.  
XX 01-DEC-1999; 99WO-US28301.  
XX 16-DEC-1999; 99WO-US28634.  
XX 20-DEC-1999; 99WO-US30095.  
XX 06-JAN-2000; 2000WO-US00219.  
XX 06-JAN-2000; 2000WO-US00376.  
XX 11-FEB-2000; 2000WO-US03565.  
XX 18-FEB-2000; 2000WO-US04341.  
XX 22-FEB-2000; 2000WO-US04914.  
XX 24-FEB-2000; 2000WO-US05004.

XX	Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Griemaldi JC, Gurney AL, Kijavrin IU, Napier MA, Pan Y, Roy VM, Stewart TA, Tamas D, Watanabe CK, Williams PM, Zhang Z, WPI: 2003-247093/24.	XX
XX	P-PSDB; ABUS9174.	XX
XX	Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346 and PRO1375, which stimulate proliferation of stimulated T-lymphocytes are therapeutically useful for enhancing immune response and in cancer treatments	XX
XX	Claim 2; Fig 291; 648pp; English.	XX
XX	The invention describes an isolated human PRO polypeptide. The PRO polypeptides are useful in detecting PRO polypeptides in a sample, in linking a bioactive molecule to a cell expressing a PRO polypeptide, and in modulating at least one biological activity of a cell expressing a PRO polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186 stimulate adrenal cortical capillary endothelial growth and PRO826, PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126, PRO1360 and PRO1387 induce c-fos in endothelial cells and are thus useful for treating conditions or disorders where angiogenesis would be beneficial, e.g. wound healing and antagonist of this polypeptide are useful for treating cancerous tumours. PRO812 inhibits vascular endothelial growth factor (VEGF) stimulated proliferation of endothelial cells and is thus useful for inhibiting endothelial cell growth in mammals which would be beneficial in inhibiting tumour growth. PRO826, PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of stimulated T-lymphocytes and are therapeutically useful for enhancing immune response. PRO828, PRO826, PRO1068 or PRO1126 enhance survival of retinal neurons cells (PRO1132 is also enhances survival/proliferation of rod photoreceptor cells) and therefore are useful for treating retinal disorders of injuries, e.g. retinitis pigmentosum. AMD. PRO819, PRO813 and PRO1066 induce proliferation of mammalian kidney mesangial cells, and therefore are useful for treating kidney disorders associated with decreased mesangial cell function such as Berger disease or other nephropathies associated with dermatitis, herpetic disease or Crohn's disease. PRO1310, PRO844, PRO1112, PRO1192 and PRO1387 induce the proliferation and/or redifferentiation of chondrocytes in culture and are thus useful for treating sports injuries, and arthritis. This sequence represents a novel human PRO protein polynucleotide.	XX
XX	Sequence 570 BP; 129 A; 190 C; 170 G; 81 T; 0 other;	XX
XX	Query Match 16.0%; Score 90; DB 25; Length 570; Best Local Similarity 100.0%; Pred. No. 7.9e-09; Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX
XX	474 GCGAGACCGGGTATAGAACCTCTGCGGCTTGGCCGGCAGCCGAGTTCCCGGGC 533	XX
XX	Db 1 GCGAGACCGGGTATAGAACCTCTGCGGCTTGGCCGGCAGCCGAGTTCCCGGGC 60	XX
XX	534 GCCCGAGCCCCCGCGCATGAACTCGCC 563	XX
XX	Db 61 GCCCGAGCCCCCGCGCATGAACTCGCC 90	XX
XX	RESULT 11	XX
XX	ABX80890	XX
XX	ID ABX80890 standard; cDNA; 570 BP.	XX
XX	ABX80890;	XX
XX	22-APR-2003 (first entry)	XX
XX	Human secreted/transmembrane protein cDNA, #163.	XX
XX	Human; gene; ss; PRO; secreted; transmembrane; pharmaceutical;	XX





PR 04-AUG-1998; 98US-095285P.  
 PR 04-AUG-1998; 98US-095301P.  
 PR 04-AUG-1998; 98US-095302P.  
 PR 04-AUG-1998; 98US-095318P.  
 PR 04-AUG-1998; 98US-095321P.  
 PR 04-AUG-1998; 98US-095325P.  
 PR 10-AUG-1998; 98US-095816P.  
 PR 10-AUG-1998; 98US-095829P.  
 PR 10-AUG-1998; 98US-096012P.  
 PR 11-AUG-1998; 98US-096143P.  
 PR 11-AUG-1998; 98US-096146P.  
 PR 12-AUG-1998; 98US-096329P.  
 PR 17-AUG-1998; 98US-096757P.  
 PR 17-AUG-1998; 98US-096766P.  
 PR 17-AUG-1998; 98US-096768P.  
 PR 17-AUG-1998; 98US-096773P.  
 PR 17-AUG-1998; 98US-096791P.  
 PR 17-AUG-1998; 98US-096867P.  
 PR 17-AUG-1998; 98US-096891P.  
 PR 17-AUG-1998; 98US-096894P.  
 PR 17-AUG-1998; 98US-096895P.  
 PR 18-AUG-1998; 98US-096897P.  
 PR 18-AUG-1998; 98US-096949P.  
 PR 18-AUG-1998; 98US-096950P.  
 PR 18-AUG-1998; 98US-096959P.  
 PR 18-AUG-1998; 98US-096960P.  
 PR 19-AUG-1998; 98US-097022P.  
 PR 20-AUG-1998; 98US-097111P.  
 PR 20-AUG-1998; 98US-097218P.  
 PR 20-AUG-1998; 98US-097661P.  
 PR 20-AUG-1998; 98US-097952P.  
 PR 20-AUG-1998; 98US-097954P.  
 PR 20-AUG-1998; 98US-097955P.  
 PR 20-AUG-1998; 98US-097971P.  
 PR 20-AUG-1998; 98US-097974P.  
 PR 20-AUG-1998; 98US-097979P.  
 PR 20-AUG-1998; 98US-097986P.  
 PR 20-AUG-1998; 98US-098014P.  
 PR 20-AUG-1998; 98US-098525P.  
 PR 16-SEP-1998; 98US-100634P.  
 PR 16-SEP-1998; 98US-100858P.  
 PR 22-DEC-1998; 98US-113296P.  
 PR 12-MAR-1999; 98US-123957P.  
 PR 23-JUN-1999; 98US-141037P.

Query Match 16.0%; Score 90; DB 25; Length 570;  
 Best Local Similarity 100.0%; Pred No. 7.9e-09;  
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 474 GCGAGGACCGGATTAAGAGCCCTCGGCGCTTCCCGGCGACCCGAGGTTCCCGCCG 533  
 DB 1 GCGAGGACCGGATTAAGAGCCCTCGGCGCTTCCCGGCGACCCGAGGTTCCCGCCG 60  
 OY 534 GCGCGGAGCCCGCGCGCATGAGCTGCGCC 563  
 DB 61 GCGCGGAGCCCGCGCGCATGAGCTGCGCC 90

RESULT 12  
 ID ABX81273 standard; DNA; 570 BP.  
 AC ABX81273;  
 DT 22-APR-2003 (first entry)  
 XX  
 DE Novel human secreted of transmembrane protein PRO1358 DNA.  
 KM Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
 KM cardiac inefficiency disorder; cancer; tumour; immune response;  
 KM adrenal cortical capillary endothelial growth; c-fos induction;  
 KM vascular endothelial growth factor inhibition; VEGF inhibition;

KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
 KW retinal neurons cell survival; rod photoreceptor cell survival;  
 KW retinal disorder; retinitis pigmentosa; kidney disorder;  
 KW mammalian kidney mesangial cell proliferation; Berger disease;  
 KW dermatitis; herpetic stomatitis; Crohn's disease; chondrocyte proliferation;  
 KW chondrocyte redifferentiation; sports injury; arthritis; gene; ds.  
 OS Homo sapiens.  
 PN US2003027985-A1.  
 PD 06-FEB-2003.  
 XX  
 XX 14-NOV-2001; 2001US-0990562.  
 XX  
 PR 05-NOV-1997; 97WO-US20069.  
 PR 16-SEP-1998; 98WO-US19330.  
 PR 17-SEP-1998; 98WO-US19437.  
 PR 07-OCT-1998; 98WO-US21141.  
 PR 01-DEC-1998; 98WO-US25108.  
 PR 05-JAN-1999; 99WO-US00106.  
 PR 08-MAR-1999; 99WO-US05028.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 01-DEC-1999; 99WO-US28634.  
 PR 16-DEC-1999; 99WO-US30095.  
 PR 20-DEC-1999; 99WO-US30911.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US04914.  
 PR 24-FEB-2000; 2000WO-US05004.  
 PR 02-MAR-2000; 2000WO-US05841.  
 PR 10-MAR-2000; 2000WO-US05841.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 20-MAR-2000; 2000WO-US07377.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 15-MAY-2000; 2000WO-US13358.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.  
 PR 30-MAY-2000; 2000WO-US14941.  
 PR 02-JUN-2000; 2000WO-US15264.  
 PR 28-JUN-2000; 2000WO-US20710.  
 PR 11-AUG-2000; 2000WO-US22031.  
 PR 23-AUG-2000; 2000WO-US23522.  
 PR 09-NOV-2000; 2000WO-US30952.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 26-FEB-2001; 2001WO-US06520.  
 PR 01-JUN-2001; 2001WO-US17800.  
 PR 20-JUN-2001; 2001WO-US19692.  
 PR 20-JUN-2001; 2001WO-US21066.  
 PR 09-JUL-2001; 2001WO-US21735.  
 PR 15-JUN-1997; 97US-049787P.  
 PR 17-OCT-1997; 97US-062250P.  
 PR 11-NOV-1997; 97US-065186P.  
 PR 11-NOV-1997; 97US-065111P.  
 PR 24-NOV-1997; 97US-066770P.  
 PR 25-FEB-1998; 98US-075945P.  
 PR 20-MAR-1998; 98US-078910P.  
 PR 28-APR-1998; 98US-083322P.  
 PR 28-APR-1998; 98US-084600P.  
 PR 28-MAY-1998; 98US-087106P.  
 PR 02-JUN-1998; 98US-087607P.  
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 PR 03-JUN-1998; 98US-087759P.  
 PR 04-JUN-1998; 98US-088021P.

PR	20-JUL-1998;	98US-093339P;
PR	30-JUL-1998;	98US-094651P;
PR	04-AUG-1998;	98US-095282P;
PR	04-AUG-1998;	98US-095285P;
PR	04-AUG-1998;	98US-095301P;
PR	04-AUG-1998;	98US-095302P;
PR	04-AUG-1998;	98US-095318P;
PR	04-AUG-1998;	98US-095331P;
PR	04-AUG-1998;	98US-095335P;
PR	10-AUG-1998;	98US-095916P;
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PR	10-AUG-1998;	98US-096012P;
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PR	20-AUG-1998;	98US-097218P;
PR	20-AUG-1998;	98US-097611P;
PR	26-AUG-1998;	98US-097952P;
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PR	26-AUG-1998;	98US-097955P;
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PR	26-AUG-1998;	98US-097974P;
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XX	01-MAY-2003		(first entry)	
XX				
DE			Human secreted/transmembrane protein CDNA, #163.	
XX				
KX			Human; gene; ss; PRO; secreted; transmembrane; signal peptide;	
KW			pharmaceutical; diagnostic; therapeutic; gene therapy.	
XX				
OS			Homo sapiens.	
XX				
PN			US2002160384-A1.	





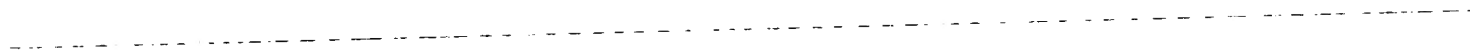
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 PR 18-AUG-1998; 98US-096949P.  
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 PR 18-AUG-1998; 98US-096959P.  
 PR 18-AUG-1998; 98US-096960P.  
 PR 19-AUG-1998; 98US-097022P.  
 PR 19-AUG-1998; 98US-097141P.  
 PR 20-AUG-1998; 98US-097218P.  
 PR 24-AUG-1998; 98US-097661P.  
 PR 26-AUG-1998; 98US-097952P.  
 PR 26-AUG-1998; 98US-097954P.  
 PR 26-AUG-1998; 98US-097955P.  
 PR 26-AUG-1998; 98US-097971P.  
 PR 26-AUG-1998; 98US-097974P.  
 PR 26-AUG-1998; 98US-097978P.  
 PR 26-AUG-1998; 98US-097979P.  
 PR 26-AUG-1998; 98US-097986P.  
 PR 31-AUG-1998; 98US-098014P.  
 PR 31-SEP-1998; 98US-098525P.  
 PR 16-SEP-1998; 98US-100634P.  
 PR 17-SEP-1998; 98US-100858P.  
 PR 22-DEC-1998; 98US-113296P.  
 PR 12-MAR-1999; 98US-123957P.  
 PR 23-JUN-1999; 98US-141037P.  
 PR 07-JUL-1999; 98US-143048P.

Query Match 16.0%; Score 90; DB 25; Length 570;  
 Best Local Similarity 100.0%; Pred. No. 7.9e-09;  
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 474 GCGAGGACCGGGATATAGAGGCTGTGCGCTTGCGCGGAGCGCGGAGTTCCCGCGC 533  
 Db 1 GCGAGGACCGGGATATAGAGGCTGTGCGCTTGCGCGGAGCGCGGAGTTCCCGCGC 60  
 Qy 534 GCGCGAGCGCGCGCGCGCATGAGCTCGCGC 563  
 Db 61 GCGCGAGCGCGCGCGCGCATGAGCTCGCGC 90

RESULT 15  
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 ID ABE79570 standard; CDNA; 570 BP.  
 XX  
 AC ABE79570;  
 XX  
 DT 17-APR-2003 (first entry)  
 XX  
 DE Human secreted/transmembrane protein CDNA, #163.  
 XX  
 KW Human; gene; ss; PRO; secreted; transmembrane; signal peptide;  
 KW pharmaceutical; diagnostic; biosensor; bioreactor; tumour; therapeutic;  
 KW colon cancer; lung cancer; breast cancer;cancer; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2002142961-A1.  
 XX  
 PD 03-OCT-2002.  
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 PF 19-NOV-2001; 2001US-0989721.  
 XX  
 PR 05-NOV-1997; 97WO-US20069.  
 PR 17-SEP-1998; 98WO-US19437.  
 PR 07-OCT-1998; 98WO-US21141.  
 PR 01-DEC-1998; 98WO-US25108.  
 PR 05-JAN-1999; 99WO-US00106.  
 PR 08-MAR-1999; 99WO-US12522.  
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 PR 15-SEP-1999; 99WO-US21547.  
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 PR 30-NOV-1999; 99WO-US28313.  
 PR 01-DEC-1999; 99WO-US28301.  
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 PR 16-DEC-1999; 99WO-US30095.  
 PR 20-DEC-1999; 99WO-US30911.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04431.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US04914.  
 PR 02-MAR-2000; 2000WO-US05004.  
 PR 10-MAR-2000; 2000WO-US05841.  
 PR 15-MAR-2000; 2000WO-US06319.  
 PR 30-MAR-2000; 2000WO-US07377.  
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 PR 15-MAY-2000; 2000WO-US13358.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 30-MAY-2000; 2000WO-US14941.  
 PR 02-JUN-2000; 2000WO-US15264.  
 PR 28-JUL-2000; 2000WO-US20710.  
 PR 11-AUG-2000; 2000WO-US22031.  
 PR 23-AUG-2000; 2000WO-US23328.  
 PR 24-AUG-2000; 2000WO-US23328.  
 PR 08-NOV-2000; 2000WO-US30952.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 28-FEB-2001; 2001WO-US06520.  
 PR 01-JUN-2001; 2001WO-US17800.  
 PR 20-JUN-2001; 2001WO-US19692.  
 PR 29-JUN-2001; 2001WO-US21066.  
 PR 09-JUL-2001; 2001WO-US21735.  
 PR 16-JUN-1997; 97US-049787P.  
 PR 17-OCT-1997; 97US-062250P.  
 PR 12-NOV-1997; 97US-065186P.  
 PR 13-NOV-1997; 97US-065311P.  
 PR 24-NOV-1997; 97US-065770P.  
 PR 25-FEB-1998; 98US-075945P.  
 PR 20-MAR-1998; 98US-076910P.  
 PR 28-APR-1998; 98US-083322P.  
 PR 07-MAY-1998; 98US-084600P.







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Run on: November 6, 2003, 14:25:31 ; Search time 56 Seconds

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Pred. No. is the number of results predicted by chance to have a  
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and is derived by analysis of the total score distribution.

## SUMMARIES

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5	48.4	8.6	4411529	3	US-09-103-840A-1
6	47.2	8.4	7218	1	US-08-233-463-14
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9	46.6	8.3	932	1	US-08-459-254-1
10	46.6	8.3	932	1	US-08-458-165-8
11	46.2	8.2	3937	3	US-08-814-098-7
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15	45.4	8.1	1327	4	US-08-483-537-36
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21	44.8	8.0	6453	3	US-08-306-691B-14
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23	44.8	8.0	6453	3	US-09-356-952-8
24	44.6	7.9	4257	2	US-08-690-473-1
25	44.6	7.9	4257	3	US-09-259-821A-1
26	44.6	7.9	4257	3	US-08-843-659-1
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31	44.4	7.9	12001	1	US-08-458-568A-11	Sequence 11, Appli
32	44.2	7.9	450	4	US-09-252-991A-6540	Sequence 6540, Ap
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34	43.8	7.8	53526	3	US-08-658-136-2	Sequence 2, Appli
35	43.8	7.8	53577	3	US-08-658-136-1	Sequence 1, Appli
36	43.4	7.7	2990	3	US-08-572-951-1	Sequence 1, Appli
37	43.2	7.7	1327	3	US-08-483-533-36	Sequence 36, Appli
38	43.2	7.7	1327	4	US-09-283-477A-36	Sequence 1, Appli
39	42.8	7.6	1590	4	US-09-434-288-1	Sequence 1, Appli
40	42.8	7.6	2887	4	US-09-679-298A-1	Sequence 1, Appli
41	42.8	7.6	35100	2	US-08-770-379-17	Sequence 17, Appli
42	42.8	7.6	35100	4	US-08-757-669A-17	Sequence 17, Appli
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## ALIGNMENTS

RESULT 1  
US-09-996-243-407  
Sequence 407, Application US/09996243  
Patent No. 6478825  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deonoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Goddard, Audrey E.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C13  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: US/09/996,243  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28

us-10-081-817a-19-plus-1-12-of-sev3.rnj

Page 2

PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 16.0%; Score 90; DB 4; Length 570;  
Best Local Similarity 100.0%; Pred. No. 2.4e-10;  
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GCGAGGACCGCGATTAAGAGCTCTGCTTCCCGGCGACCGCGAGCTTCCCGGCG 60

QY 534 GCGCGAGCGCGCGCGCATGAAGCTCGCC 563  
DB 61 GCGCGAGCGCGCGCGCATGAAGCTCGCC 90

## RESULT 2

PCT-US91-06532-1/c  
Sequence 1: Application PC/TUS9106532  
GENERAL INFORMATION:  
APPLICANT: Roizman, Bernard  
TITLE OF INVENTION: Recombinant Herpes Simplex Viruses  
TITLE OF INVENTION: Vaccines and Methods  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESS: Bicknell  
STREET: Two First National Plaza Suite 2100  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US91/06532  
FILING DATE: 19910910  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Gruber, Lewis S.  
REGISTRATION NUMBER: 30,060  
REFERENCE/DOCKET NUMBER: 27373/8235  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/346-5750  
TELEFAX: 312/984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ. ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1335 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
PCT-US91-06532-1

Query Match 8.8%; Score 49.4; DB 5; Length 1335;  
Best Local Similarity 48.0%; Pred. No. 0.046;  
Matches 169; Conservative 0; Mismatches 182; Indels 1; Gaps 1;

QY 169 GCGAGGAGCTCCCTCAACNAGAGGAGTCCCTCACCGCCCAAGCTTCGAGGGAG 228  
DB 723 GGGGAGAGAGCGACCGCGCGGGGTGCGGGGGTTCGGGGGTTCGGGGGTTCGGGG 664

QY 229 GCGGTTGGGTCAAGACCGCAAGCGAAGTTCGGGGCGGGGTTCGGGGGTTCGGGG 288  
DB 663 GGTTCGGGGGTTCGGGGGTTCGGGGGTTCGGGGGTTCGGGGGTTCGGGGGTTCGGGG 604

QY 289 GCGCGGCGCTGCTCTCTCAAGGCGCCCGAGCGCTTCGCAAGAGAACTCTCGAGGCC 348  
DB 603 CGCGCGCGCTCTCTCTCTCAAGGCGCCCGAGCGCTTCGCAAGAGAACTCTCGAGGCC 544

QY 349 GCGCAGGAGAGGGGCGACGGGCTTCCAGAGGCCCGCGCGCAGAGAACTTCGCGAG 408  
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DB 483 GTTAGCG 424

QY 468 GGAAGCGCGAGAGCGCGGTATTAAGAGCTCTGCGCTTCCCGCGAGCGG 519  
DB 423 GTTGGCGCGCGCTTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 372

## RESULT 3

US-09-103-840A-2  
Sequence 2: Application US/09103840A  
Patent No. 6284328  
GENERAL INFORMATION:  
APPLICANT: FLEISCHMAN, Robert D.  
APPLICANT: WHITE, Owen R.  
APPLICANT: FRASER, Claire M.  
APPLICANT: VENTER, John C.  
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
TITLE OF INVENTION: TUBERCULOSIS  
FILE REFERENCE: 24366-20007.00  
CURRENT APPLICATION NUMBER: US/09/103,840A  
CURRENT FILING DATE: 1998-06-24  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: Patent Ver. 2.1  
SEQ ID NO 2  
LENGTH: 4403765  
TYPE: DNA  
ORGANISM: Mycobacterium tuberculosis  
FEATURE:  
OTHER INFORMATION: CDC 1551  
OTHER INFORMATION: "n" bases at various positions throughout the sequence  
OTHER INFORMATION: represent a, t, c or g  
US-09-103-840A-2

Query Match 8.7%; Score 48.8; DB 3; Length 4403765;  
Best Local Similarity 46.7%; Pred. No. 0.079;  
Matches 231; Conservative 0; Mismatches 253; Indels 11; Gaps 2;

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QY 61 CGCAGAGCGCGCGCGCGAGAGCCCGAGTGCAGCGTTCGACAGTCTGGATCAGAG 120  
DB 841169 CGCGCGCGCGAGAAAGCGCAGATCTGTTGGCGCGCGCGCGCGCGCGCGCG 841228

QY 121 CAGGAGCAGGAGCGAGAACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180  
DB 841229 ATTCTGAAGCGCGTGCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 841288

QY 181 CCTCACNAGAGAGTCTCCCTCAACCGGC---CAGCGCTGAGGCGGCGCGG 237  
DB 841289 TGGCGCGGAGAGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCG 841348

QY 238 GTCAAGCGCGAAGCGAGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 297  
DB 841349 GCGCGCGCGCGAAGCGCGGAGCGCTCGCACTGTATAGCGGCGCGCGCGCGCG 841408

QY 298 TGCCTCTCTCAAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 357  
DB 841409 CGCTAGTTCGAGCGGCGGATTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 841468

QY 358 AGGAGGAGCGGCTTCCCAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 412



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STATE: VA
COUNTRY: USA
ZIP: 2213-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELEFAX: (703) 683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: PT29pt-f18
US-08-232-463-14

Query Match      8.4%; Score 47.2; DB 1; Length 7218;
Best Local Similarity 4.4%; Pred. No. 0.14; Indels 0; Gaps 0;
Matches 13; Conservative 171; Mismatches 114;

QY 223 AGGGGGGGCGTGGGTGACAGCCGAAAGAGTGGCGGGCGGCTGGCGCGCA 282
DB 1339 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
QY 283 GACAAAGCGCGGCTGCTCTCAGAGGCGCCAGCGGCTGCAAGAGAGTCTCG 342
DB 1279 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
QY 343 AGCGCGCGGCGAGGAGGCGGCGGCTTCCAGGCGCGCGCGCGCAGCAGAAATT 402
DB 1219 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
QY 403 GGCGAGGCGAGCGCGTGAAGAGCGGCGGCGGCGGCTTCTCAGAGCGGCGGCGGCG 462
DB 1159 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
QY 463 GGCGTGAAGGCGGAGGAGCGGGTAAAGAGCTGTGAGGCTTCCCGGCGAGCGCG 520
DB 1099 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
TITLE OF INVENTION: DEACTYLASE GENES FOR THE PRODUCTION OF
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TITLE OF INVENTION: PHOSPHINOTHRICIN OR
TITLE OF INVENTION: PHOSPHINOTHRICYL-ALANYL-ALANINE, AND THEIR USE
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Curtis, Morris & Safford
ADDRESSEE: c/o William F. Lawrence
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,912
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,498
FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Lawrence, William F.
REGISTRATION NUMBER: 28,029
REFERENCE/DOCKET NUMBER: 514410-2892
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-0712
TELEFAX: (212) 840-3333
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 932 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-458-912-1

Query Match      8.3%; Score 46.6; DB 1; Length 932;
Best Local Similarity 48.5%; Pred. No. 0.17;
Matches 164; Conservative 0; Mismatches 165; Indels 9; Gaps 1;

QY 184 TCACCGAGGAGAGTCCCTCACCAGGCGGCGGCGGCGGCGGCGGCGGCGG 243
DB 744 TCGTGTACAGGACTCTCTCGGAACCGACCTGATGACAGGCGGCGGCGGCGGCGG 685
QY 244 CCGCAAGGAGAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 303
DB 684 TCGCGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 625
QY 304 TCTCAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 363
DB 624 GCGATGCGGAGAGTCTGCGGTCTCAGAGAGATCTGCGCTCTTGGGCGGAGCGTGC 565
QY 364 CAGGCGCTTCCAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 423
DB 564 GAGGCGGCTCTCAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 505
QY 424 GGAG-----CGGCGAGGCGCTTCTCAGAGGCGGCGGCGGCGGCGGCGGCGG 474
DB 504 GGCTCCCGCGCGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 445
QY 475 CGAGAGCGGAGTAAAGAGCTGTGAGCTTGGCGGCGGCGGCGGCGGCGGCGG 512
DB 444 TCACCGCGAGAGTATCCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 407
```

APPLICANT: Broer, Inge  
APPLICANT: Hillemann, Doris  
APPLICANT: Puhler, Alfred  
APPLICANT: Wohleben, Wolfgang  
APPLICANT: Mullner, Gunter  
APPLICANT: Mullner, Hubert  
APPLICANT: Bartsch, Klaus  
TITLE OF INVENTION: DEACETYLASE GENES FOR THE PRODUCTION OF  
TITLE OF INVENTION: PHOSPHINOTHRICIN OR  
TITLE OF INVENTION: PHOSPHINOTHRICIN-ALANYL-ALANINE,  
TITLE OF INVENTION: PROCESSES FOR THEIR ISOLATION, AND THEIR USE  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Curtis, Morris & Safford  
ADDRESSEE: c/o William F. Lawrence  
STREET: 530 Fifth Avenue  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/461,179  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/926,498  
FILING DATE: 07-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Lawrence, William F.  
REGISTRATION NUMBER: 28,029  
REFERENCE/DOCKET NUMBER: 514410-2882  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 840-3333  
TELEFAX: (212) 840-0712  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 932 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-461-179-1

Query Match 8.3%; Score 46.6; DB 1; Length 932;  
Best Local Similarity 48.5%; Pred. No. 0.17;  
Matches 164; Conservative 0; Mismatches 165; Indels 9; Gaps 1;

DB 184 TCACNAGAGGAGCTCCCTCACCAGGCGCCAGCCCTCGAGAGGGCGCGTGGGTCA 243  
DB 744 TCCTGTCAGACGACTTCTCGAACCAGCTGATGACGAGGGGGGCAACCGGTCA 685  
QY 244 CCGCAAGCGAAGGTGCGGCGCGGGGTGGGCTTCGCGAGACAAAGCCGGCTGCTC 303  
DB 684 TCCTGTCAGACGACTTCTCGAACCAGCTGATGACGAGGGGGGCAACCGGTCA 625  
QY 304 TCTCAGAGGGCCCGAGGCGCTGCGAAGAGTCTCGAGGCCCGGAGGAGAGGGG 363  
DB 624 GCATGCGGAGCGAGTCTCTGAGTCTCAGAGAGATCTCCGCTCTTGCGGGTGAAGTC 565  
QY 364 CACGAGCTTCCAGGCGCGCGCGCGCGAGCAGAGAGTGGCCAGGCGACCGGCTGAGC 423  
DB 564 GAGGCGGCTCGAGGCGCAGGTGCGCCAGAGGCGAATGCAACCGCGGCGCGGAGC 505  
QY 424 GAGG-----CGGCGAGGCGCTTCTCAGAGCGCGGCGCGGCGCGGCTGAGAGGG 474  
DB 504 GGGTCCCGGCGGCGGCGAGCAGCTGAGAGGGGGGCGAGCGGCGAGGCGCGGCGAG 445  
QY 475 CGAGACCGGGGTATAGAGGCTCTGAGGCTTGGCGCGG 512

DB 444 TCACCGGCGAAGTGATCCCGCGGCGGAGGCGCCG 407  
RESULT 9  
US-08-459-254-1/c  
Sequence 1, Application US/08459254  
Patent No. 5767370  
GENERAL INFORMATION:  
APPLICANT: Broer, Inge  
APPLICANT: Hillemann, Doris  
APPLICANT: Puhler, Alfred  
APPLICANT: Wohleben, Wolfgang  
APPLICANT: Mullner, Gunter  
APPLICANT: Mullner, Hubert  
APPLICANT: Bartsch, Klaus  
TITLE OF INVENTION: DEACETYLASE GENES FOR THE PRODUCTION OF  
TITLE OF INVENTION: PHOSPHINOTHRICIN OR  
TITLE OF INVENTION: PHOSPHINOTHRICIN-ALANYL-ALANINE,  
TITLE OF INVENTION: PROCESSES FOR THEIR ISOLATION, AND THEIR USE  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Curtis, Morris & Safford  
ADDRESSEE: c/o William F. Lawrence  
STREET: 530 Fifth Avenue  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/459,254  
FILING DATE: 02-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/926,498  
FILING DATE: 07-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Lawrence, William F.  
REGISTRATION NUMBER: 28,029  
REFERENCE/DOCKET NUMBER: 514410-2882  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 840-0712  
TELEFAX: (212) 840-3333  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 932 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-459-254-1

Query Match 8.3%; Score 46.6; DB 1; Length 932;  
Best Local Similarity 48.5%; Pred. No. 0.17;  
Matches 164; Conservative 0; Mismatches 165; Indels 9; Gaps 1;

DB 184 TCACNAGAGGAGCTCCCTCACCAGGCGCCAGCCCTCGAGAGGGCGCGTGGGTCA 243  
DB 744 TCCTGTCAGACGACTTCTCGAACCAGCTGATGACGAGGGGGGCAACCGGTCA 685  
QY 244 CCGCAAGCGAAGGTGCGGCGCGGGGTGGGCTTCGCGAGACAAAGCCGGCTGCTC 303  
DB 684 TCCTGTCAGACGACTTCTCGAACCAGCTGATGACGAGGGGGGCAACCGGTCA 625  
QY 304 TCTCAGAGGGCCCGAGGCGCTGCGAAGAGTCTCGAGGCCCGGAGGAGAGGGG 363  
DB 624 GCATGCGGAGCGAGTCTCTGAGTCTCAGAGAGATCTCCGCTCTTGCGGGTGAAGTC 565  
QY 364 CACGAGCTTCCAGGCGCGCGCGCGCGAGCAGAGAGTGGCCAGGCGACCGGCTGAGC 423

Db 564 GAGGCGCCCTCGCAGGCCAGGTGGCCGAGGCGAGATGCACACCCGCGCGCCGCGCAGC 505  
QY 424 GGAG-----CGGCGAGGAGCTTTCTCAGAGAGCGCGGCGAGGCGCGCTTGAGGG 474  
Db 504 GGGTCCCCCGCGCTCGGCGAGCCTTGAGAGCGGCGAGCCGCGCCGCGCGAG 445  
QY 475 CGAGACCGGATTAAGAGCCTCGTGCGCTTGCCCG 512  
Db 444 TCACGCGGAGGTATCGCCCGCGCGAGCCCG 407

RESULT 10  
US-08-459-255-1/c  
Sequence 1, Application US/08459255  
Patent No. 5767371

GENERAL INFORMATION:  
APPLICANT: Broer, Inge  
APPLICANT: Hillemann, Doris  
APPLICANT: Puhler, Alfred  
APPLICANT: Wohlenberg, Wolfgang  
APPLICANT: Donn, Gunter  
APPLICANT: Mullner, Hubert  
APPLICANT: Bartsch, Klaus  
TITLE OF INVENTION: DACTYLASE GENES FOR THE PRODUCTION OF  
TITLE OF INVENTION: PHOSPHOTRISIN OR  
TITLE OF INVENTION: PHOSPHOTRISIN-ALANINE  
TITLE OF INVENTION: PROCESSES FOR THEIR ISOLATION, AND THEIR USE  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Curtis, Morris & Safford  
ADDRESSEE: c/o William F. Lawrence  
STREET: 530 Fifth Avenue  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/459,255  
FILING DATE: 02-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/926,498  
FILING DATE: 07-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Lawrence, William F.  
REGISTRATION NUMBER: 28,029  
REFERENCE/DOCKET NUMBER: 514410-2882  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 840-0712  
TELEFAX: (212) 840-3333  
INFORMATION FOR SEQ. ID NO.: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 932 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-459-255-1

Query Match 8.3%; Score 46.6; DB 1; Length 932;  
Best Local Similarity 48.5%; Pred. No. 0.17; Mismatches 165; Indels 9; Gaps 1;  
Matches 164; Conservative 0;

QY 184 TCACGAGGAGGAGCTCCCTCAGCCGCGCCAGCCCTCGAGAGGGGCGGTGAGCAGA 243  
Db 744 TCGTGTACAGACTCTCTCGAAGCCAGCTGATGACAGGGGCGAGACCGGTCA 685  
QY 244 CCGAAGCGAAGGTGCGGCGCGGGGTGCGCTCGCGAACAAGCCGCGCTGCTC 303

Db 684 TCGCGTGGGCGGCGAGGCCAGGCGGCTTCTGGATCGGTCCGCGCAGTACGCCGCC 625  
QY 304 TCTCAGAGGCGCCAGCGCTTCCCAAGAGATCTTCAGAGCCCGGCGAGGAGG 363  
Db 624 GCCATCGGAGAGAGTCTCTCGGTGTCCAGAGATCTCGCTCTTGCGGGTGA 565  
QY 364 CAGGAGCTTCCAGAGGCGCGCGCGCGCGAGGAGAGTGTGCGCAGGCGAGGCGCTTAC 423  
Db 564 GAGGCGCTCGCAGGCGAGGTGCGCCAGGCGAGATGCACACCGCGCGCGAGC 505  
QY 424 GGAG-----CGGCGAGGCTTTCTCAGAGCGCGGCGAGGCGCGCTGAGGG 474  
Db 504 GGGTCCCCCGCGCTCGCGAGCCTGAGAGCGGCGAGCGGCGAGCCCGCGCGAG 445  
QY 475 CGAGACCGGATTAAGAGCCTCGTGCGCTTGCCCG 512  
Db 444 TCACGCGGAGGTATCGCCCGCGCGAGCCCG 407

RESULT 11  
US-08-586-165-8/c  
Sequence 8, Application US/08586165  
Patent No. 6054298

GENERAL INFORMATION:  
APPLICANT: Lauder, Edward M.  
APPLICANT: Orozco, Olivia E.  
APPLICANT: Tabin, Clifford U.  
TITLE OF INVENTION: Fringe Proteins and Pattern Formation  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Millia Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: US  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/586,165  
FILING DATE: 16-JAN-1996  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: H095-05  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 861-6240  
TELEFAX: (617) 861-9540  
INFORMATION FOR SEQ. ID NO.: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3937 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-586-165-8

Query Match 8.2%; Score 46.2; DB 3; Length 3937;  
Best Local Similarity 48.1%; Pred. No. 0.21; Mismatches 173; Indels 2; Gaps 1;  
Matches 162; Conservative 0;

QY 207 CCGGCGCCAGCCTTGAGGAGGCGCGGTGAGTCAAGCCGAAAGCGAAGTGGCGCG 266  
Db 455 CCGATGGAGACTCTCGCGAAGGCGACGAGCTACCGGAGCCCGCGCGCGCG 396  
QY 267 GGGTGGCTCGCGAGAGCAAGAGCGCGCTCTCTCAAGAGGCGCGCGCGCGCTGC 326  
Db 395 GCTCCGAGCGCGCGCGCGCGGTCCCGGAGCTCTCCCGCGCGCGCGCTCCGC 336

QY 327 CAGAGGAGTCTCGAGCCCGGCGAG--GAGAGGGGGCAGCGGCTTCCAGGCGCG 384  
Db 335 TTCGGGGAGGCGCTCTGCGCCCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 276  
QY 389 CGGCGGCGAGGAGATTGGCCAGGCGACGGCCCTGAGCGGAGCGGCGAGGCTTCTCA 444  
Db 275 TGTCCCGGGGCGACGACGACGAGAGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 216  
QY 445 GAGGCGCGGCGAGGCG 504  
Db 215 GCGTCTGCGAGCG 156  
QY 505 TTGCGCGGCGAGCGCGAGGTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 541  
Db 155 CTGCGCGGCGAGCTCAATGGCCCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCG 119

## RESULT 12

US-08-814-095-7

Sequence 7, Application US/08814095

Patent No. 6025183

GENERAL INFORMATION:

APPLICANT: Soreq, Hermona

APPLICANT: Zakut, Haim

APPLICANT: Shani, Moshe

TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR

TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTANCES

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: KOHN &amp; ASSOCIATES

STREET: 30500 No. 6025183thwestern Highway, Suite 410

CITY: Farmington Hills

STATE: Michigan

COUNTRY: U.S.

ZIP: 48334

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/814,095

FILING DATE:

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Montgomery, Ilene N.

REGISTRATION NUMBER: 38,972

REFERENCE/DOCKET NUMBER: 2391.00066

TELECOMMUNICATION INFORMATION:

TELEPHONE: (248) 539-5050

TELEFAX: (248) 539-5050

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 3506 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "Cosmid including Ache

HYPOTHEICAL: promoter, Ache gene and Ars gene"

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

POSITION IN GENOME:

CHROMOSOME/SEGMENT: 7q22

FEATURE:

NAME/KEY: promoter

LOCATION: 4089..22464

OTHER INFORMATION: /function= "Ache Promotor"

OTHER INFORMATION: /standard\_name= "Ache Promotor"

FEATURE:

NAME/KEY: exon

LOCATION: 22465..22537  
OTHER INFORMATION: /function= "non-translated"  
OTHER INFORMATION: /gene= "ACHE"  
OTHER INFORMATION: /number= 1  
FEATURE:  
NAME/KEY: exon  
LOCATION: 24090..25177  
IDENTIFICATION METHOD: experimental  
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OTHER INFORMATION: 24110)"  
OTHER INFORMATION: /evidence= EXPERIMENTAL  
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OTHER INFORMATION: /number= 2  
FEATURE:  
NAME/KEY: exon  
LOCATION: 25524..26009  
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OTHER INFORMATION: /number= 3  
FEATURE:  
NAME/KEY: exon  
LOCATION: 27005..27274  
IDENTIFICATION METHOD: experimental  
OTHER INFORMATION: /evidence= EXPERIMENTAL  
OTHER INFORMATION: /gene= "ACHE"  
OTHER INFORMATION: /number= 4  
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NAME/KEY: exon  
LOCATION: 27255..28007  
IDENTIFICATION METHOD: experimental  
OTHER INFORMATION: /evidence= EXPERIMENTAL  
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OTHER INFORMATION: /number= 5  
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NAME/KEY: terminator  
LOCATION: 27385..27387  
FEATURE:  
NAME/KEY: exon  
LOCATION: 28008..28129  
IDENTIFICATION METHOD: experimental  
OTHER INFORMATION: /evidence= EXPERIMENTAL  
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OTHER INFORMATION: /number= 6  
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LOCATION: 28129..28131  
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NAME/KEY: exon  
LOCATION: 34528..34895  
OTHER INFORMATION: /function= "arsenite resistance  
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OTHER INFORMATION: /number= 1  
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NAME/KEY: exon  
LOCATION: 34092..34358  
OTHER INFORMATION: /gene= "AR"  
OTHER INFORMATION: /number= 2  
FEATURE:  
NAME/KEY: exon  
LOCATION: 33779..33963  
OTHER INFORMATION: /gene= "AR"  
OTHER INFORMATION: /number= 3  
FEATURE:  
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LOCATION: 33493..33591  
OTHER INFORMATION: /gene= "AR"  
OTHER INFORMATION: /number= 4  
FEATURE:  
NAME/KEY: exon  
LOCATION: 33297..33408  
OTHER INFORMATION: /gene= "AR"



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		FEATURE:							
		NAME/KEY: exon							
		LOCATION: complement (32959..33094)							
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		OTHER INFORMATION: /number= 6							
		FEATURE:							
		NAME/KEY: exon							
		LOCATION: complement (32569..32628)							
		OTHER INFORMATION: /gene= "AR"							
		OTHER INFORMATION: /number= 7							
		FEATURE:							
		NAME/KEY: exon							
		LOCATION: complement (32386..32468)							
		OTHER INFORMATION: /gene= "AR"							
		OTHER INFORMATION: /number= 8							
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		NAME/KEY: exon							
		LOCATION: complement (31894..32080)							
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		OTHER INFORMATION: /number= 9							
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		NAME/KEY: exon							
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		OTHER INFORMATION: /number= 10							
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		OTHER INFORMATION: /number= 11							
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		NAME/KEY: exon							
		LOCATION: complement (30816..31011)							
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		OTHER INFORMATION: /number= 12							
		FEATURE:							
		NAME/KEY: exon							
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		OTHER INFORMATION: /number= 13							
		FEATURE:							
		NAME/KEY: exon							
		LOCATION: complement (30187..30274)							
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		OTHER INFORMATION: /number= 14							
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		FEATURE:							
		NAME/KEY: exon							
		LOCATION: complement (29664..29856)							
		OTHER INFORMATION: /gene= "AR"							
		OTHER INFORMATION: /number= 16							
		US-08-814-095-7							
		Query Match							
		Best Local Similarity							
		Matches							
		151							

QY 331 AGGAAGTCTTCGAGCGCCGGCGAGAGGAAAGGGGGCAACGGGCTTTCCAGAGGCCCGCGC 390

Db 28445 AGGGAGACTCCGAGCGGGCGGCAGGCGCAAGGCCAACCCCTTAGCCCTCGCCGCGGGCG 28504

OY 391 CAGCAGGAAGTTGGCCA--GGGCACGGCTGTAGCGGAGCGGGGCGAGGGCTTTCTCAGAG 448

Db 28505 GAGCTCCGCGCTCGTAATAGAGCCCGCAGCGAGGCTACTGTGCAACGGCGAGGGAGA 28564

OY 449 CGCGGGCGAGCGCGCGCTTGAGAGGGCGCAGACCGSGTATAAAGAGCTCGTGGCTTGC 508

Db 28565 GAGGGGAGGGGAGGGAGGAGGGAGGGGCGGGCGCGGCGAGCATTTGGAGACTC 28624

OY 509 CCGGAGCAGCCGAGGT 524

Db 28625 CTCGGTCGTCGCCGT 28640

RESULT 13  
US-08-483-533-4  
Sequence 4, Application US/08483533  
Patent No. 6172017  
GENERAL INFORMATION:  
APPLICANT: Roizman, Bernard  
APPLICANT: Chou, Joany  
TITLE OF INVENTION: Method for Treating Tumorigenic  
TITLE OF INVENTION: Diseases  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
City: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,533  
FILING DATE: 07-MAR-95  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/419,853  
FILING DATE: 11-APR-95  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/861,233  
FILING DATE: 31-MAR-92  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, James P.  
REGISTRATION NUMBER: 28,491  
REFERENCE/DOCKET NUMBER: 28097/32742  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 595 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-483-533-4

Query Match 8.1%; Score 45.4; DB 3; Length 595;  
Best Local Similarity 46.2%; Pctd. No. 0.29; Indels 1; Gaps 1  
Matches 183; Conservative 0; Mismatches 212;

23 TGAGGCTGATGTCCTGGGCGCTCCACCTCCCCAGGCGCAGAGAGCCGCCACGAGAGC 82

Db 50 TCACGCCCCCTTCCGCGCCGCGCTCCGCTCCGCTGCGCCTCAACCGAGAGAC 109  
Qy 83 CCCAGTGGCCCGAGCTTGGCAAGCTCTGGGATCAAGGCAAGGACCAAGGAGCGAGAAC 142  
Db 110 CTGGCGGCGCTCGCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 169  
Qy 143 TGGCG 202  
Db 170 CCGCGACCG 229  
Qy 203 CTACCG 262  
Db 230 ACCCG 289  
Qy 263 GCGCGGCTGGGCTCG-CGAGACAAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 321  
Db 290 CACCTGCTGCTGGGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 349  
Qy 322 CTGCGCAAGAGAGTCTCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 381  
Db 350 CCG 409  
Qy 382 CG 417  
Db 410 TGCCTGGGCG 445

RESULT 14  
US-09-283-471A-4  
Sequence 4, Application US/09283471A  
Patent No. 6340673  
GENERAL INFORMATION:  
APPLICANT: Roizman, Bernard  
APPLICANT: Chou, Joany  
TITLE OF INVENTION: Method For Treating Tumorigenic Diseases  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/283,471A  
FILING DATE: 04-APR-1999  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/861,233  
FILING DATE: 31-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/419,853  
FILING DATE: 11-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/483,533  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, James P.  
REGISTRATION NUMBER: 28,491  
REFERENCE/DOCKET NUMBER: 27373/32742A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SPO. ID NO.: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 595 base pairs  
TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-283-471A-4  
Query Match  
Best Local Similarity 46.2%; Score 45.4; DB 4; Length 595;  
Matches 183; Conservative 0; Mismatches 212; Indels 1; Gaps 1;  
Qy 23 TGAAGCTGATGCTCCCTGCGCGCTTCACCTCCGAGCGAGAGGCGCCACAGAGAC 82  
Db 50 TCACGCCCCCTTCCGCGCCGCGCTCCGCTCCGCTGCGCCTCAACCGAGAGAC 109  
Qy 83 CCCAGTGGCCCGAGCTTGGCAAGCTCTGGGATCAAGGCAAGGACCAAGGAGCGAGAAC 142  
Db 110 CTGGCGGCGCTCGCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 169  
Qy 143 TGGCG 202  
Db 170 CCGCGACCG 229  
Qy 203 CTACCG 262  
Db 230 ACCCG 289  
Qy 263 GCGCGGCTGGGCTCG-CGAGACAAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 321  
Db 290 CACCTGCTGCTGGGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 349  
Qy 322 CTGCGCAAGAGAGTCTCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 381  
Db 350 CCG 409  
Qy 382 CG 417  
Db 410 TGCCTGGGCG 445

RESULT 15  
US-08-483-533-36  
Sequence 36, Application US/08483533  
Patent No. 6172047  
GENERAL INFORMATION:  
APPLICANT: Roizman, Bernard  
APPLICANT: Chou, Joany  
TITLE OF INVENTION: Method For Treating Tumorigenic  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,533  
FILING DATE: 07-MAR-95  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/419,853  
FILING DATE: 11-APR-95  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/861,233  
FILING DATE: 31-MAR-92  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, James P.  
REGISTRATION NUMBER: 28,491

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REFERENCE/DOCKET NUMBER: 28097/32742
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 1327 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-483-533-36

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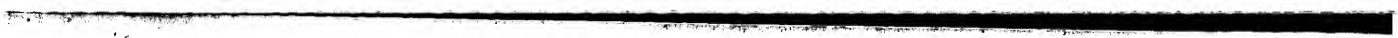
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Query Match      8.1%; Score 45.4; DB 3; Length 1327;
Best Local Similarity 46.2%; Pred. No. 0.3;
Matches 183; Conservative 0; Mismatches 212; Indels 1; Gaps 1;

QY 23 TGAAGGCTATGCTGCGCGCTCCACCTCCCGAGGCGCAAGAGCCCAAGAGAGC 82
DB 491 TCAAGCCCTTCGCTTCGCGCGCTCCACCTCCCGAGGCGCAAGAGAGC 550
QY 83 CCCCAATGCCCCGACGTTGCAAGGATCTGAGATCAGAGCAAGAGCAAGAGAGC 142
DB 551 CTGGCTGCGCTGCGCTGCGAGCGCGAGGAGAGAGAGAGAGAGAGAGAGAGC 610
QY 143 TGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 202
DB 611 CCGCGAGCCCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 670
QY 203 CTGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 262
DB 671 ACCCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 730
QY 263 GCGGAGGCTGCGCTCG-CGAGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 321
DB 731 CACTGTGTGTCTGAGGCTCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 790
QY 322 CTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 381
DB 791 CGGAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 850
QY 382 CGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 417
DB 851 TGCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 886

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Search completed: November 6, 2003, 16:18:18  
Job time : 75 secs





Db 61 CGCAGAGGCGCCACAGAGACCCCAAGTCCCGACGTTGCCAGCTGTGATCAGAG 120  
Qy 121 CAGGAGCAGAGGAGCCAGGAACTGCGCGCGCCCGCCCTGCGCTGCGGAGGAACT 180  
Db 121 CAGGAGCAGAGGAGCCAGGAACTGCGCGCGCCCGCCCTGCGCTGCGGAGGAACT 177  
Qy 181 CCCTACACAGAGGAGGAGCTCCCTCACCGCGCCAGCCCTGCGAGGGGGCGCGTGGGTC 240  
Db 178 CCCTACACAGAGGAGGAGCTCCCTCACCGCGCCAGCCCTGCGAGGGGGCGCGTGGGTC 236  
Qy 241 AACCCGCAAGAGAGAGTGGCGGGCGGGGCTGCGAGAGCAAAAGCCGGCCCTGCG 300  
Db 237 AACCCGCAAGAGAGTGGCGGGCGGGGCTGCGAGAGCAAAAGCCGGCCCTGCG 296  
Qy 301 CTCTCTCAGAGGAGCCCGACGCGCTGCGCAAGAGAACTCTGAGGCGCGGCGAGGAAAG 360  
Db 297 CTCTCTCAGAGGAGCCCGACGCGCTGCGCAAGAGAACTCTGAGGCGCGGCGAGGAAAG 356  
Qy 361 GGGCAGCGGCTTCCAGGGCGCGCGCGCGCGAGAGAACTTGGCCAGAGGCAAGCGCGTG 420  
Db 357 GGGCAGCGGCTTCCAGGGCGCGCGCGCGCGAGAGAACTTGGCCAGAGGCAAGCGCGTG 416  
Qy 421 AGCGGAGCGGAGGCTTCTCAGAGAGCGCGGCGAGGCGCGCTGAGAGGCGAGGA 480  
Db 417 AGCGGAGCGGAGGCTTCTCAGAGAGCGCGGCGAGGCGCGCTGAGAGGCGAGGA 476  
Qy 481 CCGGATATAGAGAGCTCGTGGCTTGGCCCGGCGAGCGCGAGGTTCCCGCGCGCCCGCA 540  
Db 477 CCGGATATAGAGAGCTCGTGGCTTGGCCCGGCGAGCGCGAGGTTCCCGCGCGCCCGCA 536  
Qy 541 GCGCCCGCGCC 551  
Db 537 GCGCCCGCGCC 547

## RESULT 2

US-10-059-579-120  
Sequence 120 Application US/10059579  
Publication No. US20030138783A1  
GENERAL INFORMATION:  
APPLICANT: THE JOHN HOPKINS UNIVERSITY SCHOOL OF MEDICINE  
APPLICANT: SUKUMAR, Saraswati  
APPLICANT: EVRON, Ella  
APPLICANT: DOOLEY, William C.  
APPLICANT: DAVIDSON, Nancy  
APPLICANT: FACKLER, Mary Jo.  
FILE REFERENCE: JHU1630-1  
CURRENT APPLICATION NUMBER: US/10/059,579  
CURRENT FILING DATE: 2003-02-03  
PRIOR APPLICATION NUMBER: US 09/771,357  
PRIOR FILING DATE: 2001-01-26  
NUMBER OF SEQ ID NOS: 136  
SOFTWARE: Patent in version 3.1  
SEQ ID NO 120  
LENGTH: 1794  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (359) (359)  
OTHER INFORMATION: n 1st any nucleotide  
US-10-059-579-120

Query Match 62.2%; Score 350.4; DB 12; Length 1794;  
Best Local Similarity 97.9%; Pred. No. 2,2e-66;  
Matches 366; Conservative 0; Mismatches 6; Indels 2; Gaps 1;  
Qy 190 CAGGAGAGTCCCTCAGAGCCCGGCGCAAGCCCTGCGAGGGGGCGCGTGGGCTCAGAGCCGCA 249  
Db 812 CAGGAGAGTCCCTCAGAGCCCGGCGCAAGCCCTGCGAGGGGGCGCGTGGGCTCAGAGCCGCA 869  
Qy 250 AGCGAGGTGCGGCGCGGGGTGGCTCGCGAGAGCAAAAGCGCGGCTGCTCTCAG 309

Db 870 AGCGAGGTGCGGCGCGGGGTGGGCTCGCGAGAGCAAAAGCGCGGCTGCTCTCAG 929  
Qy 310 AGGAGCCAGCGCTCTCAGAGAGAGTCTCAGAGGCGCGGCGAGAGAGGAGGAGCGAG 369  
Db 930 AGGAGCCAGCGCTCTCAGAGAGAGTCTCAGAGGCGCGGCGAGAGAGGAGGAGCGAG 989  
Qy 370 CTTCAGAGGCGCGCGCGCGCGAGAGTGGCGAGGAGCGCGGCGGAGGAGCGGAGCG 429  
Db 990 CTTCAGAGGCGCGCGCGCGCGAGAGTGGCGAGGAGCGCGGCGGAGGAGCGGAGCG 1049  
Qy 430 GCGAGGCTTCTCAGAGAGCGGCGGAGAGCGCGGCTGAGAGGCGAGAGCGGATTA 489  
Db 1050 GCGAGGCTTCTCAGAGAGCGGCGGAGAGCGCGGCTGAGAGGCGAGAGCGGATTA 1109  
Qy 490 AGAGCTCTGCTGCTTGGCCCGGAGCGCGAGGTTCCCGCGCGCCCGAGCCCGCGG 549  
Db 1110 AGAGCTCTGCTGCTTGGCCCGGAGCGCGAGGTTCCCGCGCGCCCGAGCCCGCGG 1169  
Qy 550 CCATGAAGCTCGCC 563  
Db 1170 CCATGAAGCTCGCC 1183

## RESULT 3

US-10-027-632-196114/c  
Sequence 196114 Application US/10027632  
Publication No. US20030204075A9  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
FILE REFERENCE: 108827, 129  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
Polymorphisms in the Human Genome  
CURRENT APPLICATION NUMBER: US/10/027,632  
CURRENT FILING DATE: 2002-04-30  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 196114  
LENGTH: 533  
TYPE: DNA  
ORGANISM: Human  
US-10-027-632-196114

Query Match 25.5%; Score 143.6; DB 12; Length 533;  
Best Local Similarity 94.8%; Pred. No. 3.7e-22;  
Matches 181; Conservative 0; Mismatches 5; Indels 5; Gaps 3;

Qy 1 CCGCGCGGAGAGCGCGCGGAGTGAAGGCTGATGCTGCGGCTGCGCTCAGCTCCAGG 60  
Db 189 CCGCGCGGAGAGCGCGCGGAGTGAAGGCTGATGCTGCGGCTGCGCTCAGCTCCAGG 130  
Qy 61 CCGAGAGGCGCCCGCAGAGAGAGTGGCGGCGCGGCTGCGAGAGTGGAGTCAAGG 120  
Db 129 CCGAGAGGCGCCCGCAGAGAGAGTGGCGGCGCGGCTGCGAGAGTGGAGTCAAGG 70  
Qy 121 CAGAGAGAGAGAGAGTGGCGGCGCGGCTGCGAGAGTGGAGTCAAGG 179  
Db 69 CAGAGAGAGAGAGAGTGGCGGCGCGGCTGCGAGAGTGGAGTCAAGG 14

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QY 180 TCCCTCACCNG 190
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      13 TCCCTCACCNG 3

RESULT 4
US-10-027-632-196114/c
; Sequence 196114, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Mang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 196114
; LENGTH: 533
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-196114

Query Match      25.5%; Score 143.6; DB 13; Length 533;
Best Local Similarity 94.8%; Pred. No. 3.7e-22;
Matches 181; Conservative 0; Mismatches 5; Indels 5; Gaps 3;

QY 1 CGGCGGAGGAGGCGGCGGAGTGTGAGGCTGATCTCTCCCTGCGGCTTCACCTTCCCGAG 60
DB 189 CGGCGGAGGAGGCGGCGGAGTGTGAGGCTGATCTCTCCCTGCGGCTTCACCTTCCCGAG 130
QY 61 CGGAGAGGAGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120
DB 129 CGGAGAGGAGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 70
QY 121 CA-GGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 179
DB 69 CAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 14

QY 180 TCCCTCACCNG 190
      |||||
      13 TCCCTCACCNG 3

RESULT 5
US-10-237-435-6
; Sequence 6, Application US/10237435.
; Publication No. US20030124580A1
; GENERAL INFORMATION:
; APPLICANT: Walker, Michael G.
; APPLICANT: Murty, Lynn E.
; APPLICANT: Spiro, Peter A.
; TITLE OF INVENTION: LONG SURFACTANT MOLECULES
; FILE REFERENCE: PB-0019 US
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US/10/237,435
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 60/317,822
; PRIOR FILING DATE: 09-07-2001
; NUMBER OF SEQ ID NOS: 9
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; SOFTWARE: PERL Program
; SEQ ID NO: 6
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030124580A1 242745.1
US-10-237-435-6

Query Match      22.7%; Score 128; DB 14; Length 561;
Best Local Similarity 100.0%; Pred. No. 7.6e-19;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 436 GCTTCTCAGAGGCGGCGGAGGCGGCGGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 495
DB 1 GCTTCTCAGAGGCGGCGGAGGCGGCGGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 60
QY 496 CTGCTGAGGCTTGTGCGGCGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 555
DB 61 CTGCTGAGGCTTGTGCGGCGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120
QY 556 AGCTCGCC 563
DB 121 AGCTCGCC 128

RESULT 6
US-10-210-951-27
; Sequence 27, Application US/10210951
; Publication No. US20030170228A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Masters, Scott A.
; APPLICANT: Pan, James
; APPLICANT: Pitti, Robert M.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stone, Donna M.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR
; FILE REFERENCE: P293191.1
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/014699
; PRIOR FILING DATE: 1996-04-01
; PRIOR APPLICATION NUMBER: 60/026943
; PRIOR FILING DATE: 1996-09-23
; PRIOR APPLICATION NUMBER: 60/059121
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/062037
; PRIOR FILING DATE: 1997-10-10
; PRIOR APPLICATION NUMBER: 60/063755
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063045
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/06511
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066772
; PRIOR FILING DATE: 1997-11-24
; REMAINING PRIOR APPLICATION DATA REMOVED - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 258
; SEQ ID NO: 27
; LENGTH: 569
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TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-210-951-27

Query Match  
Best Local Similarity 100.0%; Score 90; DB 12; Length 569;  
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 474 GCGAGACCGGGTATTAAGAGCTCTGTCGCTTGCCCGGAGCCGCGAGTTCCCGCGC 533  
Db 1 GCGAGACCGGGTATTAAGAGCTCTGTCGCTTGCCCGGAGCCGCGAGTTCCCGCGC 60

Qy 534 GCGCGAGCGCGCGCGCGCATGAAGCTCGCC 563  
Db 61 GCGCGAGCGCGCGCGCGCATGAAGCTCGCC 90

RESULT 7

US-10-211-884-27  
Sequence 27, Application US/10211884  
Publication No. US20030175900A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Goddard, Audrey  
APPLICANT: Goddard, Paul J.  
APPLICANT: Guiney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Marsters, Scot A.  
APPLICANT: Pan, James  
APPLICANT: Pizzi, Robert M.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Smith, Victoria  
APPLICANT: Stone, Donna M.  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR  
FILE REFERENCE: P2931R1C1  
CURRENT APPLICATION NUMBER: US/10/211,884  
PRIORITY FILING DATE: 2002-08-02  
PRIOR APPLICATION NUMBER: 60/014699  
PRIOR FILING DATE: 1996-04-01  
PRIOR APPLICATION NUMBER: 60/026943  
PRIOR FILING DATE: 1996-09-23  
PRIOR APPLICATION NUMBER: 60/059121  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/059352  
PRIOR FILING DATE: 1997-09-19  
PRIOR APPLICATION NUMBER: 60/062037  
PRIOR FILING DATE: 1997-10-10  
PRIOR APPLICATION NUMBER: 60/063755  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063045  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063046  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/066511  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/066772  
PRIOR FILING DATE: 1997-11-24  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 258  
SEQ ID NO 27  
LENGTH: 569  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-211-884-27

Query Match  
Best Local Similarity 100.0%; Score 90; DB 12; Length 569;  
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 474 GCGAGACCGGGTATTAAGAGCTCTGTCGCTTGCCCGGAGCCGCGAGTTCCCGCGC 533

Db 1 GCGAGACCGGGTATTAAGAGCTCTGTCGCTTGCCCGGAGCCGCGAGTTCCCGCGC 60  
Qy 534 GCGCGAGCGCGCGCGCGCATGAAGCTCGCC 563  
Db 61 GCGCGAGCGCGCGCGCGCATGAAGCTCGCC 90

RESULT 8

US-09-989-722-407  
Sequence 407, Application US/09989722  
Patent No. US20020072067A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
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APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C63  
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APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
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APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
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/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Botstein, David
/ APPLICANT: Deamoys, Luc
/ APPLICANT: Baton, Dan L.
/ APPLICANT: Perrara, Napoleone
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PRIOR FILING DATE: 1998-07-09

Query Match 16.0%; Score 90; DB 9; Length 570;  
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QY 534 GCGCGAGCGCGCGCGCGCGATGAAGTGGC 563  
DB 61 GCGCGAGCGCGCGCGCGCGATGAAGTGGC 90

RESULT 11  
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Sequence 407, Application US/09989727  
Patent No. US20020072497A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Denoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerbasi, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Guiney, Austin L.  
APPLICANT: Kijavini, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tamas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same  
FILE REFERENCE: P27301165  
CURRENT APPLICATION NUMBER: US/09/989,727  
PRIOR FILING DATE: 1997-06-16  
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Sequence 407, Application US/09989731
Patent No. US20020103125A1
GENERAL INFORMATION:
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APPLICANT: Ashkenazi, Avi J.
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APPLICANT: Desnoyers, Luc
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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Query Match 16.0%; Score 90; DB 10; Length 570;  
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QY 474 GCGAGACCGCGGTATTAAGAGCTTGCGCTTGGCCCGGCGAGCCGCAAGTTCCCGGCC 533  
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RESULT 13  
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Patent No. US20020123463A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David

APPLICANT: Desnoyers, Ildic  
 APPLICANT: Factor, Dan L.  
 APPLICANT: Fong, Shaomee  
 APPLICANT: Gerber, Hanspeter  
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; APPLICANT: Botstein, David
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Maranabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
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; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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APPLICANT: Desnoyers, Luc  
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APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerlitsen, Maty E.

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 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 APPLICANT: Zhang, Zemin  
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OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	86.6	15.4	982	13	BX415111	BX415111 BX415111
2	81.2	14.4	935	29	CNS006XK	AL066051 Drosophila
3	81	14.4	982	13	BX415111	BX415111 BX415111
4	78	13.9	1313	29	AG032885	AG032885 Pan trogl

5	77.6	13.8	1203	29	CNS015Y4	AL106054 Drosophila
6	77.2	13.7	925	29	CNS0091P	AL1053013 Drosophila
7	77.2	13.7	1281	12	BG852363	BG852363 1024034A0
8	74.8	13.3	949	29	AG043499	AG043499 Pan trogl
9	73.6	13.1	1065	13	BO681076	BO681076 Drosophila
10	73.6	13.1	1101	29	CNS0175Y	AL106431 SEMMCO06
11	72.6	13.0	1040	12	BG786331	BG786331 Drosophila
12	72.6	12.9	1201	13	BX405071	BX405071 Pan trogl
13	72.4	12.9	1085	29	AG152796	AG152796 Pan trogl
14	72.4	12.9	1085	29	AG152796	AG152796 Pan trogl
15	72.2	12.8	1143	13	BX442207	BX442207 Drosophila
16	72.2	12.8	1100	29	CNS017KO	AL106855 Drosophila
17	72.2	12.8	1100	29	CNS017KO	AL106855 Drosophila
18	71.6	12.7	888	12	BG809572	BG809572 mgc1001A
19	71.4	12.6	970	29	CNS010C9	AL109878 Drosophila
20	71.2	12.6	1030	29	AG126333	AG126333 Pan trogl
21	71.2	12.6	1030	29	AG126333	BZ690979 MO37E05 G
22	70.8	12.6	1144	13	BX415926	BX415926 Drosophila
23	70.8	12.6	1144	13	BX415926	AL1053013 Drosophila
24	70.4	12.5	925	29	CNS0091P	BM547577 AGENCOURT
25	70.4	12.5	925	29	CNS0091P	BM547577 AGENCOURT
26	70.4	12.5	925	29	CNS0091P	BM547577 AGENCOURT
27	70.4	12.5	925	29	CNS0091P	BM547577 AGENCOURT
28	69.6	12.4	932	29	CNS00720	AL066742 Drosophila
29	69.6	12.4	932	29	CNS00720	AL066742 Drosophila
30	69.6	12.4	1201	13	BX405071	BX405071 AGENCOURT
31	69.6	12.4	1273	12	BM542096	BM542096 AGENCOURT
32	69.4	12.3	845	13	BO721449	BO721449 AGENCOURT
33	69.4	12.3	1073	13	BO721449	BO721449 AGENCOURT
34	69.2	12.3	924	13	BO721449	BO721449 AGENCOURT
35	69.2	12.3	1581	29	AG052690	AG052690 Pan trogl
36	69.2	12.3	776	29	CNS010YK	AL1099332 Drosophila
37	69.2	12.3	803	29	AG162326	AG162326 Pan trogl
38	68.4	12.1	935	29	CNS006XK	BO951911 AGENCOURT
39	68.4	12.1	1052	13	BO951911	BO951911 AGENCOURT
40	68.4	12.1	1184	12	AG187356	AG187356 SP 1008 B
41	68.2	12.1	822	28	AG187356	AG187356 SP 1008 B
42	68.2	12.1	873	13	BO721449	BO721449 AGENCOURT
43	68.2	12.1	1073	13	BO721449	BO721449 AGENCOURT
44	67.8	12.0	1542	29	AG032943	AG032943 Pan trogl
45	67.6	12.0	1200	13	BX456467	BX456467 Drosophila

ALIGNMENTS

RESULT 1  
BX415111/c 982 bp mRNA EST 15-MAY-2003  
LOCUS BX415111 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP004Y120  
DEFINITION 5-PRIME. mRNA sequence.  
ACCESSION BX415111  
VERSION BX415111.1 GI:30765470  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1. (bases 1 to 982)  
AUTHORS Mammals; Metazoa; Chordata; Vertebrata; Euteleostomi;  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished  
COMMENT Genoscope Centre National de Sequencage  
BP 191 91006 Evry cedex - France  
Email: seqre@genoscope.cns.fr Web: www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com URL:  
http://fulllength.invitrogen.com/Invitrogen Corporation 1600  
Faraday Avenue Genoscope sequence ID: CS0CAP004BBI00P1.  
Location/Qualifiers  
Loc982  
1..982  
/organism="Homo sapiens"

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/mo1_type="mRNA"
/db_xref="taxon:9606"
/c1one="CS0CAP004Y120"
/r1ssue_type="THYMUS"
/c1one_l1b="Homo sapiens THYMUS"
/note="Vector: pCMVSPORT 6, 1st strand cDNA was primed
with a NotI-Oligo(dT) primer, 5' end enriched,
double-strand cDNA was digested with NotI and
cloned into the NotI and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalised."
BASE COUNT
ORIGIN
177 a 257 c 333 g 18 t 207 others

```

[illegible]

RESULT 2			
CNS006XK LOCUS		935 bp DNA linear	GSS 03-JUN-1998
DEFINITION		Drosophila melanogaster genome survey sequence T7 end of BAC # BAIRL1N09 of RGC1-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.	
ACCESSION VERSION		AL066051 AL066051.1 GI:4945019 GSS.	
SOURCE ORGANISM		Drosophila melanogaster (fruit fly)	
REFERENCE TITLE		Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephyroidea; Drosophilidae; Drosophila.	
AUTHORS JOURNAL		Genoscope. Direct Submission Submitted (02-JUN-1998) Genoscope - Centre National de Séquençage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr Web : www.genoscope.cns.fr ) Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila	
COMMENT			

melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BdpD Drosophila melanogaster BAC library was prepared by Kazunyo Oosawa and Aaron Mammoser in Pierer de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCL-98 and was constructed in Buffalo, BACI digestion of Drosophila DNA provided by the BDP from the 18ogenic strain y2; cn bw sp, the same strain used for the BDP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

Location/Qualifiers  
1..935

BASE COUNT	257 a	170 c	162 g	96 t	250 others
ORIGIN					

Query Match	14.4%	Score 81.2;	DB 29;	Length 935;
Best Local Similarity	32.9%	Pred. No. 1;	5e-05;	

[illegible]

538 CSCTGTCCTSSCTSCMCSCTGTGCKCGCGCGCTSCSSSSCCSBBSYSTCSCIBCTK

[illegible]

26 CGGGGCGGCGCTCGGCGGAGACAAAGGCGGCGGCTGCTCTCTCAAGGGGCCCCAGCGGCT

325 GCCAAGAGGAGTCTTCGAGGCCGGGCGAGGAGGAGGGGCACGSGCTTCCCAAGGCCCGG

385 CGGCCGCGCAGGAAGTTGGACAGGCACCCCCCCCCTTCCGCTTC

[illegible]

838 SGGCGCGSSCCSGCGCGSGGSSCCSGGCGGAGACCGGCTATAGAGAGCTCGTGCC

505 TTGCCCCGCGACCGGAGTTCCCGCGCGCCCCG 539

BSIII T 3 532

[illegible][illegible]

ORGANISM	SOURCE
Homo sapiens (human)	ES1.
Homo sapiens	
Homo sapiens	

REFERENCE  
Lukavý, J. 1982. Mammalia; Euteria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 982).  
Euteleostom  
Chordata; Craniata; Vertebrata; Euteleostom  
Metazoa; Chordata; Craniata; Vertebrata; Euteleostom  
Euteleostom

unpublished

COMMENT  
Contact: Genoscope

Genoscope - Centre National de Sequencage  
BP 191 91006 Evry cedex - France  
Email: seque@genoscope.cns.fr, Web: www.genoscope.cns.fr  
Library was constructed by life technologies, a division of  
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com URL:  
http://fulllength.invitrogen.com/Invitrogen Corporation 1600  
Faraday Avenue Genoscope sequence ID: CS0CAP004BEI00P1.

## FEATURES

source

1. .982  
/organism="Homo sapiens"  
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/db\_xref="taxon:9606"  
/clone="CS0CAP004Y120"  
/issue\_type="THYMUS"  
/note="Vector: PCWVSPORT 6; 1st strand cDNA was primed  
with a NotI-oligo (gt) primer. Five prime end enriched,  
double-strand cDNA was digested with Not I and cloned into  
the Not I and EcoRV sites of the PCWVSPORT 6 vector.  
Library was not normalized."  
Location/Qualifiers  
177 a 257 c 323 g 18 t 207 others

## BASE COUNT

Query Match 14.4%; Score 81; DB 13; Length 982;  
Best Local Similarity 32.7%; Pred. No. 1.6e-05;  
Matches 145; Conservative 97; Mismatches 202; Indels 0; Gaps 0;

100 GCCACGCTGTGATCAGAGCAGGACCCAGGAGCCAGAACTGCGCCGCCGCC 159  
129 SSSGAGGAGSS 188  
160 TGCCCTGAGCGGAGGAGGAGCTCCCTCAGGAGGAGGAGCTCCCTCAGG 219  
189 KCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 248  
220 TGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 279  
249 CCC 308  
280 GGAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 339  
309 GCGSSSCGSGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 368  
340 TCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 399  
369 CCGSSSCGSGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 428  
400 GTTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 459  
429 CCGSSSCGSGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 488  
460 CCGGCGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 519  
489 GGGGCGSSCGSGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 548  
520 CAGGTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 548  
549 GCCCCCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 572

RESULT 4  
AG032885 1313 bp DNA linear GSS 01-NOV-2001  
LOCUS Pan troglodytes DNA, clone: PTB-007M05.F, genomic survey sequence.  
DEFINITION AG032885  
ACCESSION AG032885.1 GI:16559758  
VERSION  
KEYWORDS  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM  
REFERENCE  
AUTHORS  
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,

Totoki, Y., Matanabe, H. and Sakaki, Y.  
BAC end sequences of library PTB  
Unpublished  
2 (bases 1 to 1313)  
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,  
Totoki, Y., Matanabe, H. and Sakaki, Y.  
Direct Submission  
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
1-7-22 Suicho-chou, Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan  
(E-mail: chimbes@sc.riken.go.jp, URL: http://bgp.gsc.riken.go.jp/,  
Tel: 81-45-503-9111, Fax: 81-45-503-9170)  
Clones are derived from the chimpanzee BAC library PTB. This BAC end  
was generated during the R&D process and may have higher chance of  
clone tracking errors.

## COMMENT

Sequencing: -21M13  
LIBRARY  
Vector : pKS145  
R.Site 1 : SacI  
R.Site 2 : SacI

## FEATURES

source

1. .1313  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
/clone="PTB-007M05.F"  
/sex="male"  
/cell\_type="lymphoblast"  
/clone\_id="PTB Chimpanzee Male BAC Library"  
BASE COUNT 65 a 389 c 502 g 132 t 225 others

Query Match 13.9%; Score 78; DB 29; Length 1313;  
Best Local Similarity 43.3%; Pred. No. 5.8e-05;  
Matches 231; Conservative 0; Mismatches 303; Indels 0; Gaps 0;

27 GCTGATGCTGCTGAGGCTCTCACTCCAGGAGGAGGAGGAGGAGGAGGAGG 86  
412 GCGGCG 471  
87 AGTGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 146  
472 GCGGCG 531  
147 CCGGCG 206  
532 GCGGCG 591  
207 CCGGCG 266  
592 GCGGCG 651  
267 GGTGAGGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 326  
652 CCGGCG 711  
327 CAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 386  
712 GCGGCG 771  
387 GCGGCG 446  
772 CCGGCG 831  
447 AGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 506  
832 CCGGCG 891  
507 GCGGCG 560  
892 GCGGCG 945

[illegible]

	RESULT: 6
CNS0091P/c	
LOCUS	Drosophila melanogaster genome survey sequence 1c73 end of BAC #
DEFINITION	BACRP19D6 of RPCT-98 library from Drosophila melanogaster (fruit fly), genomic DNA sequence.
ACCESSION	AL053013.1 GI:4934461
VERSION	GSS.
KEYWORDS	Drosophila melanogaster (fruit fly)
SOURCE ORGANISM	Drosophila melanogaster (Insecta; Pterygota; Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Epiphytoidae; Drosophilidae; Drosophila).
REFERENCE	1 (bases 1 to 925) Genoscope.
AUTHORS	Direct Submission
TITLE	Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
JOURNAL	BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr Web : www.genoscope.cns.fr)
COMMENT	determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Ososawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCT-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES	location/Qualifiers
source	1..925
	/organism="Drosophila melanogaster"
	/mol_type="genomic DNA"
	/db_xref="taxon:7227"
	/clone="BACRP19D6"
	/clone_11b="RPCT-98"
	/note="end : 1c73"
BASE COUNT	120 a 61 c 61 g 172 t 511 others
ORIGIN	
Query Match	13.7%; Score 77.2; DB 29; Length 925;
Best Local Similarity	13.3%; Pred. No. 8.1e-05;
Matches	48; Conservative 185; Mismatches 128; Indels 0; Gaps 0;
Oy	178 GCCTCCATCAAGGAGAAGTCCCTCCATCCAGCCGCACCGCAGCCGTGAGAGCAAAGCCGGCCG 237
Db	:::     :::     :::     :::     :::     :::     :::     :::     :::
Oy	918 SCGCSBSBCSSSMSTSSNSBSCSSBSBSSSTRSMSSBSBSSSSSSSSSSSSSSSSSSSSSSSSA 859
Db	:::     :::     :::     :::     :::     :::     :::     :::
Oy	238 GTTCAGCCGGAAGAAAGTGCC 297
Db	:::     :::     :::     :::     :::     :::     :::     :::
Oy	858 CTKCMASBSCGCCCGMAABCMCMSSSSSSCCGSASAGVVRVASGAKRGKSGSGASASH 799
Db	:::     :::     :::     :::     :::     :::     :::     :::
Oy	298 TGCCTCTCTCAAGAGGCCCAAGCGCCTCCACAAGAAGTCTCTCAAGCGCCGGAGAGGA 357
Db	:::     :::     :::     :::     :::     :::     :::     :::
Oy	798 SSSASCBSSSSSCASASASSSSSSASSSSRGGAGAGSASSSSSSSSSSSSSSSSSSSSSSAGSV 739
Db	:::     :::     :::     :::     :::     :::     :::     :::
Oy	358 AGGGGCAAGGCGTTCCAGAGGCCCGCGGCGCGCACAGAGAAATTGGCCAGGCAAGCGCC 417
Db	:::     :::     :::     :::     :::     :::     :::     :::



Db 738 SSASSSSSSSSSSVASMSCSBSSSSASASSSSSSSASCSGCTTWSGSC 679

Qy 418 GTAGCGGAGCGGAGCGCTTCTCAGACCGCGGCGGCGCTGAGGAGCA 477

Db 678 STASMSAARSSSSSSSSSSSSSSASSSSSSSSSSSSSSSGACGSGSGG 619

Qy 478 GAGCGGATTAAGAGCTCTGCGCTTCCCGGCGGAGGATCCCGCGGCC 537

Db 618 SGGSASSSGWSVSSSGRSGSGGCGGCGGSSSGSGSGSGSGSGSGGCMCNC 559

Qy 538 C 538

Db 558 S 558

RESULT 7  
BG852363/c 1281 bp mRNA linear EST 29-MAY-2001  
LOCUS 1024034A03.y2 C. reinhardtii CC-1690, normalized, lambda Zap II  
DEFINITION Chlamydomonas reinhardtii cDNA, mRNA sequence.  
ACCESSION BG852363  
VERSION BG852363.1 GI:14233547  
KEYWORDS EST.  
SOURCE Chlamydomonas reinhardtii  
ORGANISM Chlamydomonas reinhardtii  
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;  
Chlamydomonadaceae; Chlamydomonas.  
REFERENCE 1 (bases 1 to 1281)  
Grossman, A., Davies, J., Federspiel, N., Harris, E., Lefebvre, P.,  
McDermott, J. P., Silflow, C., Stern, D. and Surzycki, R.  
Analyses of the Chlamydomonas reinhardtii Genome: A Model,  
Universal System for Analyzing Gene Function and Regulation in  
Unpublished  
Vascular Plants; project phase 2  
JOURNAL  
COMMENT Contact: Charles Hauser  
DCMB Box 91000  
Duke University  
Durham, NC 27708-1000  
Tel: 919 613 8159  
Fax: 919 613 8177  
Email: chause@duke.edu

FEATURES  
source location/Qualifiers  
1..1281  
/organism="Chlamydomonas reinhardtii"  
/mol\_type="mRNA"  
/strain="CC-1690 wild type mt+ 21gr"  
/db\_xref="taxon:3055"  
/clone\_lib="C. reinhardtii CC-1690, normalized, lambda Zap II"  
/note="Vector: pBluescript II SK-; Site 1: EcoRI; Site 2: XhoI; This library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells grown to mid-log phase in RAP (acetate-containing) medium in the light, RAP medium in the dark, HS (minimal) medium in ambient levels of CO2 and HS medium bubbled with 5% CO2. PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda Zap II (Stratagene) in the EcoRI (5') and XhoI (3') sites. pBluescript II SK- plasmids were excised from the lambda Zap clones by superinfection with ExSist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al (1996) Genome Research 6: 791-806."

BASE COUNT 30 a 697 c 456 g 15 t 83 others

ORIGIN

Query Match 13.7%; Score 77.2; DB 12; Length 1281;  
Best Local Similarity 45.8%; Pred. NO. 8.2e-05;  
Matches 250; Conservative 0; Mismatches 294; Indels 2; Gaps 1;

Qy 1 CGCGCGGAGGAGCGGCGGCGGAGTGAGGCTGATCGTCCCTGCGGCTCCACTCCCGCAG 60

Db 1068 CCAGNGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1009

Qy 61 CGCAGAGCGCGCCACGAGAGACCCCGAGTGCCGACGTTGCGACGCTGCGATCAGAG 120

Db 1008 CCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 949

Qy 121 CAGGAGCAGGAGGACGAGAACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180

Db 948 GGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 889

Qy 181 CCGTACCGNAGAGGAAGTCCCTTCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240

Db 888 CCG 829

Qy 241 AGACCGCAAAGGAGAGTGTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300

Db 828 GCG 769

Qy 301 CTCTCTCAG--AGGCG 358

Db 768 CGGGGNGCGCGCGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 709

Qy 359 GGGGCG 418

Db 708 GCGGCG 649

Qy 419 TGAGCGGAGCGGCG 478

Db 648 CG 589

Qy 479 GACCGGATTAAGAGCTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 538

Db 588 GCG 529

Qy 539 GAGCGG 544

Db 528 GCGCGG 523

RESULT 8  
AC043499/c 949 bp DNA linear GSS 01-NOV-2001  
LOCUS Pan troglodytes DNA, clone: PTB-021N08.F, genomic survey sequence.  
DEFINITION AG043499  
ACCESSION AG043499.1 GI:16572224  
VERSION  
KEYWORDS GSS.  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes (chimpanzee)  
REFERENCE 1  
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,  
Totoki, Y., Matanabe, H. and Sakaki, Y.  
BAC end sequences of Library PTB  
Unpublished  
2 (bases 1 to 949)  
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,  
Totoki, Y., Matanabe, H. and Sakaki, Y.  
Direct Submission  
Submitted (02-AUG-2001) Aao Fujiyama, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC), Japan  
(E-mail: chimp@res.riken.go.jp, url: http://hsp.gsc.riken.go.jp/,  
Tel: 81-45-503-9111, Fax: 81-45-503-9170).  
Clones are derived from the chimpanzee BAC library PTB. This BAC end  
was generated during the Rad process and may have higher chance of  
clone tracking errors.  
PRIMERS  
Sequencing: -21M13  
LIBRARY  
Vector : pKS145  
R.Site 1 : SacI  
R.Site 2 : SacI  
Location/Qualifiers  
1..949

FEATURES  
source





Db 875 SSSSVVSAASASSSSSASASMAVAAAAVAVSVASVSSSSSSSSSSASVVSA 934  
 QY 424 GAGCGCGGAGGCTTTCTCAGAGAGCGCGGCGGCGCTGAGAGGCGGAGACCG 483  
 Db 935 SVASASVSSSSSSSVSTSSASVSVASVMSVSSASSSSSSVSVSAVAAASAA 994  
 QY 484 GGTATTAAGAGCTTCGTGCTTGGCCCGGCGAGCCGCAAGTTCCCGCGCGCCGAGCC 543  
 Db 995 AAAAAAASASVAVSVASVSSSSSSSSSSSSSSSVSVSSSSSVSVSSSS 1054  
 QY 544 CCC 546  
 Db 1055 VSV 1057

RESULT 12  
 BG786331/c 1040 bp mRNA linear EST 20-MAY-2001  
 LOCUS SEAMC006288 Sea urchin primary mesenchyme cell cDNA library  
 DEFINITION Strongylocentrotus purpuratus CDNA clone PC\_0028\_A2\_g12\_MR 5', mRNA  
 sequence.  
 ACCESSION BG786331.1 GI:14157344  
 VERSION EST  
 KEYWORDS Strongylocentrotus purpuratus  
 SOURCE Strongylocentrotus purpuratus  
 ORGANISM Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
 Echinoidea; Euechinoidea; Echinacea; Echinoida;  
 Strongylocentrotidae; Strongylocentrotus.  
 1 (bases 1 to 1040)  
 Zhu,X., Mahalax,G., Illies,M.R., Cameron,R.A., Davidson,E.H. and  
 Ettensohn,C.A.  
 A large scale analysis of mRNAs expressed by primary mesenchyme  
 cells of the sea urchin embryo  
 Development 128 (13), 2615-2627 (2001)  
 21384984  
 11493577  
 CONTACT: Ettensohn CA  
 Dept. Biol. Sci.  
 Carnegie Mellon University  
 4400 Fifth Avenue, Pittsburgh, PA 15213, USA  
 Tel: +1 412 268 15849  
 Email: ettensohn@andrew.cmu.edu.  
 Location/Qualifiers  
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 /mol\_type="mRNA"  
 /db\_xref="taxon:7668"  
 /clone="PC\_0028\_A2\_g12\_MR"  
 /tissue\_type="embryo"  
 /cell\_type="primary mesenchyme cells"  
 /lab\_host="E.coli"  
 /clone\_lib="Sea urchin primary mesenchyme cell cDNA  
 library"  
 /note="Vector: pSPORT1, Site\_1: NotI, Site\_2: SalI; oligo  
 dt priming from poly A+ RNA, directionally cloned"  
 499 c 472 g 44 t 5 others

BASE COUNT 20 a  
 ORIGIN

Query Match 13.0%; Score 73.2; DB 12; Length 1040;  
 Best Local Similarity 46.9%; Pred. No. 0.00044;  
 Matches 259; Conservative 0; Mismatches 290; Indels 3; Gaps 1;

QY 7 GGAAGAGCGCGCGGAGTGAGGCTGATGTCCTGAGCGCTCACTCCCGAGGCGAGA 66  
 Db 872 GCAC 813  
 QY 67 AGGCGCCAGAGAGCCCGCAGTCCGAGCTTCCCGAGTCTGAGTCAAGAGCGAGGA 126  
 Db 812 GCAC 753  
 QY 127 CCAGGAGCCAGAGACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCA 186

Db 752 GAGCG 693  
 QY 187 CUNAGAGGAAGCTCCCTCACCACCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 246  
 Db 692 GCG 633  
 QY 247 CAAGGAGAGTCCG 306  
 Db 632 GCG 573  
 QY 307 CAGAGGCG 366  
 Db 572 CCG 513  
 QY 367 GGGCTTCCAGAGCG 426  
 Db 512 GGGCG 453  
 QY 427 GCGCGAGAGCTTTCTCAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 486  
 Db 452 GCG 394  
 QY 487 ATAGAAGCTGATGCTTGCCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 546  
 Db 393 --CG 336  
 QY 547 GCGCCATGAGC 558  
 Db 335 CG 324

RESULT 13  
 BX405071 1201 bp mRNA linear EST 13-MAY-2003  
 LOCUS BX405071 Homo sapiens B CELLS (RAMOS CELL LINE) Homo sapiens cDNA  
 DEFINITION clone CS0D006Y06 3-PRIME, mRNA sequence.  
 ACCESSION BX405071  
 VERSION BX405071.1 GI:30648111  
 KEYWORDS EST  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 1201)  
 Li,W.B., Gruber,C., Jessee,J. and Poljates,D.  
 Full-length cDNA libraries and normalization  
 Unpublished  
 CONTACT: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 Library was constructed by Life Technologies, a division of  
 Invitrogen. This sequence belongs to sequence cluster 10245..r For  
 more information about this cluster, see  
 http://www.genoscope.cns.fr/  
 cgi-bin/custer.cgi?seq=CS0AG006BD03NP1&cluster=10245..r. Contact :  
 Feng Liang Email : fliang@life.techn.com URL :  
 http://fulllength.invitrogen.com/invitrogen Corporation 1600  
 Faraday Avenue Genoscope sequence ID : CS0AG006BD03NP1.  
 Location/Qualifiers  
 1..1201  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="CS0D006Y06"  
 /tissue\_type="B CELLS (RAMOS CELL LINE)"  
 /cell\_line="RAMOS CELL LINE"  
 /clone\_lib="Homo sapiens B CELLS (RAMOS CELL LINE)"  
 /note="Vector: pCMVSPORT\_6, 1st strand cDNA was primed  
 with a NotI-oligo(dT) primer. Five prime end enriched,  
 double-strand cDNA was digested with Not I and cloned into  
 the Not I and EcoRV sites of the pCMVSPORT 6 vector.  
 Library was not normalized."

FEATURES  
 source

BASE COUNT 62 a 448 c 462 g 5 t 224 others  
 ORIGIN  
 Query Match 12.9%; Score 72.6; DB 13; Length 1201;  
 Best Local Similarity 35.4%; Pred. No. 0.00058;  
 Matches 196; Conservative 87; Mismatches 268; Indels 3; Gaps 1;

1 CGGCGCGGAGGAGGCGCGGAGTGAGGCTGATGTCCTCGGCGCTCCACCTCCCGCAG 60  
 555 MCGCGCGGCG 614  
 61 CGGAGAGGAGGCG 120  
 615 CGGAGCG 674  
 121 CAGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 177  
 675 GCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 734  
 178 GCTCCTCTCACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 237  
 735 CGGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 794  
 238 GTCGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 297  
 795 GCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 854  
 298 TGCCTCTCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 357  
 855 CGGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 914  
 358 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 417  
 915 GCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 974  
 418 GTGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 477  
 975 GCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1034  
 478 GAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 537  
 1035 MCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1094  
 538 CGAGCG 551  
 1095 CGBCAVCAAMGCC 1108

RESULT 14  
 AG080291/c 937 bp DNA linear GSS 03-NOV-2001  
 LOCUS AG080291 Pan troglodytes DNA, clone: PTB-076G14.F, genomic survey sequence.  
 DEFINITION AG080291  
 VERSION AG080291.1 GI:16632093  
 KEYWORDS GSS.  
 SOURCE Pan troglodytes (chimpanzee)  
 ORGANISM Pan troglodytes  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.  
 1 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.  
 BAC end sequences of Library PTB  
 2 (bases 1 to 937)  
 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.  
 Direct Submission  
 Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC), Japan  
 1-7-22, Suenho-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 E-mail: chimpanzee@sc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/,  
 tel: 81-45-503-9111, Fax: 81-45-503-9170

COMMENT Clones are derived from the chimpanzee BAC library PTB. This BAC end was generated during the RAD process and may have higher chance of clone tracking errors.  
 PRIMERS  
 Sequencing: -21M13  
 LIBRARY  
 Vector : pRS145  
 R Site 1 : SacI  
 R Site 2 : SacI  
 Location/Qualifiers  
 1. 937  
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 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9598"  
 /clone="PTB-076G14.F"  
 /sex="male"  
 /cell\_type="lymphoblast"  
 /clone\_lib="PTB Chimpanzee Male BAC library"

BASE COUNT 28 a 414 c 454 g 24 t 17 others  
 ORIGIN  
 Query Match 12.9%; Score 72.4; DB 29; Length 937;  
 Best Local Similarity 46.5%; Pred. No. 0.00062;  
 Matches 261; Conservative 0; Mismatches 296; Indels 4; Gaps 1;

6 GGGGAGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 65  
 868 GTGGGGGGGCG 809  
 66 AAGGCGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 125  
 808 GCGGCG 749  
 126 ACCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 185  
 748 CCGGCG 689  
 186 ACNAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 245  
 688 GTCCCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 629  
 246 GCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 305  
 628 GCGGCG 569  
 306 TCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 361  
 568 GCGGCG 509  
 362 GGCAGGCGGCTTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 421  
 508 GGGGCG 449  
 422 GCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 481  
 448 GCGGCG 389  
 482 CGGAGTATAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 541  
 388 CCGGCG 329  
 542 CCGGCG 562  
 328 GCGGCG 308

RESULT 15  
 AG152796 1085 bp DNA linear GSS 09-JAN-2002  
 LOCUS AG152796 Pan troglodytes DNA, clone: RP43-016F02.TV, genomic survey sequence.  
 DEFINITION AG152796  
 VERSION AG152796.1 GI:16682474

KEYWORDS GSS.  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.  
REFERENCE 1  
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,  
Toto, Y., Watanabe, H. and Sakaki, Y.  
TITLE BAC end sequences of library RPCI-43  
JOURNAL Unpublished  
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,  
Toto, Y., Watanabe, H. and Sakaki, Y.  
TITLE Direct Submission  
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Japan  
1-7-22 Saitama-shi, Saitama, Japan, Yokohama, Kanagawa 230-0045, Japan  
(E-mail: chimpes@riken.go.jp, URL: http://hgp.gsc.riken.go.jp/,  
Tel: 81-45-503-9211, Fax: 81-45-503-9170)  
Clones are derived from the chimpanzee BAC library RPCI-43. This BAC  
end was generated during the R&D process and may have higher chance  
of clone tracking errors.  
PRIMERS  
Sequencing: TJ  
LIBRARY  
Vector : pBACe3.6  
R.Site 1 : EcoRI  
R.Site 2 : EcoRI  
Location/Qualifiers  
1. 1085  
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/db\_xref="taxon:9598"  
/clone="RP43-016F02.TJ"  
/sex="male"  
/cell\_type="lymphocytes"  
/clone\_lib="RPCI-43 Chimpanzee Male BAC Library"  
BASE COUNT 45 a 445 c 468 g 31 t 96 others  
ORIGIN  
Query Match 12.9% Score 72.4; DB 29; Length 1085;  
Best Local Similarity 44.9%; Pred. No. 0.00062;  
Matches 226; Conservative 0; Mismatches 277; Indels 0; Gaps 0;  
QY 1 CGGCGGAGGAGCGCGCGGAGTATCGTCCCTGCGCGCTTCCATCCAGG 60  
DB 573 CGGCGGAGGAGCGCGCGGAGTATCGTCCCTGCGCGCTTCCATCCAGG 60  
QY 61 CGCAGAAAGCGCCACAGAGACCCCAATGCCGATGTCACAGTGGATCAGAG 120  
DB 633 NCGCCCG 692  
QY 121 CAGGAGCCAGGAGCCAGGAACTGCGCGCGCGCGCGCGCGCGCGCGCGCG 180  
DB 693 GCGGCG 752  
QY 181 CCTTACCGAGAGAGTCCCTTACCGCGCGCGCGCGCGCGCGCGCGCGCG 240  
DB 753 CGGCG 812  
QY 241 AGACCGCAAGAGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300  
DB 813 CGGNNNGGCGGNNNGGCGGNNNGGCGGNNNGGCGGNNNGGCGGNNNGGCG 872  
QY 301 CTCTCTCAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360  
DB 873 CGGCG 932  
QY 361 GGGCAGCGGCTTCCAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420  
DB 933 CGCCCG 992  
QY 421 AGCGAGCG 480

DB 993 CGGCG 1052  
QY 481 CCGGATATAAGACCTCGTGGC 503  
DB 1053 ACCACAACAACAAGATCGACGC 1075  
Search completed: November 6, 2003, 16:16:47  
Job time: 1938 secs



JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Unpublished  
2 (bases 1 to 127488)  
DOE Joint Genome Institute.  
Submitted (26-JAN-2000) Production Sequencing Facility, DOE Joint  
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
On Apr 20, 2001 this sequence version replaced gi:7711676.  
-----Genome Center  
Center: Joint Genome Institute  
Center Code: JGI  
Web site: <http://www.jgi.doe.gov>  
-----  
Project Information  
Center Project Name: 78060  
Center clone name: CIT978SKB\_36B8  
-----  
Summary Statistics  
Consensus quality: 110477 bases at least Q40  
Consensus quality: 117221 bases at least Q30  
Consensus quality: 120225 bases at least Q20  
Estimated insert size: 131000; pulse-field gel estimation  
Quality coverage: 7.48 in Q20 bases; sum-of-contigs estimation  
Quality coverage: 7.76 in Q20 bases; sum-of-contigs estimation.  
NOTE: This is a 'working draft' sequence. It currently  
\* consists of 13 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* as soon as it is available and the accession number will  
\* be preserved.

1  
1117 1116: contig of 1116 bp in length  
1217 1216: gap of unknown length  
1217 1254: contig of 1038 bp in length  
2255 2354: gap of unknown length  
3412 3412: contig of 1058 bp in length  
3512 3512: gap of unknown length  
5005 5005: contig of 1493 bp in length  
5105 5105: gap of unknown length  
7647 7647: contig of 2542 bp in length  
7748 7747: gap of unknown length  
10238 10237: contig of 2490 bp in length  
10338 10337: gap of unknown length  
12441 12440: contig of 2103 bp in length  
12541 12540: gap of unknown length  
15936 15935: contig of 3385 bp in length  
16036 16035: gap of unknown length  
24397 24396: contig of 8361 bp in length  
24487 24486: gap of unknown length  
34088 34087: contig of 14589 bp in length  
39186 39185: gap of unknown length  
60545 60545: contig of 21360 bp in length  
60546 60545: gap of unknown length  
79490 79490: contig of 18845 bp in length  
79491 79590: gap of unknown length  
79591 127488: contig of 47898 bp in length.  
Location/Qualifiers  
1. 127488  
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/mol\_type="Genomic DNA"  
/db\_xref="taxon:9606"  
/chromosome="5"  
/clone="CTB-36B8"  
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BASE COUNT 31643 a 32392 c 31616 g 30626 t 1211 others  
ORIGIN  
Query Match 79.6%; Score 200.6; DB 2; Length 127488;  
Best Local Similarity 91.3%; Pred. No. 3.2e-28;  
Matches 230; Conservative 0; Mismatches 5; Indels 17; Gaps 1;  
1 CGGCGGAGGAGCGCGCGGAGCTGATCGTCCTCGCGCTCCACCTCCACG 60

Db 84291 CGGCGGAGGAGCGCGCGGAGCTGATCGTCCTCGCGCTCCACCTCCACG 84232  
Qy 61 CGCAGAGGCGCCACAGAGACCCCGAGTCGCCAGCTTGCCAGGTCGGATCAGAG 120  
Db 84231 CGCAGAGGCGCCACAGAGACCCCGAGTCGCCAGCTTGCCAGGTCGGATCAGAG 84172  
Qy 121 CAGGAGCAGAGGCGCAGAACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180  
Db 84171 CAGGAGCAGAGGCGCAGAACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 84112  
Qy 181 CCGTCACGAGGAGGAGGAGCTCCCTCAGCCCGGCGCGCGCGCGCGCGCGCGCG 240  
Db 84111 CCGCTCAGC-----CGGAGCCAGCCCTGCGAGGCGCGCGCGCGCGCG 84069  
Qy 241 AGACCGCAAGC 252  
Db 84068 AGACCGCAAGC 84057  
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RESULT 2  
AC108083/c 130129 bp DNA linear HTG 25-JAN-2002  
LOCUS Homo sapiens chromosome 5 clone CTD-2013L15, WORKING DRAFT  
DEFINITION  
ACCESSION AC108083.1 GI:18369929  
VERSION HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_ACTIVEFIN.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1  
1 (bases 1 to 130129)  
DOE Joint Genome Institute.  
Submitted (25-JAN-2002) Production Sequencing Facility, DOE Joint  
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
-----Genome Center  
Center: Joint Genome Institute  
Center Code: JGI  
Web site: <http://www.jgi.doe.gov>  
-----  
Project Information  
Center Project Name: 632820  
Center clone name: CITB-H1\_2013L15  
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Summary Statistics  
Consensus quality: 124488 bases at least Q40  
Consensus quality: 128031 bases at least Q30  
Consensus quality: 128842 bases at least Q20  
Estimated insert size: 135000; agarose-gel estimation  
Quality coverage: 7.97 in Q20 bases; agarose-gel estimation  
Quality coverage: 7.66 in Q20 bases; sum-of-contigs estimation  
Quality coverage: 7.97 in Q20 bases; sum-of-contigs estimation.  
NOTE: This is a 'working draft' sequence. It currently  
\* consists of 4 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* as soon as it is available and the accession number will  
\* be preserved.

1  
4321 4320: contig of 4320 bp in length  
4421 4420: gap of unknown length  
23713 23712: contig of 19292 bp in length  
23813 23812: gap of unknown length  
48602 48602: contig of 24790 bp in length  
48702 48702: gap of unknown length  
48703 130129: contig of 81427 bp in length.



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FEATURES
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  Best Local Similarity 90.9%; Pred. No. 9.6e-28;
  Matches 229; Conservative 0; Mismatches 5; Indels 18; Gaps 1;

  1 CGGCGGGGAGGCGGCGGAGTGAAGCGCTGATCGTCCCTGCGCGCTCCCACTCCCGAGG 60
  Db CGGCGGGGAGGCGGCGGAGTGAAGCGCTGATCGTCCCTGCGCGCTCCCACTCCCGAGG 24510
  QY CGGCGAGGCGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
  Db CGGAGAGGCGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 24450
  QY 121 CAGGAGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
  Db 24449 CAGGAGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 24390
  QY 181 CCTCACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
  Db 24389 C-----CCTCACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 24348
  QY 241 AGACCGCAAGC 252
  Db 24347 AGACCGCAAGC 24336

RESULT 3
LOCUS AC106813 166777 bp DNA linear HTG 07-MAR-2002
DEFINITION Homo sapiens chromosome 5 clone RP11-566L9, WORKING DRAFT SEQUENCE,
ACCESSION AC106813.3 GI:19224876
VERSION HTG: HTGS PHASE2; HTGS_DRAFT; HTGS_ACTIVEFIN.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
  AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  TITLE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
  JOURNAL DOE Joint Genome Institute.
  TITLE Sequencing of Human Chromosome 5
  JOURNAL Unpublished
  TITLE 2. (bases 1 to 166777)
  JOURNAL DOE Joint Genome Institute.
  TITLE Direct Submission
  JOURNAL Submitted (12-JAN-2002) Production Sequencing Facility, DOE Joint
  Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
  TITLE 3. (bases 1 to 166777)
  JOURNAL DOE Joint Genome Institute.
  TITLE Direct Submission
  JOURNAL Submitted (07-MAR-2002) Production Sequencing Facility, DOE Joint
  Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
  TITLE On Mar 7, 2002 this sequence version replaced gi:18369924.
  JOURNAL -----Genome Center
  TITLE Center: Joint Genome Institute
  JOURNAL Center Code: JGI
  JOURNAL Web site: http://www.jgi.doe.gov
  JOURNAL -----
  JOURNAL Project Information
  JOURNAL Center Project Name: 1519801
  JOURNAL Center clone name: RP11-566L9
  JOURNAL -----
  JOURNAL Summary Statistics

```

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Consensus quality: 163497 bases at least Q40
Consensus quality: 16071 bases at least Q30
Consensus quality: 166432 bases at least Q20
Estimated insert size: 166250; agarose-fp estimation
Estimated insert size: 166577; sum-of-contigs estimation
Quality coverage: 9.4 in Q20 bases; agarose-fp estimation
Quality coverage: 10.51 in Q20 bases; sum-of-contigs estimation
NOTE: This is a 'working draft' sequence. It currently
  consists of 3 contigs. Gaps between the contigs
  are represented as runs of N. The order of the sizes
  is believed to be correct as given, however the sizes
  of the gaps between them are based on estimates that have
  been provided by the submitter.
  * This sequence will be replaced
  * by the finished sequence as soon as it is available and
  * the accession number will be preserved.
  1 62238 62237: contig of 62237 bp in length
  * 62338 75837: gap of unknown length
  * 75838 75837: gap of unknown length
  * 75938 166777: contig of 90840 bp in length.
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      /mol_type="genomic DNA"
      /db_xref="taxon:9606"
      /chromosome="5"
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      /clone_11b="RP11-566L9"
      /clone_11c="Caltech human BAC library D"
      /clone_11d="30949 g 31146 t 300 others"
BASE COUNT
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ORIGIN
  Query Match 78.6%; Score 198; DB 2; Length 166777;
  Best Local Similarity 90.9%; Pred. No. 8.9e-28;
  Matches 229; Conservative 0; Mismatches 5; Indels 18; Gaps 1;

  1 CGGCGGGGAGGCGGCGGAGTGAAGCGCTGATCGTCCCTGCGCGCTCCCACTCCCGAGG 60
  Db 119104 CGGCGGGGAGGCGGCGGAGTGAAGCGCTGATCGTCCCTGCGCGCTCCCACTCCCGAGG 119163
  QY 61 CGGAGAGGCGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
  Db 119164 CGGAGAGGCGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 119223
  QY 121 CAGGAGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
  Db 119224 CAGGAGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 119283
  QY 181 CCTCACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
  Db 119284 C-----CCTCACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 119325
  QY 241 AGACCGCAAGC 252
  Db 119326 AGACCGCAAGC 119337

RESULT 4
LOCUS AC025336/c 168347 bp DNA linear HTG 25-MAR-2000
DEFINITION Homo sapiens chromosome 5 clone RP11-451H23 map 5, WORKING DRAFT
ACCESSION AC025336.2 GI:7328761
VERSION HTG: HTGS PHASE1; HTGS_DRAFT.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
  AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  TITLE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
  JOURNAL 1. (bases 1 to 168347)
  JOURNAL Birren, B., Linton, L., Nusbaum, C. and Lander, E.
  JOURNAL Homo sapiens chromosome 5, clone RP11-451H23
  JOURNAL Unpublished

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Query Match 78.6%; Score 198; DB 2; Length 168347;

Best Local Similarity 90.9%; Pred. No. 8.9e-28; Mismatches 5; Indels 18; Gaps 1;

Matches 229; Conservative 0; Mismatches 5; Indels 18; Gaps 1;

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QY 1 CGGCGGGGAGGCGCGCGGAGTGAAGGCTGATGCTGCTGCGGCGCTCCCACTCCCAAG 60
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QY 61 CGGAGAGGCGCGCGCGGAGTGAAGGCTGATGCTGCTGCGGCGCTCCCACTCCCAAG 120
DB 145142 CGGAGAGGCGCGCGCGGAGTGAAGGCTGATGCTGCTGCGGCGCTCCCACTCCCAAG 145083
QY 121 CAGGAGCCAGGAGCCAGGAACTGCGCGCGCGCGCGCGCTGCGGCGCGGAGAAAGCT 180
DB 145082 CAGGAGCCAGGAGCCAGGAACTGCGCGCGCGCGCGCGCTGCGGCGCGGAGAAAGCT 145023
QY 181 CCTCACCAGGAGGAGAACTGCGCGCGCGCGCGCGCTGCGGCGCGGAGAAAGCT 240
DB 145022 CCTCACCAGGAGGAGAACTGCGCGCGCGCGCGCGCTGCGGCGCGGAGAAAGCT 144981
QY 241 AGACCGCAAGC 252
DB 144980 AGACCGCAAGC 144969

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RESULT 5  
AC122714/c 190024 bp DNA linear PRI 04-MAR-2003  
LOCUS Homo sapiens chromosome 5 clone RP11-451H23, complete sequence.  
DEFINITION AC122714  
ACCESSION AC122714.2 GI:28827858  
VERSION  
KEYWORDS HTG.

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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euteleostomi; Primates; Catarrhini; Homiidae; Homo.
TITLE DOE Joint Genome Institute and Stanford Human Genome Center.
JOURNAL Direct Submission
REFERENCE Unpublished
AUTHORS 2 (bases 1 to 190024)
JOURNAL Direct Submission
TITLE DOE Joint Genome Institute.
REFERENCE Submitted (25-MAY-2002) Production Sequencing Facility, DOE Joint
AUTHORS Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
JOURNAL 3 (bases 1 to 190024)
REFERENCE DOE Joint Genome Institute and Stanford Human Genome Center.
AUTHORS Submitted (04-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell
JOURNAL Drive, Walnut Creek, CA 94598, USA
COMMENT On Mar 4, 2003 this sequence version replaced gi:212062277.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40.99.8% of Sequence;
Estimated Total Number of Errors is 0.9.
NOTE: Shatter Libraries failed to verify the dinucleotide repeat
region 124370-125308. Unsure number of repeat copies
124370-125308. Forced join 124996.
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124370..125308
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dinucleotide repeat region 124370-125308. Unsure number
of repeat copies 124370-125308. Forced join 124996."
BASE COUNT 45607 a 46028 c 46121 g 52268 t
ORIGIN

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Query Match

Best Local Similarity 78.6%; Score 198; DB 9; Length 190024;

Matches 229; Conservative 0; Mismatches 5; Indels 18; Gaps 1;

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QY 1 CGGCGGGGAGGCGCGCGGAGTGAAGGCTGATGCTGCTGCGGCGCTCCCACTCCCAAG 60
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QY 61 CGGAGAGGCGCGCGCGGAGTGAAGGCTGATGCTGCTGCGGCGCTCCCACTCCCAAG 120
DB 81411 CGGAGAGGCGCGCGCGGAGTGAAGGCTGATGCTGCTGCGGCGCTCCCACTCCCAAG 81352
QY 121 CAGGAGCCAGGAGCCAGGAACTGCGCGCGCGCGCGCGCTGCGGCGCGGAGAAAGCT 180
DB 81351 CAGGAGCCAGGAGCCAGGAACTGCGCGCGCGCGCGCGCTGCGGCGCGGAGAAAGCT 81292
QY 181 CCTCACCAGGAGGAGAACTGCGCGCGCGCGCGCGCTGCGGCGCGGAGAAAGCT 240
DB 81291 CCTCACCAGGAGGAGAACTGCGCGCGCGCGCGCGCTGCGGCGCGGAGAAAGCT 81250
QY 241 AGACCGCAAGC 252
DB 81249 AGACCGCAAGC 81238

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RESULT 6  
PM4A12G 931 bp DNA linear STS 09-MAR-2002  
LOCUS Penicillium marneffei STS, clone pm4a12.9, sequence tagged site.  
DEFINITION AL885775  
ACCESSION AL885775.1 GI:19337810  
VERSION



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Query Match 18.3% Score 46.2; DB 14; Length 156789; Best Local Similarity 50.9%; Pred. No. 8; Matches 108; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

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QY 26 GGGCTGATGTCCTTCGCGCTCCACCTTCCGAGGCGAGAAAGGCCACGAGAACCC 85
Db 139583 GGGCTGATGTCCTTCGCGCTCCACCTTCCGAGGCGAGAAAGGCCACGAGAACCC 85
QY 86 CAGTCCCGCAGCTTGGCAGCTCTGGGATCAGAGCGAGGAGCAGAGAACCTCG 145
Db 139643 TCGTCCCGCAGCTTGGCAGCTCTGGGATCAGAGCGAGGAGCAGAGAACCTCG 145
QY 146 GCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 205
Db 139703 GCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 205
QY 206 ACCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 237
Db 139763 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 237
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RESULT 8  
AC023530/c  
LOCUS 70097 bp DNA linear HTG 13-UTL-2000  
DEFINITION Homo sapiens clone RP11-28L5, LOW-PASS SEQUENCE SAMPLING.  
ACCESSION AC023530  
VERSION AC023530.2 GI:9137803  
KEYWORDS HTG; HTGS PHASE0.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
1 (bases 1 to 70097)  
2 (bases 1 to 70097)  
AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.  
TITLE Unpublished  
JOURNAL  
REFERENCE  
1. Birren, B., Linton, L., Nusbaum, C. and Lander, E.  
2. (bases 1 to 70097)  
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,  
Anderson, S., Baldwin, J., Barna, N., Beda, F., Boguslavsky, L.,  
Bouckgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A.,  
Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,  
Dearellano, K., Dewar, K., Dodge, S., Domino, M., Doyle, M.,  
Fenster, J., Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D.,  
Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,



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* 45782 45845: contig of 764 bp in length
* 46546 46645: gap of 100 bp in length
* 46646 47417: contig of 772 bp in length
* 47418 47517: gap of 100 bp in length
* 47518 48297: contig of 780 bp in length
* 48298 48397: gap of 100 bp in length
* 48398 48462: contig of 765 bp in length
* 49163 49263: gap of 100 bp in length
* 49263 49788: contig of 716 bp in length
* 49789 50079: gap of 100 bp in length
* 50079 50845: contig of 766 bp in length
* 50845 50944: gap of 100 bp in length
* 50945 51765: contig of 820 bp in length
* 51765 51865: gap of 100 bp in length
* 51865 52627: contig of 762 bp in length
* 52627 53055: gap of 100 bp in length
* 53055 53506: contig of 779 bp in length
* 53506 54392: gap of 100 bp in length
* 54392 54491: contig of 786 bp in length
* 54491 55275: gap of 100 bp in length
* 55275 55376: contig of 784 bp in length
* 55376 56138: gap of 100 bp in length
* 56138 56239: contig of 763 bp in length
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* 57018 57119: contig of 780 bp in length
* 57119 57893: gap of 100 bp in length
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Query Match 17.9%; Score 45; DB 2; Length 70097;

Best Local Similarity 49.1%; Pred. No. 17; Mismatches 115; Indels 0; Gaps 0;

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Matches 111; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

Qy 4 CCGGAGAGGCGCGCGAGTGGCTGATGCTCCCTGCGCCCTCCCACTCCCGAGCGC 63
Db 69065 CCGGAGAGGCGCGCGAGTGGCTGATGCTCCCTGCGCCCTCCCACTCCCGAGCGC 69006
Qy 64 AGAAGAGCGCGCGAGTGGCTGATGCTCCCTGCGCCCTCCCACTCCCGAGCGC 123
Db 69005 TCGGCGCGCGCGCGAGTGGCTGATGCTCCCTGCGCCCTCCCACTCCCGAGCGC 68946
Qy 124 GGACCGAGGAGCGCGAGTGGCTGATGCTCCCTGCGCCCTCCCACTCCCGAGCGC 183
Db 68945 GCGCGCGCGCGCGAGTGGCTGATGCTCCCTGCGCCCTCCCACTCCCGAGCGC 68886
Qy 184 TCACGAGGAGGAGTGGCTGATGCTCCCTGCGCCCTCCCACTCCCGAGCGC 229
Db 68885 CCGGAGAGGCGCGCGAGTGGCTGATGCTCCCTGCGCCCTCCCACTCCCGAGCGC 68840

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RESULT 9  
 TMI270035 786 bp DNA linear VRT 01-SEP-2000  
 LOCUS Tetracodon nigroviridis 18S rRNA gene (partial), 5.8S rRNA gene (partial) and internal transcribed spacer 1 (ITS1), clone COA019AD11.  
 ACCESSION AJ270035  
 VERSION AJ270035.1 GI:6689431  
 KEYWORDS 18S ribosomal RNA; 18S rRNA gene; 5.8S ribosomal RNA; 5.8S rRNA gene; internal transcribed spacer 1; ITS1.  
 SOURCE Tetracodon nigroviridis  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorphi; Acanthopterygii; Percormorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.

REFERENCE 1 Roest Crolius, H., Jallion, O., Dasilva, C., Bouneau, L., Fisher, C.,

TITLE Bernot, A., Fizames, C., Wincker, P., Brothier, P., Quetier, F., Saurin, W., and Weissenbach, J.  
 JOURNAL Estimate of human gene number provided by genome-wide analysis using Tetracodon nigroviridis DNA sequence  
 MEDLINE Nat Genet. 25 (2), 235-238 (2000)  
 PUBMED 10835645

REFERENCE 2 Roest Crolius, H., Jallion, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A., and Weissenbach, J.  
 TITLE Characterization and repeat analysis of the compact genome of the freshwater puterfish Tetracodon nigroviridis  
 JOURNAL Genome Res. 10 (7), 939-949 (2000)  
 MEDLINE 20359837  
 PUBMED 10899143

REFERENCE 3 (bases 1 to 786)  
 Roest Crolius, H.  
 TITLE Direct Submission  
 JOURNAL Submitted (27-SEP-1999) Roest Crolius H., Tetracodon Group, Genoscope, 2, rue Gaston Crémieux, 91057 Evry Cedex, FRANCE  
 COMMENT The full annotated consensus sequence of the complete Tetracodon nigroviridis rRNA gene cluster is available at <http://www.genoscope.cns.fr/> (URL provided by the submitter) This sequence corresponds to position 2151-2937 of the consensus.

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BASE COUNT 131 a 266 c 253 g 110 t 26 others  
 ORIGIN

Query Match 17.7%; Score 44.6; DB 5; Length 786;  
 Best Local Similarity 50.0%; Pred. No. 77;  
 Matches 89; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

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Qy 114 TCAGAGGAGGAGGCGCGAGTGGCTGATGCTCCCTGCGCCCTCCCACTCCCGAGCGC 173
Db 275 AGGAGGAGGAGGCGCGAGTGGCTGATGCTCCCTGCGCCCTCCCACTCCCGAGCGC 334
Qy 174 GGAAGTCTCTACGAGGAGGAGTGGCTGATGCTCCCTGCGCCCTCCCACTCCCGAGCGC 231
Db 335 GCGGCTGCTGCGCGAGGAGTGGCTGATGCTCCCTGCGCCCTCCCACTCCCGAGCGC 392

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RESULT 10  
 AB074432 14447 bp DNA linear VRL 11-JAN-2002  
 LOCUS Cercopithecine herpesvirus 1 US1, US2, US3, US4, US5, US6, US7, US8, US9, US10, US11, US12 genes, complete and partial cds.  
 ACCESSION AB074432  
 VERSION AB074432.1 GI:18157353  
 KEYWORDS Cercopithecine herpesvirus 1 (monkey B virus)  
 SOURCE Cercopithecine herpesvirus 1



REFERENCE	1	Virus; dsDNA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Simplexvirus.
AUTHORS		Ohsawa, K., Black, D. H., Sato, H. and Eberle, R.
TITLE		Sequence and genetic arrangement of the (U)S region of the monkey B virus (cercopithecine herpesvirus 1) genome and comparison with the (U)S regions of other primate herpesviruses
JOURNAL		J. Virol. 76 (3) 1516-1520 (2002)
MEDLINE		21635528
PUBMED		11773425
REFERENCE	2	(bases 1 to 14447)
AUTHORS		Ohsawa, K. and Eberle, R.
TITLE		Direct Submission
JOURNAL		Submitted (15-NOV-2001) Kazuraka Ohsawa, Nagasaki University School of Medicine, Laboratory Animal Center for Biomedical Research; 1-12-4 Sakamoto, Nagasaki 852-8523, Japan
		(E-mail: kohna@net.nagasaki-u.ac.jp, Tel: 81-95-849-7134, Fax: 81-95-849-7148)
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TATA_signal		7028. 7035
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TATA_signal		9874. 9879
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PSAQPPRPAAPRAALVGLIYGAVALVAGLSVMACTCRPAAPRAVAKRDIAMP
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Db 5544 TCGTCCCGCCCATTTGCCACGAGAGGGGGCGGGGACAGCGCCAGGGGGGGCGCTCGCG 5603
OY 146 GCGCGCCCCCGCCCTGCGCGCGCGCGAGAGGAAGCTCCCTCACACGAGAGGAGCTCCCTC 205
Db 5604 GCGGCGGAGACCGAGCGCGCCCCCGCGCAGACCCCTTCACTCCCGCTCGAGGCTCTGACT 5663
OY 206 ACCCGGCGCAAGCCTTGACGAGGGGGCGCGCTGGG 237
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ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AC130306  
AC130306.1 GI:22165240  
HTG, HTGS PHASED  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS

Barren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,  
Barra,N., Baeclen,J., Bloom,C., Boguski,Y., L., Bourkhalter,B.,  
Carnata,J., Chang,J., Chazaro,B., Choepl,Y., Collymore,A.,  
Cook,A., Correl,P., Dearlano,K., Dewar,K., Diaz,J.S., Dodge,S.,  
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Karats,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,  
Liu,G., Maclean,C., Macdonald,P., Major,J., Matthews,C.,  
McCarthy,M., Meldrum,J., Menais,L., Mhlova,T., Mlenga,V.,  
Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,  
O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K.,  
Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,  
Roman,J., Roy,A., Schauer,S., Schupack,R., Seaman,S., Severy,P.,  
Smith,C., Spencer,B., Stange-Thoman,N., Stojanovic,N., Talamas,J.,  
Teafaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,  
Viell,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zaitoun,J.,  
Zembek,L., Zimmer,A. and Zody,M.

Direct Submission  
Submitted (99-AUG-2002) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
All repeats were identified using RepeatMasker:  
Smit,A.P.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WITR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
----- Project Information  
Center project name: L27898  
Center clone name: L26\_H\_19

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\* NOTE: This record contains 80 individual  
\* sequencing reads that have not been assembled into  
\* configs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

\* 1  
\* 736 835: contig of 735 bp in length  
\* 736 835: gap of 100 bp  
\* 836 1572: contig of 737 bp in length  
\* 1572: gap of 100 bp  
\* 1573 2398: contig of 727 bp in length  
\* 2398: gap of 100 bp  
\* 2400 2498: gap of 100 bp  
\* 2498: contig of 721 bp in length  
\* 3220 3320: gap of 100 bp  
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\* 3321 4037: gap of 100 bp  
\* 4037: contig of 717 bp in length  
\* 4038 4138: gap of 100 bp  
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\* 4138 4881: gap of 100 bp  
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\* 4882 5714: gap of 100 bp  
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\* 5715 6541: gap of 100 bp  
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8215	8314:	gap of 100 bp	in length
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9057	9156:	gap of 100 bp	in length
9157	9156:	contig of 760 bp	in length
98017	10016:	gap of 100 bp	in length
10017	10723:	contig of 716 bp	in length
10733	10832:	gap of 100 bp	in length
10833	11534:	contig of 711 bp	in length
11544	11643:	gap of 100 bp	in length
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12493	13324:	contig of 732 bp	in length
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14046	14145:	gap of 100 bp	in length
14146	14894:	contig of 749 bp	in length
14895	14994:	gap of 100 bp	in length
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15727	15826:	gap of 100 bp	in length
15827	16562:	contig of 736 bp	in length
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16663	17400:	contig of 738 bp	in length
17401	17500:	gap of 100 bp	in length
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19142	19860:	contig of 719 bp	in length
19861	19960:	gap of 100 bp	in length
19961	20680:	contig of 720 bp	in length
20681	20780:	gap of 100 bp	in length
20781	21508:	contig of 728 bp	in length
21509	21609:	gap of 100 bp	in length
21609	22316:	contig of 708 bp	in length
22317	22316:	gap of 100 bp	in length
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25696	25796:	gap of 100 bp	in length
25796	26518:	contig of 723 bp	in length
26519	26618:	gap of 100 bp	in length
26619	27359:	contig of 741 bp	in length
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28201	28300:	gap of 100 bp	in length
28301	29009:	contig of 709 bp	in length
29010	29109:	gap of 100 bp	in length
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32452	33177:	contig of 726 bp	in length
33178	33277:	gap of 100 bp	in length
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33999	34099:	gap of 100 bp	in length
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34914	35633:	contig of 717 bp	in length
35637	35737:	gap of 100 bp	in length
35737	36449:	contig of 713 bp	in length
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Matches 110;	Conservative	0;	Mismatches 114;	Indels 0;	Gaps 0;	
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20553	GC	CGG	GGG	CGG	CGG	CGG
63	CAG	AA	CGG	CGG	CGG	CGG
20493	CGT	GGG	GGG	CGG	CGG	CGG
123	GGG	AA	CGG	CGG	CGG	CGG
20433	TGG	AA	CGG	CGG	CGG	CGG
183	CTC	AA	CGG	CGG	CGG	CGG
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RESULT 12  
AC093712/c 133924 bp DNA linear MAM 10-OCT-2002  
LOCUS AC093712  
DEFINITION Canis familiaris clone RP81-229G11, complete sequence.  
ACCESSION AC093712  
VERSION AC093712.2 GI:17352412  
KEYWORDS HTG.  
SOURCE  
ORGANISM Canis familiaris (dog)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
REFERENCE  
AUTHORS Akter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakeley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Ho, S.-L., Idol, J.R., Karlins, E., Latic, P., Lee-Lin, S.-Q., Legaaspi, R., Maduro, Q.L., Maduro, V.B., Masiello, C., Mastrian, S.D., McLooney, J.C., McDowell, J., Pearson, R., Prasad, A., Schandler, K., Stantirlop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Taurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Zhang, L.-H., and Green, E.D.  
TITLE NISC Comparative Sequencing Initiative  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 133924)  
AUTHORS Green, E.D.  
TITL Direct Submission  
JOURNAL Submitted (08-SEP-2001) NIH Intramural Sequencing Center, 8717  
REFERENCE 3 (bases 1 to 133924)  
AUTHORS Green, E.D.  
TITL Direct Submission  
JOURNAL Submitted (05-DEC-2001) NIH Intramural Sequencing Center, 8717  
REFERENCE 4 (bases 1 to 133924)  
AUTHORS Green, E.D.  
TITL Direct Submission  
JOURNAL Submitted (10-OCT-2002) NIH Intramural Sequencing Center, 8717  
REFERENCE 5 (bases 1 to 133924)  
AUTHORS Green, E.D.  
TITL Direct Submission  
JOURNAL Submitted (10-OCT-2002) NIH Intramural Sequencing Center, 8717  
COMMENT  
----- Genome Center  
Center: NIH Intramural Sequencing Center  
Center code: NISC  
Web site: http://www.nisc.nih.gov  
Contact: nisc.zoo@hgrl.nih.gov  
----- Project Information  
Center project name: cia  
Center clone name: 229G11

This sequence was finished as follows unless otherwise noted:  
all regions were double-stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

CLONE LENGTH: This sequence represents the entire insert of this clone unless otherwise noted. If there are overlapping clones, the overlaps are noted in the beginning and end of the Features section.

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ORIGIN

Query Match 17.7%; Score 44.6; DB 4; Length 133924;  
Best Local Similarity 49.2%; Pred. No. 16;  
Matches 116; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

RESULT 13  
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LOCUS AC134963  
DEFINITION Canis familiaris clone RP81-262L7, WORKING DRAFT SEQUENCE, 7  
ACCESSION AC134963  
VERSION AC134963.2 GI:24022401  
KEYWORDS HTG; HTGS; PHAS2; HTGS\_DRAFT.  
SOURCE  
ORGANISM Canis familiaris (dog)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
REFERENCE  
AUTHORS Akter, N., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakeley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Carleaga, K., Coleman, B., Dietrich, N.L., Engle, J., Granite, S., Guan, X., Gupta, J., Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E., Latic, P., Lee-Lin, S.-Q., Legaaspi, R., Maduro, Q.L., Maduro, V.B., Margulies, E.H., Masiello, C., Mastrian, S.D., McLooney, J.C., McDowell, J., Paguirigan, C., Pearson, R., Portnoy, M.E., Prasad, A., Reddix-Dugue, N., Schandler, K., Schueler, M.G., Sison, C., Stantirlop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Vogt, J.L., Walker, M., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H., and Green, E.D.  
TITLE NISC Comparative Sequencing Initiative  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 156221)  
AUTHORS Green, E.D.  
TITL Direct Submission  
JOURNAL Submitted (03-OCT-2002) NIH Intramural Sequencing Center, 8717  
REFERENCE 3 (bases 1 to 156221)  
AUTHORS Green, E.D.  
TITL Direct Submission  
JOURNAL Submitted (16-OCT-2002) NIH Intramural Sequencing Center, 8717  
COMMENT  
----- Genome Center  
Center: NIH Intramural Sequencing Center  
Center code: NISC  
Web site: http://www.nisc.nih.gov  
Contact: nisc.zoo@hgrl.nih.gov  
----- Project Information  
Center project name: dgp  
Center clone name: 262L07

The sequence data in this record represents an 'enhanced' version of a phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones; overlaps with neighboring clones; alignment with available reference sequence (e.g.,



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* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
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785      784: gap of 100 bp
1480     1479: contig of 695 bp in length
1580     1579: gap of 100 bp
2282     2281: contig of 702 bp in length
3092     3091: gap of 100 bp
3192     3191: contig of 710 bp in length
3872     3871: contig of 680 bp in length
3972     3971: gap of 100 bp
4678     4677: contig of 706 bp in length
4778     4777: gap of 100 bp
5500     5499: contig of 722 bp in length
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6323     6322: contig of 723 bp in length
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8823     8822: gap of 100 bp
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12809    12808: gap of 100 bp
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14451    14450: gap of 100 bp
15114    15113: contig of 664 bp in length
15215    15214: gap of 100 bp
15900    15900: contig of 686 bp in length
16001    16000: gap of 100 bp
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17484    17483: contig of 684 bp in length
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22327    22326: contig of 717 bp in length
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36007    36714: contig of 708 bp in length
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40661    40760: contig of 704 bp in length
40761    41487: gap of 100 bp
41487    41587: contig of 727 bp in length
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42334    42424: gap of 100 bp
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44775    44874: gap of 100 bp
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45565    46261: gap of 100 bp
46262    46461: contig of 697 bp in length
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47172    47271: contig of 710 bp in length
47272    47961: contig of 690 bp in length
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48062    48776: contig of 715 bp in length
48777    48876: gap of 100 bp
48877    49578: contig of 702 bp in length
49579    49678: gap of 100 bp
49679    50385: contig of 707 bp in length
50386    50485: gap of 100 bp
50486    51192: contig of 707 bp in length
51193    51292: gap of 100 bp
51293    51984: contig of 692 bp in length
51985    52084: gap of 100 bp
52085    52786: contig of 702 bp in length
52787    52886: gap of 100 bp
52887    53588: contig of 702 bp in length
53589    54373: gap of 100 bp
54374    54473: contig of 685 bp in length
```

[illegible]

Center project name: L113327	
Center clone name: 314_C_119	
-----	
* NOTE: This record contains 85 individual	
* sequencing reads that have not been assembled	
* contigs. Runs of N are used to separate the r	
* and the order in which they appear is complet	
* arbitrary. Low-pass sequence sampling is usefu	
* identifying clones that may be gene-rich and	
* overlap relationships among clones to be dedu	
* However, it should not be assumed that this c	
* will be sequenced to completion. In the event	
* the record is updated, the accession number w	
* be preserved.	
1	720: contig of 720 bp in length
721	560: gap of 100 bp in length
821	1557: gap of 100 bp in length
1558	1557: gap of 737 bp in length
1558	1637: gap of 100 bp in length
1558	2494: contig of 747 bp in length
2405	2504: gap of 100 bp in length
2505	3259: contig of 795 bp in length
3300	3359: gap of 100 bp in length
3400	4153: contig of 754 bp in length
4154	4253: gap of 100 bp in length
4254	4978: contig of 725 bp in length
4979	5078: gap of 100 bp in length
5079	5815: contig of 737 bp in length
5816	5915: gap of 100 bp in length
5916	6648: contig of 733 bp in length
6649	6748: gap of 100 bp in length
6749	7520: contig of 772 bp in length
7521	7620: gap of 100 bp in length
7621	8347: contig of 727 bp in length
8348	8447: gap of 100 bp in length
8448	9227: contig of 780 bp in length
9228	9327: gap of 100 bp in length
9328	10052: contig of 725 bp in length
10053	10152: gap of 100 bp in length
10153	10865: contig of 717 bp in length
10870	10966: gap of 100 bp in length
10970	11718: contig of 749 bp in length
11719	11818: gap of 100 bp in length
11819	12587: contig of 739 bp in length
12588	12657: gap of 100 bp in length
12658	13414: contig of 755 bp in length
13413	13512: gap of 100 bp in length
13513	14255: contig of 743 bp in length
14256	14355: gap of 100 bp in length
14356	15086: contig of 731 bp in length
15087	15186: gap of 100 bp in length
15187	15901: contig of 715 bp in length
15902	16001: gap of 100 bp in length
16002	16711: contig of 710 bp in length
16712	16811: gap of 100 bp in length
16812	17533: contig of 728 bp in length
17534	17639: gap of 100 bp in length
17640	18351: contig of 712 bp in length
18352	18451: gap of 100 bp in length
18452	19163: contig of 711 bp in length
19163	19263: gap of 100 bp in length
19263	20054: contig of 792 bp in length
20055	20154: gap of 100 bp in length
20155	20891: contig of 737 bp in length
20892	21820: gap of 100 bp in length
21821	21920: contig of 729 bp in length
21921	22555: contig of 733 bp in length
22554	22655: gap of 100 bp in length
22655	23420: contig of 767 bp in length
23421	23520: gap of 100 bp in length
23521	24230: contig of 714 bp in length
24232	24330: gap of 100 bp in length
24335	25065: contig of 735 bp in length

<div>Record contains 85 individual reads that have not been assembled</div>					
<div>reads of N are used to separate the r</div>					
<div>in which they appear is complete</div>					
<div>low-pass sequence sampling is useful</div>					
<div>clones that may be gene-rich and c</div>					
<div>relationships among clones to be deduc</div>					
<div>should not be assumed that this c</div>					
<div>is updated, the accession number w</div>					
object name: L11327	720:	contig of 720 bp	in length		
clone name: 314_C19	820:	gap of 100 bp	in length		
	1557:	contig of 737 bp	in length		
	1557:	gap of 100 bp	in length		
	2404:	contig of 747 bp	in length		
	2504:	gap of 100 bp	in length		
	3299:	contig of 795 bp	in length		
	3399:	gap of 100 bp	in length		
	4153:	contig of 754 bp	in length		
	4253:	gap of 100 bp	in length		
	4978:	contig of 725 bp	in length		
	5078:	gap of 100 bp	in length		
	5815:	contig of 737 bp	in length		
	5915:	gap of 100 bp	in length		
	6648:	contig of 733 bp	in length		
	6748:	gap of 100 bp	in length		
	7550:	contig of 772 bp	in length		
	7630:	gap of 100 bp	in length		
	8347:	contig of 727 bp	in length		
	8447:	gap of 100 bp	in length		
	9227:	contig of 780 bp	in length		
	9337:	gap of 100 bp	in length		
	10052:	contig of 725 bp	in length		
	10152:	gap of 100 bp	in length		
	10669:	contig of 717 bp	in length		
	10969:	gap of 100 bp	in length		
	11718:	contig of 749 bp	in length		
	11878:	gap of 100 bp	in length		
	12557:	contig of 739 bp	in length		
	12677:	gap of 100 bp	in length		
	13142:	contig of 755 bp	in length		
	13512:	gap of 100 bp	in length		
	14255:	contig of 743 bp	in length		
	14355:	gap of 100 bp	in length		
	15086:	contig of 731 bp	in length		
	15186:	gap of 100 bp	in length		
	15901:	contig of 715 bp	in length		
	16001:	gap of 100 bp	in length		
	16711:	contig of 710 bp	in length		
	16811:	gap of 100 bp	in length		
	17539:	contig of 728 bp	in length		
	17639:	gap of 100 bp	in length		
	18311:	contig of 712 bp	in length		
	18451:	gap of 100 bp	in length		
	1912:	contig of 711 bp	in length		
	1912:	gap of 100 bp	in length		
	20054:	contig of 792 bp	in length		
	20154:	gap of 100 bp	in length		
	20891:	contig of 737 bp	in length		
	20991:	gap of 100 bp	in length		
	21780:	contig of 729 bp	in length		
	21830:	gap of 100 bp	in length		
	22553:	contig of 733 bp	in length		
	22653:	gap of 100 bp	in length		
	23420:	contig of 767 bp	in length		
	23540:	gap of 100 bp	in length		
	24234:	contig of 714 bp	in length		
	24334:	gap of 100 bp	in length		
	25069:	contig of 735 bp	in length		

25170	25169:	gap of 100 bp	in length
25170	25915:	contig of 746 bp	in length
25916	25915:	gap of 100 bp	in length
26016	26751:	contig of 736 bp	in length
26652	26851:	gap of 100 bp	in length
27575	27574:	contig of 723 bp	in length
27575	28437:	gap of 100 bp	in length
28437	28437:	contig of 763 bp	in length
28438	28258:	gap of 100 bp	in length
28258	29259:	contig of 721 bp	in length
29259	29959:	contig of 710 bp	in length
30069	30169:	gap of 100 bp	in length
30919	30918:	gap of 750 bp	in length
30919	31078:	contig of 100 bp	in length
31078	31770:	gap of 752 bp	in length
31770	31870:	contig of 100 bp	in length
31870	32658:	contig of 788 bp	in length
32659	32758:	gap of 100 bp	in length
32759	33501:	contig of 743 bp	in length
33502	33601:	gap of 100 bp	in length
33602	34347:	contig of 746 bp	in length
34348	34447:	gap of 100 bp	in length
34448	35165:	contig of 718 bp	in length
35166	35265:	gap of 100 bp	in length
35266	35998:	contig of 733 bp	in length
35999	36098:	gap of 100 bp	in length
36099	36802:	contig of 704 bp	in length
36803	36902:	gap of 100 bp	in length
36903	37632:	contig of 730 bp	in length
37633	37732:	gap of 100 bp	in length
37733	38454:	contig of 722 bp	in length
38455	38554:	gap of 100 bp	in length
38555	39275:	contig of 721 bp	in length
39276	39375:	gap of 100 bp	in length
39376	40113:	contig of 738 bp	in length
40114	40213:	gap of 100 bp	in length
40214	40948:	contig of 735 bp	in length
40949	41048:	gap of 100 bp	in length
41049	41792:	contig of 744 bp	in length
41793	41892:	gap of 100 bp	in length
41893	42630:	contig of 738 bp	in length
42631	42730:	gap of 100 bp	in length
42731	43459:	contig of 729 bp	in length
43460	43559:	gap of 100 bp	in length
43560	44277:	contig of 718 bp	in length
44378	44377:	gap of 100 bp	in length
44378	45120:	contig of 743 bp	in length
45121	45220:	gap of 100 bp	in length
45221	45942:	contig of 722 bp	in length
45943	46042:	gap of 100 bp	in length
46043	46775:	contig of 733 bp	in length
46776	46875:	gap of 100 bp	in length
46876	47609:	contig of 734 bp	in length
47610	47709:	gap of 100 bp	in length
47710	48446:	contig of 737 bp	in length
48447	48546:	gap of 100 bp	in length
48547	49285:	contig of 739 bp	in length
49286	49385:	gap of 100 bp	in length
49386	50178:	contig of 793 bp	in length
50179	50278:	gap of 100 bp	in length
50279	51008:	contig of 730 bp	in length
51009	51108:	gap of 100 bp	in length
51109	51846:	contig of 738 bp	in length
51847	52672:	gap of 100 bp	in length
52673	52772:	contig of 726 bp	in length
52773	53772:	gap of 100 bp	in length
53773	53806:	contig of 733 bp	in length
53807	54330:	gap of 100 bp	in length
54331	54430:	contig of 725 bp	in length
54431	55166:	contig of 736 bp	in length
55167	55266:	gap of 100 bp	in length

	Query Match	17.5%	Score 44.2	DB 2	Length 71032	
	Best local similarity	44.1%	Pred. No. 24			
	Matches	97	Conservative	0	Mismatches	123; Indels 0; Gaps 0;
OY	* 55267	55979:	contig of 713 bp	in length		
	*	55980	56079:	gap of 100 bp		
	*	56080	56823:	contig of 744 bp	in length	
	*	56823	56923:	gap of 100 bp		
	*	56924	57626:	contig of 703 bp	in length	
	*	57627	57726:	gap of 100 bp		
Dd	3	GCGGGGAGGCGGCGCGGATGAGGCTGTATTCGTCCCTTGCGCCTTCACTCCACAGGC	62			
Dd	28390	GCCCCNCGGGGGGGGCGCGCNCGNGAGNCCCCTGGCGGCGGANCNCNCGGGGCCNNNNCNN	2833			
OY	63	CAGAAGCGCCCAACAGAGACCCCAAGTCCCGAATTGTTCCACAGTCTTGCGATCAGAGCA	122			
Dd	28330	NGCGCGGAGCGCGCGNCGAGNCCCAGNNCCNCCCGGGGGGGGGCGCGCGCGCGNCCC	2827			
OY	123	GGACCAAGGAGCCAGGAATCTGCGCGCGCCCGCCCTGCGCTTGCGCGGAGGAAGCTCC	182			
Dd	28270	GGGNCGCCGGGGGCGCCNNCCCGCCCGCCCGCGCGCCGAGNCGGGGGGGGAGNCCNCGCC	2821			
OY	183	CTCACNAGAGGAAGTCTCCCTCAACCCGAGCCAGCCCTGC	222			
Dd	28210	NGCNCGCCCGGGGCGGTCCGTTGNTGTGTCNCTCGCGCGC	28171			
RESULT 16						
LOCUS	AC022707	88064 bp	DNA	linear	HTG-13-Jul-2000	
DEFINITION	Homo sapiens clone RP11-59L21, LOW-PASS SEQUENCE SAMPLING.					
VERSION	AC022707.2	GI:9146450				
KEYWORDS	HTG; HTGS PHASFO					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
REFERENCE	1 (bases 1 to 88064) Britten,B., Linton,L., Nussbaum,C. and Landér,E. Homo sapiens chromosome, clone RP11-59L21 Unpublished					
AUTHORS	2 (bases 1 to 88064) Britten,B., Linton,L., Nussbaum,C., Landér,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barua,N., Beckert,R., Bedalov,F., Boyslavsky,I., Boukhgalter,B., Brown,A., Burkett,G., Castle,A., Choepel,V., Collangelo,M., Collins,S., Collymore,A., Cooke,P., DeRubeis,K., Dewar,K., Domino,M., Doyle,N., Fenecher,J., Ferreira,P., FitzHugh,W., Forrest,C., Gage,D., Galagan,J., Gardland,S., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.C., Johnson,R., Jones,C., Klam,L., Karalas,A., Klein,J., Landers,T., Lebochky,J., Levine,R., Liu,C., Liu,G., Locke,K., Macdonald,P., Margulis,N., McManus,P., McGuck,A., McKernan,K., McMasters,R., Meldrum,J., Meneses,L., Morrow,J., Naylor,J., Nichols,C.H., O'Connor,T., O'Donnell,P., Oliver,T.M., Peterson,K., Pierre,N., Pisanic,C., Pollara,V., Raymond,C., Riley,R., Rochman,D., Roy,A., Santos R., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye S., Theodore J., Tirrell A., Vasilev H., Viel,R., Vo,A., Wu,X., Wymann D., Ye,W.Y., Zimmer,A. and Zody M.					
TITLE	Direct Submission					
JOURNAL	Submitted (06-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 300 Charles Street, Cambridge, MA 02141, USA On Jul 13, 2000 this sequence version replaced gi:5922799. All repeats were identified using RepeatMasker: Smtc, A.E.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html					
COMMENT	-----Genome Center Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR Web site: http://www-seq.wi.mit.edu Contact: sequence_submissions@genome.wi.mit.edu					

```
----- Project Information
Center project name: L5349
Center clone name: 59_L_21

* NOTE: This record contains 89 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

1      857: contig of 857 bp in length
858    157: gap of 100 bp
958    1863: contig of 906 bp in length
1864    1963: gap of 100 bp in length
1964    2869: contig of 906 bp in length
2870    3854: contig of 885 bp in length
3855    3954: gap of 100 bp
3955    4838: contig of 884 bp in length
4839    5830: contig of 892 bp in length
5831    5930: gap of 100 bp
5931    6826: contig of 896 bp in length
6827    6926: gap of 100 bp
6927    7854: contig of 928 bp in length
7855    7954: gap of 100 bp
7955    8854: contig of 900 bp in length
8855    8954: gap of 100 bp
8955    9857: contig of 903 bp in length
9858    9957: gap of 100 bp
9958    10830: contig of 873 bp in length
10831    10930: gap of 100 bp
10931    11813: contig of 883 bp in length
11814    11913: gap of 100 bp
11914    12788: contig of 875 bp in length
12789    12888: gap of 100 bp
12889    13770: contig of 882 bp in length
13771    13870: gap of 100 bp
13871    14745: contig of 875 bp in length
14746    14845: gap of 100 bp
14846    15751: contig of 906 bp in length
15752    15851: gap of 100 bp
15852    16748: contig of 897 bp in length
16749    16848: gap of 100 bp
16849    17762: contig of 914 bp in length
17763    17862: gap of 100 bp
17863    18750: contig of 888 bp in length
18751    18850: gap of 100 bp
18851    19733: contig of 883 bp in length
19734    19833: gap of 100 bp
19834    20703: contig of 870 bp in length
20704    20803: gap of 100 bp
20804    21815: contig of 912 bp in length
21816    21915: gap of 100 bp
21916    22738: contig of 923 bp in length
22739    22838: gap of 100 bp
22839    23737: contig of 899 bp in length
23738    23837: gap of 100 bp
23838    24702: contig of 865 bp in length
24703    24802: gap of 100 bp
24802    25686: contig of 884 bp in length
25687    25786: gap of 100 bp
25787    26682: contig of 896 bp in length
26683    26782: gap of 100 bp
26783    27686: contig of 904 bp in length
27687    28687: gap of 100 bp
28688    28787: contig of 901 bp in length
28787    29687: gap of 100 bp
29688    29787: contig of 900 bp in length
29788    30713: contig of 926 bp in length
30714    30813: gap of 100 bp
30814    31700: contig of 887 bp in length
31701    31800: gap of 100 bp
31801    32654: contig of 883 bp in length
32655    32754: gap of 100 bp
32755    33671: contig of 917 bp in length
33672    33771: gap of 100 bp
33772    34666: contig of 895 bp in length
34667    34766: gap of 100 bp
34767    35551: contig of 885 bp in length
35552    35751: gap of 100 bp
35752    36620: contig of 869 bp in length
36621    36720: gap of 100 bp
36721    37596: contig of 876 bp in length
37597    37696: gap of 100 bp
37697    38561: contig of 865 bp in length
38562    38661: gap of 100 bp
38662    39533: contig of 872 bp in length
39534    39633: gap of 100 bp
39634    40549: contig of 916 bp in length
40550    40650: gap of 100 bp
40650    41357: contig of 708 bp in length
41358    41457: gap of 100 bp
41458    42385: contig of 928 bp in length
42386    42486: gap of 100 bp
42487    43425: contig of 939 bp in length
43426    43525: gap of 100 bp
43526    44404: contig of 880 bp in length
44405    44504: gap of 100 bp
44505    45405: contig of 901 bp in length
45406    45505: gap of 100 bp
45506    46375: contig of 870 bp in length
46376    46475: gap of 100 bp
46476    47355: contig of 880 bp in length
47356    47455: gap of 100 bp
47456    48340: contig of 885 bp in length
48341    48440: gap of 100 bp
48441    49320: contig of 880 bp in length
49321    49420: gap of 100 bp
49421    50324: contig of 904 bp in length
50325    50424: gap of 100 bp
50425    51321: contig of 897 bp in length
51322    51421: gap of 100 bp
51422    52350: contig of 925 bp in length
52351    52450: gap of 100 bp
52451    53355: contig of 905 bp in length
53356    53455: gap of 100 bp
53456    54320: contig of 865 bp in length
54321    54420: gap of 100 bp
54421    55326: contig of 906 bp in length
55327    55426: gap of 100 bp
55427    56308: contig of 882 bp in length
56309    56408: gap of 100 bp
56409    57299: contig of 891 bp in length
57300    57399: gap of 100 bp
57399    58292: contig of 893 bp in length
58293    58393: gap of 100 bp
58394    59250: contig of 858 bp in length
59251    59350: gap of 100 bp
59351    60180: contig of 830 bp in length
60181    60280: gap of 100 bp
60281    61198: contig of 918 bp in length
61199    61298: gap of 100 bp
61299    62170: contig of 872 bp in length
62171    62270: gap of 100 bp
62271    63184: contig of 914 bp in length
63185    63284: gap of 100 bp
63285    64181: contig of 897 bp in length
64182    64281: gap of 100 bp
64282    65201: contig of 920 bp in length
```



```

* 65202 65301: gap of 100 bp
* 66155: contig of 854 bp in length
* 66156 66255: gap of 100 bp
* 66256 67165: contig of 910 bp in length
* 67266 67265: gap of 100 bp
* 67266 68164: contig of 899 bp in length
* 68166 68264: gap of 100 bp
* 68265 69159: contig of 895 bp in length
* 69160 69259: gap of 100 bp
* 69260 70132: contig of 873 bp in length
* 70133 70232: gap of 100 bp

Query Match 17.5% Score 44; DB 2; Length 88064;
Best Local Similarity 47.0%; Pred. No. 24;
Matches 116; Conservative 0; Mismatches 131; Indels 0; Gaps 0;

Qy 1 CGCGCGGAGAGCGCGCGGAGTGAAGCGCTGATCGTCCCTGCGCGCTCCACCTCCCGAGG 60
Db 25277 CGCGCGGAGAGCGCGCGGAGTGAAGCGCTGATCGTCCCTGCGCGCTCCACCTCCCGAGG 25336
Qy 61 CGCAGAGAGCGCGCGCGGAGTGAAGCGCTGATCGTCCCTGCGCGCTCCACCTCCCGAGG 120
Db 25337 GCGCGGAGAGCGCGCGGAGTGAAGCGCTGATCGTCCCTGCGCGCTCCACCTCCCGAGG 25396
Qy 121 CAGGAGACGAGGAGCGCGGAGTGAAGCGCTGATCGTCCCTGCGCGCTCCACCTCCCGAGG 180
Db 25397 GCGCGGAGAGCGCGCGGAGTGAAGCGCTGATCGTCCCTGCGCGCTCCACCTCCCGAGG 25456
Qy 181 CCCTCAGCGAGGAGGAGCTCCCTCAGCGCGCGGAGTGAAGCGCTGATCGTCCCTGCGCGCT 240
Db 25457 GCGCGGAGAGCGCGCGGAGTGAAGCGCTGATCGTCCCTGCGCGCTCCACCTCCCGAGG 25516
Qy 241 AGACCGC 247
Db 25517 CGCGGAGC 25523

RESULT 17
AC079420/c 239130 bp DNA 1linear HTG 01-SEP-2000
LOCUS Mus musculus chromosome 16 clone RP23-104L12, WORKING DRAFT
DEFINITION
ACCESSION AC079420
VERSION AC079420.1 GI:9958032
KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITL 1 (bases 1 to 239130)
JOURNAL DOB Joint Genome Institute.
REFERENCE
AUTHORS Sequencing of Mouse
TITL 2 (bases 1 to 239130)
JOURNAL DOB Joint Genome Institute.
REFERENCE
AUTHORS Direct Submission.
TITL Submitted (01-SEP-2000) Production Sequencing Facility, DOE Joint
JOURNAL Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 0
Center clone name: RPCI-23_104L12
-----
Summary Statistics
Consensus quality: 15414 bases at least Q40
Consensus quality: 183510 bases at least Q30
Consensus quality: 194836 bases at least Q20
Estimated insert size: 222300; agarose-fp estimation
Estimated insert size: 233130; sum-of-contigs estimation

```

```

Quality coverage: 3.12 in Q20 bases; agarose-fp estimation.
NOTE: This is a 'working draft' sequence. It currently
* consists of 61 contigs. The true order of the pieces is
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 1030: contig of 1030 bp in length
1031 1130: gap of unknown length
1131 2520: contig of 1390 bp in length
2521 2620: gap of unknown length
2621 3633: contig of 1013 bp in length
3634 3733: gap of unknown length
3734 5381: contig of 1648 bp in length
5382 5482: gap of unknown length
5483 6793: gap of unknown length
6793 6893: gap of unknown length
6893 8479: gap of unknown length
8479 8578: gap of unknown length
8578 9634: contig of 1056 bp in length
9635 9735: gap of unknown length
9735 10792: contig of 1057 bp in length
10792 10891: gap of unknown length
10891 12358: contig of 1367 bp in length
12358 12359: gap of unknown length
12359 13772: gap of unknown length
13772 13871: gap of unknown length
13871 14988: contig of 1127 bp in length
14988 15099: gap of unknown length
15099 16261: contig of 1163 bp in length
16261 17426: gap of unknown length
17426 17526: gap of unknown length
17527 18541: gap of unknown length
18541 20200: contig of 1559 bp in length
20200 20300: gap of unknown length
20300 21423: contig of 1123 bp in length
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34198 34298: gap of unknown length
34298 36147: contig of 1849 bp in length
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62566	64722	gap of unknown length
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64825	70728	contig of 5904 bp in length
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70829	74339	contig of 3505 bp in length
74334	74433	gap of unknown length
74434	80038	contig of 5662 bp in length
80038	80138	gap of unknown length
80138	84713	contig of 4518 bp in length
84714	84813	gap of unknown length
84814	89091	contig of 4278 bp in length
89092	89192	gap of unknown length
89192	94478	contig of 5287 bp in length
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98799	98898	gap of unknown length
98899	103681	contig of 4783 bp in length
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103782	109611	contig of 5836 bp in length
109618	109717	gap of unknown length
109718	115583	contig of 5872 bp in length
115589	115689	gap of unknown length
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122308	129310	contig of 7003 bp in length
129311	131067	gap of unknown length
131068	131167	contig of 5657 bp in length
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144563	151374	contig of 8722 bp in length
151375	151474	gap of unknown length
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159604	158603	gap of unknown length
159704	162375	contig of 9572 bp in length
162376	163375	gap of unknown length
163376	176542	contig of 7167 bp in length
176543	176542	gap of unknown length
176543	186218	contig of 8476 bp in length
186219	186218	gap of unknown length
186219	196151	contig of 9933 bp in length
196152	196251	gap of unknown length
196252	200073	contig of 8822 bp in length
200074	204173	gap of unknown length
204174	211011	contig of 15928 bp in length
217102	211201	gap of unknown length
217202	220352	contig of 10151 bp in length
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FEATURES				
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	/clone="RP23-104112"			
	/clone_11b="RPct mouse BAC library 23"			
BASE COUNT	63482 a	5186 c	54864 g	59989 t
ORIGIN			8929	others
Query Match	17.5%	Score 44	DB 2	Length 239130
Best Local Similarity	43.5%	Pred. 18		
Matches 101; Conservative	0	Mismatches 131	Indels	0
			Gaps	0

[illegible]

RESULT 18	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	REFERENCE	AUTHORS
AC100379	AC100379	Mus musculus clone RP2-131C19, low-PASS SEQUENCE SAMPLING.	AC100379	GI:25815482	HTG; HTGS PHASED.	Mus musculus (house mouse)	Mus musculus	Embryota; Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.	Bitren, B., Nusbaum, C. and Lander, E.	Unpublished	2 (bases 1 to 59008)	Bitren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., D.	

Anderson, S., Barina, N., Bastien, V., Boguslavskiy, L., Bourkhalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Chepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeKrellano, K., Dewar, K., Diaz, J. S., Dodge, S., Fato, S., Ferreira, P., Fitzhugh, W., Gase, D., Galagan, J., Gard-Gardna, S., Gilde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, A., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kama, A., Karatas, A., Kells, C., Lacroque, K., Lamas, R., Lamas, R., Landers, T., Lehotzky, J., Levine, R., Liu, G., Maclean, C., MacDonald, P., Major, J., Margis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPheters, R., Meldrum, J. C., Menus, L., Mhova, T., Mienga, V., Murphy, T., Naylor, C., Nguyen, C., O'Neil, C., Norman, C. H., O'Donnell, P., O'Donnell, N., Pollara, V., Oliver, J., Peterson, K., Poonkran, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Ribick, R., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schnibbek, R., Seaman, S., Severy, P., Spencer, B., Stenge-Thomann, N., Steadovic, N., Strauss, N., Subramanian, A., Talamas, J., Teisfay, S., Theodore, J., Topham, K., Travers, M., Travis, N., Triggilio, J., Vassiliev, H. C., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission  
Submitted (32-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
3 (bases 1 to 59008)  
Britten, B., Nisbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,

Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Bokuniewicz, B., Camarata, J., Chang, J., Chazaro, B., Chopely, J., Collamore, A., Cook, P., Cooke, P., Dearellano, K., Dewar, K., Diaz, J. S., Dodge, S., Fero, S., Ferreira, P., Fitzgerald, D., Gagar, D., Galagan, J., Gardya, S., Gord, S., Graham, L., Grand-Pierre, N., Hafetz, N., Hago, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamar, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Ton, K., Liu, G., Maclean, C., MacDonald, P., Major, J., Matthews, C., McCarthy, M., Meldrum, J., Meneus, I., Mihova, T., Norman, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Nolema, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Punnkhaug, P., Pierre, N., Raymond, C., Retta, R., J., Rogov, P., Roman, J., Roy, A., Schauer, S., Schnuppach, R.,

TITLE  
JOURNAL  
COMMENT

Seaman, S., Severy, P., Smith, C., Spencer, B., Strange-Thomann, N.,  
Stojanovic, N., Talamas, J., Testaye, S., Theodore, J., Toppan, K.,  
Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X.,  
Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A., and Zody, M.  
Direct Submission  
Submitted (28-NOV-2002) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Nov 28, 2002 this sequence version replaced gi:24962776.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence\_submissions@genome.wi.mit.edu  
----- Project Information  
Project name: 115213  
Center project name: 131\_C\_19  
Center clone name: 131\_C\_19

\* NOTE: This record contains 74 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

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825 824: gap of 100 bp  
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1628 1627: gap of 100 bp  
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3115 3114: contig of 690 bp in length  
3215 3214: gap of 160 bp  
3925 3924: contig of 711 bp in length  
4026 4025: gap of 160 bp  
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4829 4828: gap of 100 bp  
5539 5538: contig of 710 bp in length  
5639 5638: gap of 100 bp  
6354 6353: contig of 716 bp in length  
6455 6454: gap of 100 bp  
7153 7152: contig of 704 bp in length  
7253 7252: gap of 100 bp  
7353 7352: contig of 719 bp in length  
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Fragment Chain: 4"  
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Matches 102; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

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Db 57809 CC 57868  
QY 97 GTTGCACGGTCTGTGATCAGAGGACAGGACCAAGGAGCCAGGAACTGCGCCCGCCCGC 156  
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LOCUS Homo sapiens clone RP11-2905, LOW-PASS SEQUENCE SAMPLING.  
DEFINITION AC022663  
ACCESSION AC022663.2 GI:9139598  
VERSION HTG; HTGS; PHASE0.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 63082)  
AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.  
TITLE Homo sapiens, clone RP11-2905  
JOURNAL Unpublished  
AUTHORS 2 (bases 1 to 63082)  
Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,  
Anderson, S., Baldwin, J., Barna, N., Becker, R., Beda, F.,  
Bonislawski, L., Bonhag, A., Brown, A., Burkett, G., Castle, A.,  
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Roy, A., Santos, R., Severy, P., Spencer, B., Strange-Thomann, N.,  
Stojanovic, N., Sudbraman, A., Talamas, D., Tesfaye, S., Theodore, J.,  
Tirrell, A., Vasilev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W., J.,  
Zimmer, A. and Zody, M.

TITLE Direct Submission  
JOURNAL Submitted (06-FEB-2000) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
COMMENT On Jul 13, 2000 this sequence version replaced gi:910643.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: MIBR  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence submissions@genome.wi.mit.edu  
Project Information  
Center project name: L4854  
Center clone name: 29\_O\_5

NOTE: This record contains 77 individual  
sequencing reads that have not been assembled into  
contigs. Runs of N are used to separate the reads  
and the order in which they appear is completely  
arbitrary. Low-pass sequence sampling is useful for  
identifying clones that may be gene-rich and allows  
overlap relationships among clones to be deduced.  
However, it should not be assumed that this clone  
will be sequenced to completion. In the event that  
the record is updated, the accession number will  
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*	28738	28837	gap of 100 bp	in length
*	28838	29556	contig of 722 bp	in length
*	29560	29652	gap of 100 bp	in length
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*	31185	31284	gap of 100 bp	in length
*	31285	32011	contig of 727 bp	in length
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*	49248	49967	contig of 720 bp	in length
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*	51567	51666	gap of 100 bp	in length
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Best Local Similarity	50.2%	Pred. No. 32		
Matches 106, Conservative	0	Mismatches	105	Indels 0, Gaps 0

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61 CGCAGAAAGCGCCACGAGACCCACAGTGCACGATCTGGATCAGAG 120

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E  
FF  
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AL138694 157264 bp DNA linear PRI 09-MAY-2001

complete sequence.

AL138694.18 GL:14018244

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INTERACTION	ADAMTS-1
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AND	ADAMTS-1
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

**AUTHORS** Sycamore, N.  
**TITLE** Direct Submission

CB10 1SA, UK. E-mail enquiries: [humquerry@sanger.ac.uk](mailto:humquerry@sanger.ac.uk) Clone

COMMENT On May 11, 2001 this sequence version replaced gi:13989969.

together with a note of the overlapping clone name. Note that the

corresponding to the overlapping clone, as we submit sequences with

This sequence was finished as follows unless otherwise noted: all reactions were either double-stranded or commenced with an alternate

30): an attempt was made to resolve all sequencing problems, such as chemistry or covered by high quality data (i.e., phred quality >=

one plasmid subclone or more than one M13 subclone; and the

abbreviations are used to associate primary accession numbers given in the feature table with their source databases: EMBL, SWISS-PROT, PDB, and TrEMBL.

database can be found at

was generated from part of bacterial clone contigs of human

Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr13>

of Pieter de Jong. For further details see

http://www.chori.org/bacpac/home.htm  
VECTOR: PBAC3.6  
IMPORTANT: This sequence is not the entire insert of clone RP11-330C15. It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true right end of clone RP11-330C15 is at 157264 in this sequence. The true left end of clone RP11-465C24 is at 130978 in this sequence. The true right end of clone RP11-153J24 is at 100 in this sequence. The true right end of clone RP11-153J24 is at 100 in this sequence.

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Query Match 17.3%; Score 43.6; DB 9; Length 157264;
Best Local Similarity 52.8%; Pred. No. 24;
Matches 94; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

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RESULT 23
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VERSION HTG; HTGS; PHASE0.
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SOURCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
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Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J.,
Zimmer, A. and Zody, M.
Direct Submission
Submitted (18-AUG-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

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http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: MIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L10783
Center clone name: 461_A_14

* NOTE: This record contains 79 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

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1563 2392: contig of 731 bp in length
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not be finished!  
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OY 67 AGGCGCGCGCGCGGAGTGAAGCTGATGCTCCCTGCGCCCTTCCACTTCCCAAGCGCAGA 126  
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RESULT 28  
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DEFINITION Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1,  
BAC clone:B1075D06.

ACCESSION AP003202 BA000010  
VERSION AP003202.3 GI:20804533

KEYWORDS  
SOURCE  
ORGANISM

REFERENCE  
AUTHORS  
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Oryza sativa (japonica cultivar-group)  
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Ito, Y., Itoh, Y., Iwabuchi, A., Kamiya, K., Karasawa, M., Katagiri, S.,  
Kikuta, A., Kobayashi, N., Kono, I., Machida, K., Maehara, T.,  
Mizuno, Y., Mizubayashi, T., Mukai, Y., Nagasaka, H., Nakashima, M.,  
Nakama, Y., Nakamichi, Y., Nakamura, M., Namiki, N., Negishi, M.,  
Ohta, I., Ono, N., Saji, S., Sakai, K., Shibata, M., Shimokawa, T.,  
Shimura, A., Song, J., Takazaki, Y., Terasawa, K., Tsuji, K., Waki, K.,  
Yamaguchi, H., Yamane, H., Yano, T., Yoshida, S., Yoshikawa, K.,  
Zhong, H., Zhang, J., and Goto, T., Ito, H., Hahn, J. H., Kim, H. I., Eun, M. Y.,  
Yano, M., Wang, J., and Goto, T., Ito, H., Hahn, J. H., Kim, H. I., Eun, M. Y.,  
Zhang, H., Zhang, J., and Goto, T., Ito, H., Hahn, J. H., Kim, H. I., Eun, M. Y.,  
The genome sequence and structure of rice chromosome 1  
Nature 420 (6913), 312-316 (2002)

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
AUTHORS  
JOURNAL  
TITLE  
DIRECT SUBMISSION  
Submitted (19-FEB-2001) Takuji Sasaki, National Institute of  
Agrobiological Sciences, Rice Genome Research Program, Kannondai  
2-1-2, Tsukuba, Ibaraki 305-8602, Japan  
(E-mail:tsasaki@nias.affrc.go.jp, URL: <http://rgp.dna.affrc.go.jp/>,  
Tel:81-298-38-7441, Fax:81-298-38-7468)

## COMMENT

On May 15, 2002 this sequence version replaced gi:14456616.  
Genes were predicted from the integrated results of the following:  
GENSCAN1.0, BLASTX2.0, BLASTY2.0 as well as SplicePredictor  
(October 1998 version). The genomic sequence was searched against  
NCBI NonRedundant Protein database, or  
(<ftp://ncbi.nlm.nih.gov/blast/db>) and the cDNA sequence database at  
RGP. Protein homologues of the coding regions were searched against  
NCBI NonRedundant Protein database with BLASTP2.0. ESTs represent  
the identified cDNA sequences using BLASTN 2.0 with the  
corresponding DB accession no. and RGP clone ID.  
A gene with identity or significant homology to a protein is  
classified based on the protein name to indicate the homology level  
such as same name, 'putative-' and '-like protein'. A gene without  
significant homology to any protein but with EST homology (covering  
almost the entire length of partial sequence) is classified as an  
'unknown' protein. A gene predicted with a gene prediction program  
is classified as a 'hypothetical' protein.  
The orientation of the sequence is from -21M13 to M13rev of the  
BAC clone. This sequence of B1075D06 clone has an overlap with  
F0504D03 (DBU: AP002970) clone at the position 1 to 14,205 of 5'  
end. Detailed information on overlap and assembly quality together  
with annotation of this entry is available at  
<http://rgp.dna.affrc.go.jp/genomeseq.html>.

## FEATURES

## source

1..130528  
Location/Qualifiers

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/product="putative ribosomal protein"  
/protein\_id="BAB92227.1"  
/db\_xref="GI:20804533"

gene  
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16420..16494,16574..16783,16974..17126,17208..17431,  
17750..17867,17963..18101,18150..18391,18489..18594,  
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join(11463..11688,12261..12419,13501..13664,14223..14330,  
15140..15310,15390..15923,16019..16093,16169..16297,  
16420..16494,16574..16783,16974..17126,17208..17431,  
17750..17867,17963..18101,18150..18391,18489..18594,  
18713..18855,18928..19062,19159..19264,20469..20845)  
/gene="B1075D06.2"

CDS  
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16420..16494,16574..16783,16974..17126,17208..17431,  
17750..17867,17963..18101,18150..18391,18489..18594,  
18713..18855,18928..19062,19159..19264,20469..20845)  
/gene="B1075D06.2"

/note="hypothetical protein  
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/codon\_start=1  
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/db\_xref="GI:20804535"

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AREDLRLREFDPALPPDILVARASAPPGDPSDLEEKIAAEKIALDYDLRL  
NCAVRLRLREFDPALPPDILVARASAPPGDPSDLEEKIAAEKIALDYDLRL  
EKKITILRENETILKDNESIGAEKALISREVSANQIALRKSLPAKQDIKEKKT  
VODLKOSIDVORKEINDCRARETSLKGMHIEGRSSRLSGDGTGILPANSMEIIVL  
SEEDNLKSGESTITSLASREVSILAKKKHHEMESLGSPPREVECSPTANEGY  
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SKDALETTITVDALPKTVPYVLTINREBELDILICALEKHPDSVRLTHLLEK  
IKRDEGQRRLINDACVELAKSYGRTTEILPCOEMRLTILPPIPNIDKRYKELMEFO  
AVVREIRSLTSLISTVQDIVERASATVVERAALHNTLTLLPPIPNIDKRYKELMEFO  
LVCPDSGAVVVALKEIVPAVVMGDKDLITLILAHILASQRCPPPSGVBGALDS

HLRVLGEORERNIVDLRLMTLELPFIHOKAISTCPFAADPSTGTMPESYKSKCLKL  
YAGDTEWSPAMHTECLPDLIKLACLLPAKEDNLRVIRKYLIDVSGRGIDYLEH  
VMLPVLVAGIDSDSDTYPLATOSFMRHRTAETIAEKYICVCLPILSGILYEH  
PSKROOLEEYLRKLIQNTYKDSFMRHRTAETIAEKYICVCLPILSGILYEH  
ISDNLKTNMAALLKALVPIYSKVASTHVALITLIGSDNLCYKVAISAFAGVAV  
HKNMNVYDKIRIQMDAFEDSDHEATSVIRALAVAPHTDLREYLSIKRFLTS  
APPTNDIERREINAFCEALRAVDATDLPATVSRDLPLPSIONLKEDDLPAPK  
BALVETIARSGGKLESGKMGALHIGASMSFSGSSLLVKKESGEQDNTAATTP  
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in CDS  
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36726. .36842,37287. .37501,38530. .38685,38773. .38972.  
39372. .39529,39766. .39862,40183. .40274,40463. .40636)  
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IOLADVNLKSTPOLVELVEDSKEMELMSLSPKILLRMNFKKGGKPPRTYNTS  
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YINNVEDLRNGWVLEVIDKIAFGSVMMKANRPITLPRKVENCOVLKIKELK  
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GTVDLSHQFSGQIPASLGRLEKXYIDLTVNNLSGPIPGQALENGPALFVGNPRL  
GCPILKNCSPDAMPSPNPVPKDGSGAPGAKKKGKGAIVAVISDVAGILILA  
LVFECYRRAVASSKKGNGAGSGRCGDCGCFRDEBATESEHDTQDLVPLA  
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IGKVRHPSIVTLRAYMSYDEKLLIYDIPNGSLSAAHGRGEGMTFPLWDRRLKI  
MGVAKGLSFLHESPCKYIHGDLRPNNVLGSMNEPIYISFGGRLANIIGSPFQ  
SDHAGIERAKSQSDASVSPVKGSCCYQABEALTKLPKSMVYSVGLIMING  
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/note="3' LTR"  
complement(58729. .62637)  
/gene="B1075D06.6"  
complement(58729. .62637)  
/gene="B1075D06.6"  
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transposon TNT 1-94"  
/protein\_id="BAB92231.1"

Query Match 17.0% Score 42.8; DB 8; Length 130528;  
Best Local Similarity 48.5%; Pred. No. 36;  
Matches 116; Conservative 0; Mismatches 123; Indels 0; Gaps 0;  
Db 7 GGGAGCGCGCGGAGTGAAGCTGATCGTCCCTGCGGCTTCACCTCCAGCGCAG 66  
108065 GGGAGCGCGGAGTGAAGCTGATCGTCCCTGCGGCTTCACCTCCAGCGCAG 108124  
Db 67 AGGCGCGCGGAGTGAAGCTGATCGTCCCTGCGGCTTCACCTCCAGCGCAG 126  
108125 CCGCGCGCGGAGTGAAGCTGATCGTCCCTGCGGCTTCACCTCCAGCGCAG 108184  
Db 127 CAGAGCGCGGAGTGAAGCTGATCGTCCCTGCGGCTTCACCTCCAGCGCAG 186  
108185 GATGGAGCGCGGAGTGAAGCTGATCGTCCCTGCGGCTTCACCTCCAGCGCAG 108244  
Db 187 CCGAGCGCGGAGTGAAGCTGATCGTCCCTGCGGCTTCACCTCCAGCGCAG 245  
108245 CCGCGCGCGGAGTGAAGCTGATCGTCCCTGCGGCTTCACCTCCAGCGCAG 108303

RESULT 29  
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LOCUS Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1,  
DEFINITION BAC clone: B106H10.  
ACCESSION AP003562  
VERSION AP003562.3 GI:20805044  
KEYWORDS Oryza sativa (japonica cultivar-group)  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
REFERENCE  
1 Sasaki, T., Matsumoto, T., Yamamoto, K., Sakata, K., Baba, T.,  
Katayose, Y., Wu, J., Nishimura, Y., Cheng, Z., Nagamura, Y.,  
Antonio, B.A., Kanemori, H., Hosokawa, S., Masukawa, M., Arikawa, K.,  
Chiden, Y., Hayashi, M., Okamoto, M., Ando, T., Aoki, K., Arita, K.,  
Hamada, M., Harada, C., Hijiishi, S., Honda, M., Ichikawa, Y.,  
Ikonuma, A., Iijima, M., Ikeda, M., Ikono, M., Itoh, S., Itoh, T.,  
Itoh, Y., Itoh, Y., Iwabuchi, A., Kamaya, K., Karasawa, W., Katagiri, S.,  
Kikuta, A., Kobayashi, N., Kono, I., Machita, K., Mebara, T.,  
Mizuno, H., Mizubayashi, T., Mukai, Y., Nagasaki, H., Nakashima, M.,  
Nakama, Y., Nakamichi, Y., Nakamura, M., Nankai, N., Negishi, M.,  
Ohta, I., Ono, N., Saji, S., Sakai, K., Shibata, M., Shimokawa, T.,  
Shomura, A., Song, J., Takezaki, Y., Terasawa, K., Tsuji, K., Waki, K.,  
Yamagata, H., Yamane, H., Yoshiki, S., Yoshikawa, R., Yukawa, K.,  
Zhong, H., Iwama, H., Endo, T., Ito, H., Hahn, J.H., Kim, H.I., Eun, M.Y.,  
Yano, M., Jiang, J., and Gotohori, T.  
The genome sequence and structure of rice chromosome 1  
Nature 420 (6913), 312-316 (2002)  
JOURNAL MEDLINE 22337376  
PUBMED 12447438  
REFERENCE 2 (bases 1 to 136357)  
AUTHORS Sasaki, T., Matsumoto, T., and Yamamoto, K.  
TITLE Direct Submission



JOURNAL Submitted (02-MAY-2001) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan  
 (E-mail: tsasak@nias.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/, Tel: 81-298-38-7441, Fax: 81-298-38-7468)  
 On May 15, 2002 this sequence version replaced gi:1816331. Genes were predicted from the integrated results of the following: GENSSCAN 1.0, BLASTX 2.0, as well as SplicePredictor (October 1998 version). The genomic sequence was searched against NCBI NonRedundant Protein database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at RGP. Protein homologies of the coding regions were searched against NCBI NonRedundant Protein database with BLASTP 2.0. ESTs represent the identified cDNA sequences using BLASTV 2.0 with the corresponding DBJ accession no. and RGP clone ID.

A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative', and '-like protein'. A gene without significant homology to any protein but with EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted with a gene prediction program is classified as a 'hypothetical' protein.  
 The orientation of the sequence is from -21M3 to M13rev of the BAC clone. This sequence of B1108H10 clone has an overlap with B1075D06 (DBJ: AP003202) clone at the position 1 to 34,607 of 5' end and an overlap with B1003B09 (AP004222) at the position of 133,578 to 136,357 of 3' end. Detailed information on overlap and assembly quality together with annotation of this entry is available at <http://rgp.dna.affrc.go.jp/GenomeSeq.html>.

## FEATURES

## source

1. 136357  
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 /mol\_type="genomic DNA"  
 /cultivar="Nipponbare"  
 /db\_xref="taxon:39947"  
 /chromosome="1"

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 /note="probably inactive due to stop codon(s) in CDS"

## CDS

/gene="B1108H10.1"  
 /note="hypothetical protein"  
 /codon\_start=1  
 /protein\_id="BAB92719.1"  
 /db\_xref="GI:20805045"

## gene

7428..8396  
 /gene="B1108H10.2"  
 /note="probably inactive due to no termination codon in CDS"

## misc\_feature

7428..8396  
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 similar to Oryza sativa chromosome 1, P0035H10.7"

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 15996..16158,20154..20346)  
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## CDS

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 /protein\_id="BAB92721.1"

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 YMRKGMFPMNGHILHKKAMPQVETORANNAAGGQGNNGVARSPEAGETMDAG  
 TTSKSSVANDMSVSGSGVQVQLRRRTLTAGNGDGVDEHVIASQRAHPFLSM  
 ELTPAMNPSGSGELCWCTPVSTENHNGFTTHPECTFESTEGVKEYIEHPALIEPAK  
 ELTAMKTLIDMPTFANVS"  
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## LTR

## LTR

## LTR

## LTR

## gene

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 TIEISRTMEVAVEIAITHWEDORASIIISQTEVAVEIAIATWENORASIRISR  
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## misc\_feature

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## misc\_feature

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 probably inactive due to frameshift(s) in CDS  
 probably inactive due to no termination codon in CDS  
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## LTR

## LTR

## LTR

## gene

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 join(38213..38361,40249..40441)  
 /gene="B1108H10.8"

## CDS

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 /note="contains EST AU092422 (C50524)"  
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 /codon\_start=1  
 /protein\_id="BAB92723.1"

## LTR

## LTR

## LTR

## gene

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 IDYKPTIVNVS"  
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 /note="5' LTR"  
 43777..48553  
 /gene="B1108H10.9"  
 43777..48553

## misc\_feature



/gene="B1108H10.9"  
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pseudogene, gag-pol polyprotein"  
pseudo  
48457..49360  
/note="3' LTR"  
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CDS  
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complement(join(50166..50300,50370..50519))  
/note="hypothetical protein"  
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54602..57489,58077..58378,58667..58864))  
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Best Local Similarity 48.5%; Pred. No. 35;  
Matches 116; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

Db 7 GGGAGCGCGCGCGAGTGAAGCGCTGATGCTGCGCGCGCTCACTCCGCGAGCGAGA 66  
13954 GGGAGCGCGCGCGAGTGAAGCGCTGATGCTGCGCGCGCTCACTCCGCGAGCGAGA 14013  
Qy 67 AGCGCGCGCGAGGAGCG 126  
Db 14014 CCTCG 14073  
Qy 127 CCAGGAGCGCGAGGAGTGAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 186  
Db 14074 GATGGAGCG 14133  
Qy 187 CCNAGGAGGAGTCCCTCCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 245  
Db 14134 CCG 14192

RESULT 30  
AP005633 155328 bp DNA linear HTG 08-AUG-2002  
LOCUS Oryza sativa (japonica cultivar-group) chromosome 9 clone P0463G11,  
DEFINITION \*\*\* SEQUENCING IN PROGRESS \*\*\*  
ACCESSION AP005633.1 GI:22138857  
VERSION AP005633.1  
KEYWORDS HTG; HTGS\_PHASE2.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Euphorbiaceae; Oryzae; Oryza.  
REFERENCE  
1 Sasaki, T., Matsumoto, T. and Katayose, Y.  
Oryza sativa nipponbare (GAS) genomic DNA, chromosome 9, PAC  
clone: P0463G11  
Published Only in Database (2002)  
2 (bases 1 to 155328)  
Sasaki, T., Matsumoto, T. and Katayose, Y.  
Direct Submission  
Submitted (07-AUG-2002) Takuji Sasaki, National Institute of  
Agrobiological Sciences, Rice Genome Research Program, Kamondai  
2-1-2, Tsukuba, Ibaraki 305-8602, Japan  
(E-mail: tsasaki@nias.affrc.go.jp, URL: http://rsgp.dna.affrc.go.jp/  
Tel: 81-298-38-7441, Fax: 81-298-38-7468)  
NOTE: It currently consists of 1 contig. Gaps between the contigs  
are represented as runs of N. The order of the pieces is believed  
to be correct as given, however the sizes of the gaps between them  
are based on estimates that have provided by the submitter. This  
sequence will be replaced by the finished sequence as soon as it is

available and the accession number will be preserved.  
\* NOTE: This is a 'working draft' sequence.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.  
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1. 155328  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="genomic DNA"  
/cultivar="Nipponbare"  
/db\_xref="taxon:39947"  
/chromosome="9"  
/clone="P0463G11"  
BASE COUNT 42283 a 33769 c 34451 g 44142 t 683 others

Query Match 17.0%; Score 42.8; DB 2; Length 155328;  
Best Local Similarity 52.4%; Pred. No. 34;  
Matches 97; Conservative 0; Mismatches 87; Indels 1; Gaps 1;

Db 1 CG 60  
87963 CG 88022  
Qy 61 CGCAG-AAGCG 119  
Db 88023 CCG 88082  
Qy 120 GCAGGAGCGCGAGGAGTGAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 179  
Db 88083 CCG 88142  
Qy 180 TCCCT 184  
Db 88143 CGCCT 88147

RESULT 31  
AC020769 175493 bp DNA linear HTG 26-MAR-2000  
LOCUS Homo sapiens clone RP11-11M3, WORKING DRAFT SEQUENCE, 20 unordered  
DEFINITION  
ACCESSION AC020769  
VERSION AC020769.4 GI:7329384  
KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE  
1 (bases 1 to 175493)  
Birren, B., Linton, L., Nusbaum, C. and Lander, E.  
Homo sapiens chromosome, clone RP11-11M3  
Unpublished  
2 (bases 1 to 175493)  
Birren, B., Linton, L., Nusbaum, C., Lander, E., Abram, H., Allen, N.,  
Anderson, S., Baldwin, J., Barna, N., Becker, R., Beda, F.,  
Boguslavsky, L., Boukhalter, B., Brown, A., Burkett, G., Castle, A.,  
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DeArrellano, K., Dewar, K., Domino, M., Doyle, M., Feneclor, J.,  
Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J.,  
Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,  
Howland, J., Johnson, R., Jones, C., Kam, L., Karas, A., Klein, J.,  
Lander, T., Lechoczy, J., Levine, R., Liu, C., Liu, G., Locke, K.,  
Macdonald, P., Margulis, N., McEwan, P., McGuire, A., McKernan, K.,  
Mehners, R., Meidum, J., Menus, L., Morrison, J., Nelson, K.,  
Norman, C.H., O'Connor, T., O'Donnell, P., Oliver, T.M., Peterson, K.,  
Pierre, N., Pisan, C., Pollara, V., Raymond, C., Riley, R., Rothman, D.,  
Roy, A., Santos, R., Severi, P., Spencer, B., Stange-Thomann, N.,  
Stojanovic, N., Subramanian, A., Talama, J., Teste, S., Theodore, J.,  
Tirrell, A., Vasiliou, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W., J.,  
Zimmer, A. and Zody, M.  
Direct Submission  
Submitted (09-JAN-2000) Whitehead Institute/MIT Center for Genome



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RESULT 32
AC010550 LOCUS AC010550 DEFINITION Homo sapiens chromosome 16 clone RP11-550L9, WORKING DRAFT ACCESION AC010550.7 GI:9966237 VERSION HTGS PHASE1; HTGS_DRAFT. KEYWORDS Homo sapiens (human) SOURCE ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL COMMENT 2 (bases 1 to 197926) DOE Joint Genome Institute. Direct Submission Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Sep 4, 2000 this sequence version replaced gi:9954629. -----Genome Center Center: Joint Genome Institute Center Code: JGI Web site: http://www.jgi.doe.gov ----- Project Information Center Project Name: 617836 Center clone name: RPCI-11_550L9 ----- Summary Statistics Consensus quality: 167417 bases at least Q40 Consensus quality: 181828 bases at least Q30 Consensus quality: 187575 bases at least Q20 Estimated insert size: 184660; agarose-fp estimation Estimated insert size: 196626; sum-of-contigs estimation Quality coverage: 5.84 in Q20 bases; agarose-fp estimation Quality coverage: 5.84 in Q20 bases; sum-of-contigs estimation. * NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. * 1438: contig of 1438 bp in length * 1439 1538: gap of unknown length * 1539 2567: contig of 1029 bp in length * 2568 2667: gap of unknown length * 2668 3793: contig of 1126 bp in length * 3794 3893: gap of unknown length * 3894 6248: contig of 2655 bp in length * 6249 6548: gap of unknown length * 6549 11592: contig of 4944 bp in length * 11593 11692: gap of unknown length * 11693 17217: contig of 5525 bp in length * 17218 17317: gap of unknown length * 17319 24917: contig of 7600 bp in length * 24918 25017: gap of unknown length * 25019 36743: contig of 11726 bp in length * 36744 36843: gap of unknown length * 36844 60051: contig of 23208 bp in length * 60052 60151: gap of unknown length * 60152 96861: contig of 36710 bp in length * 96862 130047: contig of 33086 bp in length * 130048 130147: gap of unknown length * 130149 197926: contig of 67779 bp in length. Location/Qualifiers 1..197926
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						/mol_type="genomic DNA"
						/db_xref="taxon:9606"
						/chromosome="1c"
						/clone="RP11-550L9"
						/clone_1lb="RPC1 human BAC library 11"
BASE COUNT	49341 a	48870 c	48105 g	50494 t	1116 others	
ORIGIN						
Query Match	17.0%;	Score 42.8;	DB 2;	Length 197926;		
Best Local Similarity	51.9%;	Pred No. 31;	Mismatches 88;	Indels 0;	Gaps 0;	
Matches 95;	Conservative 0;	Mismatches 88;	Indels 0;	Gaps 0;		
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Db	123890	CAGAAAGCTCCGACTCGCTCCACATTCCTCCCACTCCCTCTCTGGCCGAGAGAG	123949			
OY	123	GGGACCAAGGAGCGCAGGAATCTGCGCGCCCCCGCCCTGTGCGCGCAGGAAGCTCC	182			
Db	123950	GACCCCGAAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGACCGGAC	124009			
OY	183	CTCACACNAGGAGGAACTCCCTCACCCGCGCCAGCCCTGCAGGGGGGGCGTGAGGTCA	242			
Db	124010	CCAGAGCGGCTGGGAGCGCACCGAGCGGAGCGGTGAGCGCGCGGACAGCGCTGAGCTG	124069			
OY	243	ACC 245				
Db	124070	TCC 124072				
RESULT 33						
AC009090/c	LOCUS	AC009090	198253 bp	DNA	linear	PRI 19-MAR-2003
AC009090/c	DEFINITION	Homo sapiens chromosome 16 clone RP11-407g23, complete sequence.				
AC009090	ACCESSION	AC009090				
AC009090.12	VERSION	GI:29124043				
HTG.	KEYWORDS					
ORGANISM	ORGANISM	Homo sapiens (human)				
REFERENCE	AUTHORS	Eukariota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	AUTHORS	DOE Joint Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.				
REFERENCE	TITLE	Direct Submission				
REFERENCE	JOURNAL	Unpublished				
REFERENCE	AUTHORS	2 (bases 1 to 198253)				
REFERENCE	TITLE	DOE Joint Genome Institute.				
REFERENCE	JOURNAL	Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA				
REFERENCE	AUTHORS	3 (bases 1 to 198253)				
REFERENCE	TITLE	DOE Joint Genome Institute.				
REFERENCE	JOURNAL	Submitted (04-APR-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA				
REFERENCE	AUTHORS	4 (bases 1 to 198253)				
REFERENCE	TITLE	DOE Joint Genome Institute.				
REFERENCE	JOURNAL	Submitted (17-DEC-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA				
REFERENCE	AUTHORS	5 (bases 1 to 198253)				
REFERENCE	TITLE	DOE Joint Genome Institute.				
REFERENCE	JOURNAL	Submitted (19-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA				
REFERENCE	AUTHORS	On Mar 19, 2003 this sequence version replaced gi:27151360.				
REFERENCE	TITLE	Draft Sequence Produced by DOE Joint Genome Institute				
REFERENCE	JOURNAL	www.jgi.doe.gov				
REFERENCE	AUTHORS	Finishing Completed at Stanford Human Genome Center and Los Alamos National Laboratory				
REFERENCE	TITLE	www.-shgc.stanford.edu				





TITLE  
JOURNAL  
COMMENT

Strauss, N., Subramanian, A., Talamas, J., Teefaye, S., Theodore, J.,  
Topham, K., Travels, M., Travis, N., Triggillo, J., Vassiliev, H.,  
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,  
Zainoun, U., Zemek, L., Zimmer, A. and Zody, M.  
Submitted (22-NOV-2001) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
----- Project Information  
Center project name: L13335  
Center clone name: L13\_O\_2

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\* NOTE: This record contains 83 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

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802 1801: gap of 100 bp  
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2437 2436: gap of 100 bp  
3110 3109: contig of 673 bp in length  
3210 3209: gap of 100 bp  
3941 3940: contig of 731 bp in length  
4041 4040: gap of 100 bp  
4706 4705: contig of 665 bp in length  
4806 4805: gap of 100 bp  
5494 5493: contig of 688 bp in length  
5594 5593: gap of 100 bp  
6283 6282: contig of 689 bp in length  
6383 6382: gap of 100 bp  
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7160 7159: gap of 100 bp  
7861 7860: contig of 701 bp in length  
7961 7960: gap of 100 bp  
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27555 27555: contig of 711 bp in length  
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* 51027 51126: gap of 100 bp
* 51127 51828: contig of 702 bp in length
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* 51929 52657: contig of 729 bp in length
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* 52758 53474: contig of 717 bp in length
* 53475 53574: gap of 100 bp
* 53575 54392: contig of 718 bp in length
* 54393 55060: gap of 100 bp
* 55061 55160: contig of 668 bp in length
* 55161 55857: gap of 100 bp
* 55858 55957: gap of 100 bp

```

Query Match 16.9%; Score 42.6; DB 2; Length 67126;

Best Local Similarity 49.1%; Pred. No. 47; Mismatches 115; Indels 0; Gaps 0;

```

Matches 11; Conservative 0; Mismatches 115; Indels 0; Gaps 0;
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QY 87 AGTGCAGCGAGTTCGCGCGCTGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 146
Db 4504 GCTTCCGCGCGCGCGCGCGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 4563
QY 147 CCGCCCGCGCGCGCGCGCTGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 206
Db 4564 CCGCCCGCGCGCGCGCGCGCTGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4623
QY 207 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 252
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RESULT 37
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AC024400
AC024400.2 GI:767819
VERSION HTG; HTGS_PHASE0.
KEYWORDS Homo sapiens (human)
SOURCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
ORGANISM Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 217412)
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abrahams, H., Allen, N.,
JOURNAL Anderson, S., Baldwin, J., Barna, N., Beda, F., Boguslavsky, L.,
TITLE Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A.,
AUTHORS Choquet, Y., Colangelo, M., Collins, S., Collipalmo, A., Cooke, P.,
REFERENCE Deailellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M.,
JOURNAL Fennel, J., Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D.,
AUTHORS Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
REFERENCE Grand-Pierre, N., Grant, G., Hages, B., Heatford, A., Horton, L.,
JOURNAL Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karakas, A.,
AUTHORS Klein, J., Lander, E., Lander, T., Laroque, K., Lehotzky, J., Levine, R.,
REFERENCE Lien, C., Liu, G., Locke, K., Macdonald, P., Margulis, N., McCarthy, M.,
JOURNAL McKean, P., McKernan, K., McPherson, R., Melnick, J.,
AUTHORS Menes, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Naylor, J.,

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TITLE  
JOURNAL  
COMMENT

Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Olivar, T.M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Testa, S., Theodore, J., Tirrell, A., Travers, M., Trigglio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Submitted (28-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA. On May 10, 2000 this sequence version replaced gi:7108401. All repeats were identified using RepeatMasker: Smit, A.P.A. & Green, P. (1996-1997) <http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WTHR  
Web site: <http://www.seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
----- Project Information  
Center project name: L6776  
Center clone name: 439\_D\_4

\*\*\*\*\* NOTE: This record contains 242 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

```

1 715: contig of 715 bp in length
716 815: gap of 100 bp
1555 1554: contig of 739 bp in length
1555 1654: gap of 100 bp
1655 2421: contig of 767 bp in length
2422 2521: gap of 100 bp
2522 3271: contig of 750 bp in length
3272 3371: gap of 100 bp
3372 4116: contig of 745 bp in length
4117 4216: gap of 100 bp
4217 4978: contig of 763 bp in length
4979 5078: gap of 100 bp
5079 5080: gap of 760 bp in length
5080 5938: contig of 770 bp in length
5938 6708: contig of 770 bp in length
6708 6809: gap of 100 bp
6809 7579: contig of 770 bp in length
7579 7680: gap of 100 bp
7680 8381: contig of 702 bp in length
8382 9220: gap of 100 bp
9220 9319: contig of 738 bp in length
9319 9320: gap of 100 bp
10072 10073: contig of 753 bp in length
10073 10172: gap of 100 bp
10172 10927: contig of 755 bp in length
10928 11027: gap of 100 bp
11028 11798: contig of 770 bp in length
11798 11898: gap of 100 bp
11898 12659: contig of 762 bp in length
12660 12760: gap of 100 bp
12760 13535: contig of 776 bp in length
13536 13636: gap of 100 bp
13636 14355: contig of 720 bp in length
14356 14455: gap of 100 bp
14456 15218: contig of 763 bp in length
15219 15319: gap of 100 bp
15319 16081: contig of 763 bp in length
16082 16181: gap of 100 bp

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*	16344	17688:	cont:ig of 100	bp	in	length
*	17044	17768:	cont:ig of 725	bp	in	length
*	17769	18668:	gap of 100	bp	in	length
*	17869	18613:	cont:ig of 745	bp	in	length
*	18514	18713:	gap of 100	bp	in	length
*	19461	15360:	gap of 100	bp	in	length
*	19561	20328:	cont:ig of 768	bp	in	length
*	20329	20428:	gap of 100	bp	in	length
*	20439	21151:	cont:ig of 723	bp	in	length
*	21152	21251:	gap of 100	bp	in	length
*	21252	22017:	cont:ig of 766	bp	in	length
*	22018	22117:	gap of 100	bp	in	length
*	22118	22872:	cont:ig of 755	bp	in	length
*	22873	22972:	gap of 100	bp	in	length
*	22973	23743:	cont:ig of 771	bp	in	length
*	23744	23843:	gap of 100	bp	in	length
*	23844	24684:	cont:ig of 741	bp	in	length
*	24685	24684:	gap of 100	bp	in	length
*	24685	25443:	cont:ig of 759	bp	in	length
*	25444	25543:	gap of 100	bp	in	length
*	25544	26370:	cont:ig of 727	bp	in	length
*	26371	26370:	gap of 100	bp	in	length
*	26371	27124:	cont:ig of 754	bp	in	length
*	27125	27324:	gap of 100	bp	in	length
*	27225	27980:	cont:ig of 756	bp	in	length
*	27981	28080:	gap of 100	bp	in	length
*	28081	28811:	cont:ig of 731	bp	in	length
*	28812	28911:	gap of 100	bp	in	length
*	28912	29685:	cont:ig of 784	bp	in	length
*	29686	29795:	gap of 100	bp	in	length
*	29796	30568:	cont:ig of 773	bp	in	length
*	30569	30568:	gap of 100	bp	in	length
*	30669	31488:	cont:ig of 770	bp	in	length
*	31489	31538:	gap of 100	bp	in	length
*	31539	32278:	cont:ig of 740	bp	in	length
*	32279	32378:	gap of 100	bp	in	length
*	33379	33108:	cont:ig of 730	bp	in	length
*	33109	33208:	gap of 100	bp	in	length
*	33209	33956:	cont:ig of 748	bp	in	length
*	33957	34056:	gap of 100	bp	in	length
*	34057	34840:	cont:ig of 784	bp	in	length
*	34841	34940:	gap of 100	bp	in	length
*	34941	35674:	cont:ig of 734	bp	in	length
*	35675	35774:	gap of 100	bp	in	length
*	35775	36534:	cont:ig of 760	bp	in	length
*	36535	36634:	gap of 100	bp	in	length
*	36635	37400:	cont:ig of 766	bp	in	length
*	37401	37500:	gap of 100	bp	in	length
*	37501	38289:	cont:ig of 789	bp	in	length
*	38290	38389:	gap of 100	bp	in	length
*	38390	39147:	cont:ig of 758	bp	in	length
*	39148	39247:	gap of 100	bp	in	length
*	39248	40007:	cont:ig of 760	bp	in	length
*	40008	40107:	gap of 100	bp	in	length
*	40108	40835:	cont:ig of 728	bp	in	length
*	40836	40935:	gap of 100	bp	in	length
*	40936	41677:	cont:ig of 742	bp	in	length
*	41678	41777:	gap of 100	bp	in	length
*	41778	42547:	cont:ig of 770	bp	in	length
*	42548	42647:	gap of 100	bp	in	length
*	42648	43385:	cont:ig of 738	bp	in	length
*	43386	43485:	gap of 100	bp	in	length
*	43486	44281:	cont:ig of 766	bp	in	length
*	44282	44381:	gap of 100	bp	in	length
*	44382	45108:	cont:ig of 757	bp	in	length
*	45109	45208:	gap of 100	bp	in	length
*	45209	45573:	cont:ig of 765	bp	in	length
*	45974	46643:	gap of 100	bp	in	length
*	46074	46642:	cont:ig of 769	bp	in	length
*	46843	46942:	gap of 1			

*	47693	gap of 100 bp
*	47792	contig of 761 bp in length
*	47793	48553: gap of 100 bp
*	48554	48553: contig of 714 bp in length
*	48654	49467: gap of 100 bp
*	49468	50197: contig of 730 bp in length
*	50198	50297: gap of 100 bp
*	50298	51049: contig of 752 bp in length
*	51050	51149: gap of 100 bp
*	51150	51907: contig of 758 bp in length
*	51908	52007: gap of 100 bp
*	52008	52288: contig of 721 bp in length
*	52129	52288: gap of 100 bp
*	52289	53584: contig of 766 bp in length
*	53589	53584: gap of 100 bp
*	53595	54332: contig of 738 bp in length
*	53595	54332: gap of 100 bp
*	54333	54532: gap of 763 bp in length
*	54533	55285: contig of 763 bp in length
*	55296	55385: gap of 100 bp
*	55396	56159: contig of 764 bp in length
*	56160	56259: gap of 100 bp
*	56260	57028: contig of 763 bp in length
*	57029	57128: gap of 100 bp
*	57129	57851: contig of 723 bp in length
*	57852	57951: gap of 100 bp
*	57952	58690: contig of 739 bp in length
*	58691	58790: gap of 100 bp

Query Match	Similarity	16.9%	Score 12.6	DB 2	Length 217412
Best Local	Similarity	49.8%	Pred. No. 33		
Matches	105	Conservative	0	Mismatches	106
				Indels	0
				Gaps	0
QY	12	GGCGCCGGAGAGAGAGCCGATTCGTCCTCGCGCGCTCCACTCCCGAGGCGCAGAAAGCG	71		
Db	155256	GGCGCCCGCGGGGTCCCGCGCCCGCCCAAGCGCGCGCGCGCGCCGCGCCCGCGCGCG	155197		
QY	72	CCCAAGAGAGACCCCGAGTCGCCAGGTTGCCACGCGTGGAGATCAGAGAGCAGGAGCAGG	131		
Db	155196	GCCCGCGCCCGCCCGCGACCGCCCGCGAGCGCGCGCGCGCGCGCGCGCGCGCTCCGCG	155137		
QY	132	GAGCCAGAGAACTGCG	191		
Db	155136	CCCCCGCGCGCTGCG	155077		
QY	192	GGGAAGTCCCTCATCCGCGCCCAAGCCTTCG	222		
Db	155076	GGCGCCCG	155046		

RESULT	38
LOCUS	BX088698
DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	
	<p>BX088698                      230413 bp          DNA                      linear          HTG 04-JUN-2003</p> <p>Mus musculus chromosome X clone RP23-309D15, *** SEQUENCING IN PROGRESS ***, 7 unordered pieces.</p> <p>BX088698 BX088698.5    GI:31442026 HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP. Mus musculus (house mouse) Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (baaes 1 to 230413)</p> <p>McLaren,S. Direct Submision Submitted (03-JUN-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: clonerequest@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jun 5, 2003 this sequence version replaced g1:29125140 Consortium whole genome</p>

Sequence from the mouse genome sequencing consortium. Sequence data  
shotgun may have been used to confirm this sequence. Sequence data  
from the whole genome shotgun alone has only been used where it has  
a phred quality of at least 30.





Fri Nov 7 08:10:00 2003

us-10-081-817a-19\_copy\_1\_252.rge

```

SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 2150)
AUTHORS     Uchimura,K., Muramatsu,H., Kadomatsu,K., Kannagi,R., Habuchi,O. and
            Muramatsu,T.
TITLE       Polypeptide of N-acetylglucosamine-6-O-sulfotransferase and DNA
            encoding the same
JOURNAL     Patent: US 6455289-A 1 24-SEP-2002;
FEATURES    Location/Qualifiers
            source          1..2150
                                /organism="unknown"
BASE COUNT  386 a      695 c      679 g      390 t
ORIGIN
Query Match      16.7%; Score 42.2; DB 6; Length 2150;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 104; Conservative 0; Mismatches 104; Indels 0; Gaps 0;
QY      28 CCTGATGTCCTCCCTGCGCCCTCCACCTCCCGAGGCGGAGAAAGGCGCCACAGAGACCCCA 87
Db      143 CCAAGTCTCTCTCGAGACCCGCTGCGATGGAGAGCAGCCCTGGGCGCGGGGACAGCA 202
QY      88 GTGCCCGACGTTGCCACGATCTGGGATCAAGAGGACCAAGAGCCAGAACTGGCG 147
Db      203 GCCTCTGCGCCGCGCGCGCTCGATGCGGCGCCCAATCCGCGCCCGCAGCCGCC 262
QY      148 CGCCCCCGCCCTGCGCCCTGCGCGCGAGGAAAGTCTCTCAGCAGAGGAAAGTCTCCCTCAC 207
Db      263 TGCAGCGTCTCCCTCTCTGCGGCTGCAAGGCGCGCTCCGCGCGCGCGCGCTG 322
QY      208 CCGGCCCAAGCCTGCGAGGGGAGCGCGT 235
Db      323 CTTGTGATGAGCCGACAGCTCGCGCGAG 350
```

Search completed: November 6, 2003, 08:07:07  
Job time : 1536.45.secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Comphen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 6, 2003, 06:12:36 ; Search time 182.882 Seconds  
(without alignments)  
3719.648 Million cell updates/sec

Title: US-10-081-817a-19\_COPY\_1\_252

Perfect score: 252  
Sequence: 1 cggccgggagggcggcg999.....gtggggtcagaccgcaagc 252

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: N\_Geneseq\_19Jun03:\*  
2: /SIDSI/gcgcdata/geneq/geneq-emb1/NA1980.DAT:\*  
3: /SIDSI/gcgcdata/geneq/geneq-emb1/NA1981.DAT:\*  
4: /SIDSI/gcgcdata/geneq/geneq-emb1/NA1982.DAT:\*  
5: /SIDSI/gcgcdata/geneq/geneq-emb1/NA1983.DAT:\*  
6: /SIDSI/gcgcdata/geneq/geneq-emb1/NA1984.DAT:\*  
7: /SIDSI/gcgcdata/geneq/geneq-emb1/NA1985.DAT:\*  
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14: /SIDSI/gcgcdata/geneq/geneq-emb1/NA1992.DAT:\*  
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20: /SIDSI/gcgcdata/geneq/geneq-emb1/NA1998.DAT:\*  
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22: /SIDSI/gcgcdata/geneq/geneq-emb1/NA2000.DAT:\*  
23: /SIDSI/gcgcdata/geneq/geneq-emb1/NA2001A.DAT:\*  
24: /SIDSI/gcgcdata/geneq/geneq-emb1/NA2001B.DAT:\*  
25: /SIDSI/gcgcdata/geneq/geneq-emb1/NA2002.DAT:\*  
26: /SIDSI/gcgcdata/geneq/geneq-emb1/NA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	143.6	57.0	1794	24	ABT06542
2	42.2	16.7	1951	22	AAH43895
3	42.2	16.7	2150	20	AAH87820
4	41.4	16.4	3431	22	AAH98302
5	41.4	16.4	3459	24	AAU29756
6	40.8	16.2	2666	24	ABZ53386
7	39.6	15.7	868	21	AA65433
8	38.6	15.3	840	24	ABL60745

c	9	38.4	15.2	222	22	AAE65077	Novel human polyu
c	10	38.4	15.2	3106	25	ACC46319	Human dltip zinc f
c	11	38.4	15.2	3690	25	ACC46404	Human dltip zinc f
c	12	38.4	15.2	42999	24	ABG65032	Invertebrate forag
c	13	38.2	15.2	528	22	AAE30761	Megalomycin polyke
c	14	38.2	15.2	114955	20	AAE53491	Human adenosine A1
c	15	38.2	15.1	1875	20	AAE53363	CDNA encoding HTHB
c	16	38	15.1	2875	25	ABX90552	Human kinase CDNA
c	17	38	15.1	4890	20	AAE34648	Promoter containin
c	18	37.8	15.0	1947	24	ABK99879	Human CDNA enclocl
c	19	37.8	15.0	1947	25	ABK99879	Human kinase CDNA
c	20	37.8	15.0	1947	25	ABK99879	Human kinase CDNA
c	21	37.8	15.0	1947	25	ABK99879	Human kinase CDNA
c	22	37.8	15.0	1947	25	ABK99879	Human kinase CDNA
c	23	37.8	15.0	1947	25	ABK99879	Human kinase CDNA
c	24	37.8	15.0	1947	25	ABK99879	Human kinase CDNA
c	25	37.8	15.0	1947	25	ABK99879	Human kinase CDNA
c	26	37.8	15.0	1947	25	ABK99879	Human kinase CDNA
c	27	37.8	15.0	1947	25	ABK99879	Human kinase CDNA
c	28	37.8	15.0	1947	25	ABK99879	Human kinase CDNA
c	29	37.8	15.0	1947	25	ABK99879	Human kinase CDNA
c	30	37.8	15.0	1947	25	ABK99879	Human kinase CDNA
c	31	37.8	15.0	1947	25	ABK99879	Human kinase CDNA
c	32	37.8	15.0	1947	25	ABK99879	Human kinase CDNA
c	33	37.8	15.0	1947	25	ABK99879	Human kinase CDNA
c	34	37.8	15.0	1947	25	ABK99879	Human kinase CDNA
c	35	37.8	15.0	1947	25	ABK99879	Human kinase CDNA
c	36	37.8	15.0	1947	25	ABK99879	Human kinase CDNA
c	37	37.8	15.0	1947	25	ABK99879	Human kinase CDNA
c	38	37.8	15.0	1947	25	ABK99879	Human kinase CDNA
c	39	37.8	15.0	1947	25	ABK99879	Human kinase CDNA
c	40	37.8	15.0	1947	25	ABK99879	Human kinase CDNA
c	41	37.6	14.9	137507	17	AAV19941	Human CDNA enclocl
c	42	37.6	14.9	4257	19	AAV68520	The nucleotide seq
c	43	37.6	14.9	4257	19	AAV68520	infected cell prot
c	44	37.4	14.8	2461	22	AAE44725	Novel protein kina
c	45	37.4	14.8	3400	22	AAE51952	Human polynucleoti

#### ALIGNMENTS

RESULT 1	ABT06542	standard; DNA; 1794 BP.
ID	ABT06542;	
XX	ABT06542;	
AC	07-NOV-2002 (first entry)	
XX		
DT	Human HIN-1 coding sequence.	
XX		
DE	Human HIN-1 coding sequence.	
XX		
KW	Human; methylated gene; methylation; breast cancer; marker; WT-1;	
KW	cell proliferative disorder; TWIST; HOXA5; NES-1; RARbeta; cyclin D2;	
KW	retinoic acid receptor beta; oestrogen receptor; Wilms' tumour;	
KW	14.3.3 sigma; HIN-1; RASBP1A; tumour suppressor gene; hypermethylation;	
XX	gene; promoter; ds.	
XX		
OS	Homo sapiens.	
XX		
PN	MO200259347-A2.	
XX		
PD	01-AUG-2002.	
XX		
PF	28-JAN-2002; 2002MO-US02455.	
XX		
PR	26-JAN-2001; 2001US-0771357.	
XX		
PA	(UYO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.	
XX		
PI	Sukumar S, Eylon E, Doolley WC, Sacchi N, Davidson N, Packler MJ,	
XX	WPI: 2002-599803/64.	

XX Diagnosing and/or determining a predisposition to a cellular  
 PT proliferative disorder of breast tissue, in particular breast cancer,  
 PT by determining the state of methylation of one or more nucleic acids  
 PT isolated from the subject -  
 PS  
 XX Disclosure; Fig 9A; 115pp; English.

XX The present invention relates to a method of diagnosing a cellular  
 CC proliferative disorder of breast tissue, which involves determining the  
 CC state of methylation of one or more nucleic acids isolated from the  
 CC subject, where the state of methylation of the nucleic acids as compared  
 CC with a state of methylation from a subject not having the cellular  
 CC proliferative disorder of breast tissue is indicative of a cellular  
 CC proliferative disorder of breast tissue in the subject. The nucleic acids  
 CC may be TWIST, HOKX5, NES-1, retinoic acid receptor beta (RARbeta),  
 CC oncostatin receptor, cyclin D2, Wilms tumor gene (WT-1), 14.3.3 sigma,  
 CC HIN-1 or RASSF1A. The method is useful for diagnosing and/or determining  
 CC a predisposition to a cellular proliferative disorder, in particular  
 CC breast cancer including ductal carcinoma in situ, lobular carcinoma,  
 CC colloid carcinoma, tubular carcinoma, medullary carcinoma, metaplastic  
 CC carcinoma, intraductal carcinoma in situ, lobular carcinoma in situ and  
 CC papillary carcinoma in situ. The present sequence is a gene fragment used  
 CC in the exemplification of the invention.  
 XX  
 SQ Sequence 1794 BP; 240 A; 646 C; 522 G; 318 T; 68 other;

Query Match 57.0%; Score 143.6; DB 24; Length 1794;  
 Best Local Similarity 94.8%; Pred. No. 2.3e-22;  
 Matches 181; Conservative 0; Mismatches 5; Indels 5; Gaps 3;

QY 1 CGGCGGGGAGGCGCGGGAGTGAAGCTGATGCTGCTCGGCGGCTCCACCTCCCGCAGG 60  
 DB 156 CGGCGGGGAGGCGCGGGAGTGAAGCTGATGCTGCTCGGCGGCTCCACCTCCCGCAGG 215  
 QY 61 CGAGAAAGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120  
 DB 216 CGAGAAAGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 275  
 QY 121 CA-GGAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 179  
 DB 276 CAGGGAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 331  
 QY 180 TCCCTACCGG 190  
 DB 332 TCCCTACCGG 342

RESULT 2  
 AAH43895  
 ID AAH43895 standard; DNA; 1951 BP.

XX AAH43895;

XX 04-SEP-2001 (first entry)

XX Human CLASP-7 promoter region nucleotide sequence.

XX Human; CLASP-7; cadherin-like asymmetry protein; immune response;  
 KW neuroprotective; antidiabetic; immunosuppressive; antineoplastic;  
 KW antileukemic; hypotensive; anti-HIV; cytostatic; immunostimulant;  
 KW antianemic; antiinflammatory; ophthalmological; nephrotoxic;  
 KW antithyroid; antistaphylococcal; antiallergic; antibacterial; gene therapy;  
 KW chromosome 19q13.2; autoimmune disease; multiple sclerosis; toxemia;  
 KW juvenile diabetes; rheumatoid arthritis; pruritic urticarial papule;  
 KW hypertension; Rh incompatibility; ds.

XX Homo sapiens.

XX W0200142295-A2.

XX 14-JUN-2001.

XX

PF 13-DEC-2000; 2000WO-US34152.  
 XX  
 PR 13-DEC-1999; 99US-0170453.  
 PR 14-JAN-2000; 2000US-0176195.  
 PR 14-FEB-2000; 2000US-0182296.  
 PR 11-APR-2000; 2000US-0196267.  
 PR 11-APR-2000; 2000US-0196460.  
 PR 11-APR-2000; 2000US-0196527.  
 PR 11-APR-2000; 2000US-0196528.  
 PR 11-APR-2000; 2000US-0547276.  
 PR 13-OCT-2000; 2000US-0240503.  
 PR 13-OCT-2000; 2000US-0240508.  
 PR 13-OCT-2000; 2000US-0240539.  
 PR 13-OCT-2000; 2000US-0240543.

PA (ARBO-) ARBOR VITA CORP.

PI Lu P, Garman JD, Candia AF;

XX WPI; 2001-381641/40.

XX Novel cadherin-like asymmetry protein-7 and polynucleotides encoding  
 PT the polypeptide, useful for treating autoimmune disease,  
 PT hypersensitivity, preventing transplant rejection by modulating immune  
 PT response -

XX Disclosure; Fig 6B; 151pp; English.

XX The present invention describes a human cadherin-like asymmetry protein  
 CC (CLASP), designated CLASP-7. The CLASP-7 protein (I) and its encoding  
 CC nucleotide sequence (II) have activities including: neuroprotective;  
 CC antidiabetic; immunosuppressive; antineoplastic; antileukemic; anti-HIV;  
 CC hypotensive; cytostatic; immunostimulant; antianemic; antiinflammatory;  
 CC ophthalmological; nephrotoxic; antithyroid; antistaphylococcal;  
 CC antileukic; and antibacterial. (II) and CLASP-7 antibodies (III) are  
 CC useful for detecting the CLASP-7 polypeptide. (II) is useful for  
 CC inhibiting (I) by recombinant methods. (I) or its fragment are useful for  
 CC inducing an immune response in a cell such as T cell or B cell. A  
 CC pharmaceutical composition (C), comprising (I) or (II), can be useful  
 CC for treating CLASP-7-mediated disease such as an autoimmune disease  
 CC caused or exacerbated by increased activity of T helper cells. Autoimmune  
 CC diseases which can be treated using (C) include multiple sclerosis  
 CC and Rh incompatibility. (I) is also useful as a diagnostic reagent for  
 CC juvenile diabetes and rheumatoid arthritis. (I) is useful for treating  
 CC coxsackia or pregnancy induced hypertension, pruritic urticarial papules  
 CC and immune and other disorders, since diseases characterized by  
 CC overproduction or depletion of lymphocytes in blood or other organs may  
 CC be detected by monitoring the level of (I) or its mRNA. CLASP-7 has been  
 CC mapped to the chromosomal location 19q13.2. The present sequence  
 CC represents the human CLASP-7 promoter region nucleotide sequence which  
 CC is given in the exemplification of the present invention.  
 XX

SQ Sequence 1951 BP; 437 A; 624 C; 528 G; 362 T; 0 other;

Query Match 16.7%; Score 42.2; DB 22; Length 1951;  
 Best Local Similarity 48.3%; Pred. No. 1.8;  
 Matches 116; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

QY 1 CGGCGGGGAGGCGGCGGGAGTGAAGCTGATGCTGCTCGGCGGCTCCACCTCCCGCAGG 60  
 DB 1658 CAGGCGGGGAGTGGGGGCGGCGGAGCTGATGCTGCTCGGCGGCTCCCGCCAGC 1717  
 QY 61 CGAGAAAGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120  
 DB 1718 CTAGGTTCCCGAGGCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1777  
 QY 121 CAGGACCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180  
 DB 1778 AGGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1837  
 QY 181 CCTGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240  
 DB 1838 CCGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1897

RESULT 3  
 AAX87820 standard; cDNA; 2150 BP.  
 ID AAX87820;  
 AC AAX87820;  
 XX  
 XX  
 XX 09-NOV-1999 (first entry)  
 DT  
 XX  
 DE Mouse N-acetylglucosamine-6-O-sulfotransferase cDNA.  
 XX  
 XX N-acetylglucosamine-6-O-sulfotransferase; mouse; GLYCAM-1;  
 KM L-selectin ligand; ss.  
 XX  
 OS Mus musculus.  
 XX  
 XX  
 XX Key Location/Qualifiers  
 FT 470..1921  
 CDS /\*tag= a  
 XX  
 XX EP943688-A2.  
 XX  
 XX 22-SEP-1999.  
 XX  
 XX 04-MAR-1999; 99EP-0301530.  
 XX  
 XX 24-JUN-1998; 98JP-0177844.  
 PR 05-MAR-1998; 98JP-0054007.  
 XX  
 XX (SECK) SEIKAGAKU CORP.  
 XX  
 XX Habuchi O, Kadomatsu K, Kannagi R, Muramatsu H;  
 PI Muramatsu T, Uchimura K;  
 XX  
 XX WPI: 1999-520337/44.  
 DR P-PSDB; AAY31656.  
 XX  
 XX New polypeptides of N-acetylglucosamine-6-O-sulfotransferase, useful  
 PT for synthesis of sugar chains, e.g. GLYCAM-1  
 XX  
 PS Claim 5; Page 21-23; 41pp; English.  
 XX  
 CC This is the nucleotide sequence of an isolated cDNA coding for  
 CC mouse N-acetylglucosamine-6-O-sulfotransferase (see AAY31656), an  
 CC enzyme capable of transferring a sulfate group from a sulfate group  
 CC donor to a hydroxyl group at the 6 position of an N-acetylglucosamine  
 CC residue located at the non-reducing end of an oligosaccharide  
 CC represented by the formula GlcNAc-beta1-3Gal-beta1-4GlcNAc, where  
 CC GlcNAc = N-acetylglucosamine residue, Gal = galactose residue,  
 CC beta 1-3 = beta 1-3 glycosidic linkage, and beta 1-4 = beta 1-4  
 CC glycosidic linkage. The cDNA was isolated from a mouse embryo  
 CC cDNA library by PCR amplification. The enzyme is useful for the  
 CC synthesis of sugar chains such as GLYCAM-1, a ligand of L-selectin  
 CC that is involved in homing of lymphocytes and rolling of leukocytes  
 CC occurring at the early stage of inflammation. DNA encoding the  
 CC N-acetylglucosamine-6-O-sulfotransferase, or artificial synthesis  
 CC of GLYCAM-1 using transformants which harbour the DNA.  
 XX  
 SQ Sequence 2150 BP; 386 A; 695 C; 679 G; 390 T; 0 other;  
 Query Match 16.7%; Score 42.2; DB 20; Length 2150;  
 Best Local Similarity 50.0%; Pred No. 1.7; Indels 0; Gaps 0;  
 Matches 104; Conservative 0; Mismatches 104;  
 QY 28 CCGATGTCCTCCGCGCCCTCCACCTCCCGACGCGAAGAGGCCCGACAGAGACCCCA 87  
 DB 143 CCAAGTCTCTCCGAGCCCTGCGATGAGAGAGCCCTCGCCGCGGAGACAGCA 202  
 QY 88 GTGCGCCAGCTTGGCAAGCTGTGGATCAAGAGGAGGACCAAGAGCCAGAACTGCGC 147  
 DB 203 GCTCTGCGCGCGCGCCGCTCGAGTGGCGGCGCCCACTCCGCGCGCCGCGCGCC 262

QY 148 CGCCCCCGCCCTGCGCGCGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 207  
 DB 263 TCGAGCCGTCCT 322  
 QY 208 CCGGCGCCAGCCCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 235  
 DB 323 CCGTGTATGAGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 350  
 RESULT 4  
 AAH98302/C  
 ID AAH98302 standard; cDNA; 3431 BP.  
 XX  
 XX  
 XX AAH98302;  
 AC  
 XX  
 XX 12-OCT-2001 (first entry)  
 DT  
 XX  
 XX Human EST-derived coding sequence SEQ ID NO: 159.  
 DE  
 XX  
 XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;  
 KM tomato; monkey; dog; sea urchin; expressed sequence tag; EST;  
 KM diagnostics; forensic test; gene mapping; genetic disorder;  
 KM biodiversity; gene therapy; nutrition; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200154477-A2.  
 XX  
 XX 02-AUG-2001.  
 XX  
 XX 25-JAN-2001; 2001WO-US02687.  
 XX  
 XX 25-JAN-2000; 2000US-0491404.  
 PR 17-JUL-2000; 2000US-0617746.  
 PR 03-AUG-2000; 2000US-0631451.  
 PR 15-SEP-2000; 2000US-0663870.  
 XX  
 XX (HSE-) HXSEQ INC.  
 XX  
 XX Tang YF, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;  
 PI Cao Y, Dmanac RA, Zhang J, Wehrman T;  
 XX  
 XX WPI: 2001-476164/51.  
 DR P-PSDB; AAM23643.  
 XX  
 XX Isolated polypeptide for treatment of diseases, diagnostics, raising  
 PT antibodies and research use -  
 XX  
 PS Claim 1; Page 282-283; 1275pp; English.  
 XX  
 CC The present invention provides the protein and coding sequences of novel  
 CC proteins from a variety of organisms, including human, dog, cat, horse,  
 CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea  
 CC urchin and tomato. These were derived from expressed sequence tags (ESTs)  
 CC from the organism of interest. They can be used in diagnostics,  
 CC forensics, gene mapping, identification of mutations, to assess  
 CC biodiversity and for nutritional purposes. The present sequence is a cDNA  
 CC of the invention.  
 XX  
 SQ Sequence 3431 BP; 524 A; 1312 C; 1105 G; 490 T; 0 other;  
 Query Match 16.4%; Score 41.4; DB 22; Length 3431;  
 Best Local Similarity 53.4%; Pred No. 2.6; Indels 0; Gaps 0;  
 Matches 87; Conservative 0; Mismatches 76;  
 QY 1 CGGCGGAGAGGCGCGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 60  
 DB 170 CGGCGGAGGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 111  
 QY 61 CGGAGAGGCGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120  
 DB 110 CGGAGGAGGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 51

Qy 121 CAGGACCAAGGAGCCAGGAATGCGCCGCCCCCGCCCTGCC 163  
Db 50 GAGGCGGCGCCGCGGCAGTGCAGGAGCGGAGCCGCGCCGCGCC 8

RESULT 5
AAD29756/c
ID AAD29756 standard; DNA; 3459 BP

DT 17-MAY-2002 (first entry)

DE Human hyperpolarisation-activated cyclic nucleotide-gated channel 2 DNA

KM Human; hyperpolarisation-activated cyclic nucleotide-gated channel; HCN;  
KM therapy; stroke; ischemia; head injury; epilepsy; Alzheimer's disease;  
KM Parkinson's disease; learning disorder; memory; attention disorder; pain  
KM gut disorder; irritable bowel syndrome; IBS; sleep disorder; nootropic;  
KM neuroprotective; cerebroprotective; antiinflammatory; anticonvulsant;  
KM tranquilliser; vasotropic; da.

OS Homo sapiens.

	Key	Location/Qualifiers
FH	CDS	54..2723
FT		745-1

PN WO200202630-A2

PD 10-JAN-2002.

03-JUL-2001; 2001WO-GB02959.

PR 03-JUL-2000; 2000GB-0016360.

**XXX**

XX Strijbos PJLM, Bates S, Gloger I, Davies C;  
PI

DR	WPI; 2002-188422/24.
DR	P-PSDB; AAE18676.

New HCN channel polypeptides and polynucleotides which encode the polypeptides, for the manufacture of compositions to treat stroke ischemia, head injury, epilepsy, Alzheimer's disease, Parkinson's

FI	unseabe	
XX		
PS	Claim 7; Page 52-53; 68pp; English.	

The invention relates to new uses of human hyperpolarisation-activated, cyclic nucleotide-gated (HCN) channel polypeptides and their polynucleotides. The HCN channel polypeptides and polynucleotides can be used in the manufacture of medicaments to treat stroke, ischaemia, head injury, epilepsy, Alzheimer's disease, Parkinson's disease, learning or memory and attention disorders. These compounds may also be used in treating pain, gut disorders, in particular irritable bowel syndrome (IBS) or sleep disorders. HCN polynucleotides and polypeptides may also be employed as diagnostic reagents for detection of mutations in the above stated diseases. The present sequence is human HCN2 channel DNA.

Sequence 3459 BP; 569 A; 1317 C; 1094 G; 479 T; 0 other;

Query Match	16.4%	Score 41.4;	DB 24;	Length 3459;
Best Local Similarity	53.4%;	Pred. No. 2.6;		
Matches 87; Conservative	0;	Mismatches 76;	Indels 0;	Gaps 0

**QY**      1 CGGCCGGGAGCGCCGCGAGTGAAGCTCATGTCTGCCTGCACCTCCACCAGG 60  
         ||||| | | | | | | | | | | | | | | | | | |  
**Db**     170 CGGCCGGGCGCGGCTGTGTGGGGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 111

Qy 61 CGCAGAGGCGGCCACAGAGACCCCACTGCCAGCTTGCCACGGTCTGGGATCAGAGG 120  
Ddb 110 CGCGGGGGTTCGCGCCCGGGCTCTCCCTCGGGGCGCCCGCGGCTCCCGGCGCGCTCCATGCC 51

**Db**

50 GAGGGGCGCCGCGGCAGTGCAGACCGGAGCCGCGCGGCC 8

ID	ABZ35386	standard; cDNA; 2666 BP.
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
8	8	8
9	9	9
10	10	10
11	11	11
12	12	12
13	13	13
14	14	14
15	15	15
16	16	16
17	17	17
18	18	18
19	19	19
20	20	20
21	21	21
22	22	22
23	23	23
24	24	24
25	25	25
26	26	26
27	27	27
28	28	28
29	29	29
30	30	30
31	31	31
32	32	32
33	33	33
34	34	34
35	35	35
36	36	36
37	37	37
38	38	38
39	39	39
40	40	40
41	41	41
42	42	42
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46	46	46
47	47	47
48	48	48
49	49	49
50	50	50
51	51	51
52	52	52
53	53	53
54	54	54
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56	56	56
57	57	57
58	58	58
59	59	59
60	60	60
61	61	61
62	62	62
63	63	63
64	64	64
65	65	65
66	66	66
67	67	67
68	68	68
69	69	69
70	70	70
71	71	71
72	72	72
73	73	73
74	74	74
75	75	75
76	76	76
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80	80	80
81	81	81
82	82	82
83	83	83
84	84	84
85	85	85
86	86	86
87	87	87
88	88	88
89	89	89
90	90	90
91	91	91
92	92	92
93	93	93
94	94	94
95	95	95
96	96	96
97	97	97
98	98	98
99	99	99
100	100	100

AC ABZ35386;  
XX

DT 05-FEB-2003 (first entry)

Human gene expression profile polynucleotide SEQ ID NO 497.

KW Human, artery; endothelium; umbilical, vein; aorta; pulmonary artery;  
KW bronchial epithelium; prostate; muscle; lung fibroblast; osteoblast;  
KW tumour; microarray; genome mapping; antibiotic; antiviral; antifungal;  
KW gene expression; gene, ss.

OS Homo sapiens.

PN WO200274979-A2.

PD 26-SEP-2002.

PF 20-MAR-2002; 2002WO-US08456.

PR 20-MAR-2001; 2001US-276947P.

PA (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.

PI Wan J, Wang Y;

WPI; 2002-740862/80.

PT New gene expression profile generated from primary, endothelial  
PT epithelial, and muscle cell types, useful for identifying disease  
PT pathologies involving alterations of gene expression, e.g. cancer  
XX  
PS Disclosure; Page 638-639; 850p; English.

**CC** The invention relates to a gene expression

is a coronary artery endothelium, umbilical artery or vein endothelium, aortic endothelium, dermal microvascular endothelium, pulmonary artery endothelium, myometrium microvascular endothelium, keratinocyte epithelium, bronchial epithelium, mammary epithelium, prostate epithelium, renal cortical epithelium, renal proximal tubule epithelium, small airway epithelium, renal epithelium, umbilical artery smooth muscle, aorta smooth muscle, pulmonary artery smooth muscle, dermal fibroblast, neural fibroblast, coronary artery smooth muscle, mesangial cells, coronary artery smooth muscle, bronchial smooth muscle, uterine smooth muscle, lung fibroblast, osteoblasts or prostate stromal cell. The gene expression profile is used for determining the level of RNA expression for a sample, determining the phenotype of a cell and distinguishing cell types. The gene or a protein expression profile is useful in identifying disease pathologies involving alterations of gene expression. The assessment of expression profiles may provide meaningful information with respect to tumour type and stage, treatment methods, and prognosis. The gene or protein expression profile may also be used for creating microarrays. The microarray is useful for genetic and physical mapping of genomes, DNA sequencing, genetic or medical diagnosis, genotyping of organisms, confirming cell or tissue identifications and in identifying promising antibiotics, antiviral or antifungal agents.

Query Match 16.2%; Score 40.8; DB 24; Length 2666;  
 Best Local Similarity 49.3%; Pred. No. 3.5;  
 Matches 105; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

QY 1 CGGCGGAGAGCGCGGAGTGAAGGCTGATCTGCTGCGGCTTCACCTCCCGAGG 60  
 DB 28 CAGCCCGAGCGGGGCGGGAGAGGAGCAGAGCGGCGCGCTTGTCCGAGAGAGC 87  
 QY 61 CGCAGAAAGCGGCCACGAGAGACCCCGAGGCTTGCCACGAGTCGAGATCAGAGG 120  
 DB 88 CGCGGGGCGGCCACATCTGCGCCCCCGCGGCTGATCTGCACTCAGACCCGAGC 147  
 QY 121 CAGGAGCAGAGGCGCAGAGAACTGCGCGCGCGCGCGCTGCTGCGCGAGGAACT 180  
 DB 148 GCAGAGAGCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 207  
 QY 181 CCTCTACGAGAGAAAGTCTCCCTCACTCCGCGC 213  
 DB 208 CTGAGACCCCGCGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240

RESULT 7  
 AAA65433  
 ID AAA65433 standard; DNA; 868 BP.  
 AC AAA65433;  
 XX 10-NOV-2000 (first entry)  
 DT Porcine BAC-PIGF2-1 contig 24.  
 DE Porcine; pig; wild boar; quantitative trait locus; QTL; chromosome 2;  
 KW mapping; 2p1.7; select breeding; genotype; phenotype; muscle mass;  
 KM fat deposition; IGF2; insulin-like growth factor 2; ds.  
 OS Sus scrofa.  
 XX WO200036143-A2.  
 PN 22-JUN-2000.  
 XX 16-DEC-1999; 99WO-BP10209.  
 PF 16-DEC-1998; 98BP-0204291.  
 PR (UYLI-) UNIV LIEGE.  
 PA (MELI-) MELICA HB.  
 PA (SEGH-) SEGHESGENTEC NV.  
 XX Andersson L, Georges M, Spincemalle G;  
 PI WPI; 2000-431612/37.  
 DR Selecting a domestic animal for having desired genotypic properties  
 XX comprises testing the animal for the presence of a parentally imprinted  
 PT quantitative trait locus which is related to muscle mass and/or fat  
 PT deposition -  
 XX  
 PS Example 3; Fig 6; 107pp; English.  
 CC The present invention describes a method (M1) for selecting a domestic  
 CC animal for having desired genotypic properties. The method comprises  
 CC testing the animal for the presence of a parentally imprinted  
 CC quantitative trait locus (QTL). The pig QTL is located at chromosome 2,  
 CC mapping at around position 2p1.7. Also described are: (1) an isolated  
 CC and/or recombinant nucleic acid (N1) comprising a parentally imprinted  
 CC QTL or its functional fragment; (2) an isolated and/or recombinant  
 CC nucleic acid (N2) comprising a synthetic parentally imprinted QTL  
 CC derived from at least one chromosome or its functional fragment; (3) an  
 CC animal such as pig selected for having desired genotypic or potential  
 CC phenotypic properties; (4) a transgenic animal comprising N1 or N2; and  
 CC (5) sperm or an embryo derived from the animal of (3) or (4). N1 or its

CC fragment is useful for selecting an animal destined for slaughter or a  
 CC breeding animal having desired genotypic or potential phenotypic  
 CC properties. The properties are related to muscle mass and/or fat  
 CC deposition. The sperm or an embryo are useful in breeding animals  
 CC destined for slaughter. AAA65418 to AAA65524 represent contigs 1 to 10  
 CC and 19 to 115 which were isolated from porcine BAC-PIGF2-1 which  
 CC contains the INS and IGF2 (insulin-like growth factor) genes. These  
 CC sequences were used in an example from the present invention for  
 CC generating a reference sequence of IGF2 and flanking loci in the pig.  
 SQ Sequence 868 BP; 156 A; 243 C; 323 G; 143 T; 3 other;

Query Match 15.7%; Score 39.6; DB 21; Length 868;  
 Best Local Similarity 48.4%; Pred. No. 6.5; Indels 0; Gaps 0;  
 Matches 108; Conservative 0; Mismatches 115;

QY 26 GCGCTGATCGTCTGCGCGCTTCACCTCCCGAGGCGCAGAGCGCCACGAGACCCC 85  
 DB 87 GGGCTGATGTCCTGCGCGCTTCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 146  
 QY 86 CAGTCCCGAGCTTGCCAGCGTCTGAGATCAGAGGAGGAGGAGGAGGAGGAGGAG 145  
 DB 147 TCTGCGCTGAGAGCTGAGAGGCTCCTGAACTCCCGCTGCGACCTGCGGCTCCT 206  
 QY 146 GCGCGCGCGCGCGCGCTGCGCGCGAGGAGCTCCTCAGCGAGGAGGAGGAGGAG 205  
 DB 207 CTTGCGCTGAGAGCTGCGCGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 266  
 QY 206 ACCCGGCGCAGCGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 248  
 DB 267 TGCGCGCGCGCGCAGCGGCGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 309

RESULT 8  
 ABL60745/c  
 ID ABL60745 standard; cDNA; 840 BP.  
 AC ABL60745;  
 XX 18-SEP-2002 (first entry)  
 DT Maize haemoglobin (Mhb1) encoding cDNA.  
 DE Maize haemoglobin (Mhb1) gene; ss.  
 KW Maize; haemoglobin; Hb; plant; transgenic; seed germination; metabolite;  
 KM Mhb1; gene; ss.  
 XX Zea mays.  
 OS Zea mays.  
 XX Key Location/qualifiers  
 FH 51..626  
 FT /\*tag= a  
 FT /product= "Mhb1"  
 FT /note= "haemoglobin"  
 XX US6372961-B1.  
 PN 16-APR-2002.  
 XX 17-AUG-1999; 99US-0376728.  
 PF 20-AUG-1998; 98US-097242P.  
 PR (PION-) PIONEER HI-BRED INT INC.  
 PA Tarczyński MC, Shen B;  
 PI WPI; 2002-400343/43.  
 DR P-PSDB; ABB08069.  
 XX New isolated nucleotide sequence encoding hemoglobin for enhancing seed  
 PT germination and seedling growth, manipulating the oxygen concentration  
 PT in a plant cell, and modulating hemoglobin levels in a plant cell -  
 XX







SQ Sequence 3690 BP; 1086 A; 821 C; 848 G; 935 T; 0 other;  
Query Match 15.2%; Score 38.4; DB 25; Length 3690;  
Best Local Similarity 57.5%; Pred. No. 11;  
Matches 69; Conservative 0; Mismatches 51; Indels 0; Gaps 0;  
QY 42 GCGCCCTCCACCTCCCGAGGCGGAGGCGCCACAGAGACCCCACTGCGCGAGCTTGC 101  
DB 257 GCGAGGCTCCACACGCGCGCGGCGAGGCTGCGCCCGGAGGAAAGCTGCGCCCGCTTCA 198  
QY 102 CACGGCTGGGATCAGAGGCGGAGGAGCCAGGAGCACTGCGCGCGCGCGCGCTG 161  
DB 197 CAGGCGGCGCGCGGAGGAGGAGGAGGCGCGCTCGCGAGCGGAGCGGCGCGT 138  
RESULT 12  
AB65032/C  
ID AB65032 standard; DNA; 42999 BP.  
XX  
AC AB65032;  
XX  
DT 15-NOV-2002 (first entry)  
XX  
DE Invertebrate foraging behaviour associated human DNA sequence #12.  
XX  
KW Attention deficit hyperactivity disorder; ADHD; hypertension;  
KW Invertebrate foraging behaviour; nitric oxide; hypotensive;  
KW cGMP-dependent protein kinase; human; neuroleptic; ds;  
KW gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN WO200259370-A2.  
XX  
PD 01-AUG-2002.  
XX  
PF 13-DEC-2001; 2001WO-US48087.  
XX  
PR 15-DEC-2000; 2000US-0738630.  
XX  
PA (NEUR-) NEUROSCIENCES RES FOUND INC.  
XX  
PI Greenspan RJ, Shaw PJ;  
XX  
DR WPI; 2002-636544/68.  
XX  
PT Identifying a compound that modulates an attention deficit  
PT hyperactivity disorder (ADHD) for treating e.g. ADHD or hypertension,  
PT comprising measuring a foraging behaviour an invertebrate -  
XX  
PS Claim 89; Page 182-195; 246pp; English.  
XX  
CC The present invention relates to a method of identifying a compound  
CC that modulates attention deficit hyperactivity disorder (ADHD) in  
CC a mammal. The method comprises administering a test compound to  
CC an invertebrate, and measuring a foraging behaviour of the  
CC invertebrate, where the compound that modulates the foraging behaviour  
CC of the invertebrate is characterised as a compound that modulates  
CC ADHD in a mammal. The compound identified by the new method of the  
CC invention is useful for diagnosing or treating ADHD, hypertension or  
CC other diseases associated with a nitric oxide/cGMP-dependent protein  
CC kinase network in a mammal, particularly humans. The method  
CC distinguishes a compound that has a specific effect on ADHD,  
CC hypertension or other diseases associated with a  
CC nitric oxide/cGMP-dependent kinase protein network  
CC in a mammal from a compound that has a non-specific effect. The  
CC present sequence represents a DNA sequence associated with  
CC invertebrate foraging behaviour.  
SQ Sequence 42999 BP; 6411 A; 13605 C; 11491 G; 11479 T; 13 other;  
Query Match 15.2%; Score 38.4; DB 24; Length 42999;  
Best Local Similarity 48.4%; Pred. No. 11;

Matches 105; Conservative 0; Mismatches 112; Indels 0; Gaps 0;  
QY 1 CCGCGCGGAGGCGCGCGAGTGAGGCTGATGTCCTTGCGCTCCACTCCACAG 60  
DB 7676 CCGCGCGGAGGCGCGCGCGCGCGCGCGAGAGCTGAGGACGGGCGCGCGCGG 7617  
QY 61 CGCAGAGGCGCGCGCGAGGAGCCCGAGTGCCTGCGGAGCTGAGTCAAGAG 120  
DB 7616 GCGCGCGCGCGAGCGCGAGGCGCGCGCGAGCGGAGCGACACCGCGCTCCGCGG 7557  
QY 121 CAGGAGACAGGAGGAGGAGCACTGCGCGCGCGCGCGCGCTGCGCGGAGGAGCT 180  
DB 7556 TCGCCTGCGCGGAGCAGCGGAGCCCGCGCGCGCGCGCGGCGCGCGGCT 7497  
QY 181 CCTCAGCAGGAGGAGCTCCCTCAACCGCGCGAGC 217  
DB 7496 CCGCGCGCGCGCGCGCGCGCGCGCGCGAGCGAGCGCGGCG 7460  
RESULT 13  
AAF30761/C  
ID AAF30761 standard; DNA; 528 BP.  
XX  
AC AAF30761;  
XX  
DT 21-JUN-2001 (first entry)  
XX  
DE Megalomycin polyketide synthase codon engineered module 6.  
XX  
KW Megalomycin; meg gene; polyketide synthase; antibiotic;  
KW motif; antiparasitic; mutant; de.  
XX  
OS Micromonospora megalomycina subsp. nigra.  
XX  
PN WO200127284-A2.  
XX  
PD 19-APR-2001.  
XX  
PF 05-OCT-2000; 2000WO-US27433.  
XX  
PR 08-OCT-1999; 99US-0158305.  
PR 17-MAR-2000; 2000US-0190024.  
XX  
PA (KOSA-) KOSAN BIOSCIENCES INC.  
XX  
PI McDaniel R, Volchegursky Y;  
XX  
DR WPI; 2001-282034/29.  
XX  
PT Nucleic acids encoding a domain of megalomycin polyketide synthase or a  
PT megalomycin modification enzyme, useful for the production of  
PT megalomycin for use as antibiotics, molluscides and antiparasitics -  
XX  
PS Example 2; Page 99; 189pp; English.  
XX  
CC The present sequence of that of bases 26736-27267 in a codon  
CC engineered module 6 of the Micromonospora megalomycina subsp. nigra  
CC ATCC 27587 (NRRL3275) megalomycin polyketide synthase (PKS) gene  
CC cluster (see AAF30757). Expression plasmids containing the  
CC full-length megalomycin PKS were unstable and subject to deletion  
CC in recA+ strains. To prevent homologous recombination and so  
CC stabilize the plasmids, the codons of 2 regions in module 6  
CC coding sequence that are identical to regions in module 2  
CC sequence were changed without changing the sequence of protein  
CC encoded. The 2 regions changed in module 6 were bases 26739-27267  
CC (see AAF30760) and 27697-27987 (see AAF30763), which were identical  
CC to module 2 bases 6810-7338 (see AAF30759) and 7778-8068,  
CC respectively. The start codon of the loading domain of the meg PKS  
CC was set as the first base. Codon engineering in the meg PKS  
CC stabilized meg PKS expression in bacterial host cells. The  
CC invention provides nucleic acids encoding all or a portion of  
CC the megalomycin PKS and modification enzymes, which can be used to



PI Albone EF, Kikly KK;  
XX  
DR WPI; 1999-246414/21.  
DR P-PSDB; AAY02135.  
XX  
PT New Kringle protein family member useful for diagnosing and treating  
PT diseases such as cancer, rheumatoid arthritis and AIDS  
XX  
PS Claim 2; Page 13; 22pp; English.

CC The present sequence encodes a protein designated HTB247. The  
CC protein is a member of the kringle protein family. Detection  
CC of the amount of HTB247 protein in a sample from a patient may  
CC be used to diagnose diseases such as cancer, rheumatoid arthritis,  
CC asthma, Alzheimer's disease, multiple sclerosis, septic shock,  
CC stroke and AIDS. Similarly, detection of a mutation in the gene  
CC encoding HTB247 may be used in diagnosis. The protein may be  
CC used to identify its agonists and antagonists, and to identify  
CC its membrane bound or soluble receptors.

SQ Sequence 1875 BP; 385 A; 584 C; 479 G; 427 T; 0 other;

Query Match 15.1%; Score 38; DB 20; Length 1875;  
Best Local Similarity 49.2%; Pred. No. 14;  
Matches 98; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

OY 52 CTCGCCAGGCGGAGAGGCGCCACGAGAGAGCCCGAGTCCCGATGCGACGCTGCG 111  
DB 1 CTCGCCCTCTCCATGCGCGCGCCCGCTCCCGCGCTGCGCTTACCCCGGCGCG 60  
OY 112 GATCAGAGGCGAGGAGACGAGAGAGCGAGAACTGCGCGCGCGCGCGCTGCGCG 171  
DB 61 GCGCGCGCGCGCGCGAGCTGACGCGCGCGCGCGCGCGCGCGCGCGCTGCT 120  
OY 172 AAGGAGAGCTCCCTACACNAGAGGAGCTCCCTACCGCGCGCGCGCGAGCGGCGG 231  
DB 121 CCGCGCGCGCGCTGACGCTGCGCGCGCGCGCGCGCGCGCGCGCTGCGCG 180  
OY 232 CGTGGGTCGAGACCGGAAA 250  
DB 181 CCGAGCTTTCACAGCCAA 199

## RESULT 16

ABX30552  
ID ABX30552 standard; cDNA; 2875 BP.

AC ABX30552;

DT 02-MAY-2003 (first entry)

DE Human kinase CDNA #17.

KW Human; gene; ss; kinase; phosphorylation; regulatory pathway;

KW gene therapy.

OS Homo sapiens.

PN US2002161213-A1.

PD 31-OCT-2002.

PF 12-DEC-2001; 2001US-0020079.

PR 12-DEC-2000; 2000US-255103P.

PR 08-MAY-2001; 2001US-289422P.

PA (TURNER) TURNER C A.

PA (MATHUR) MATHUR B.

PA (FRID) FRIDDLE C J.

PI Turner CA, Mathur B, Friddle CJ;

DR WPI; 2003-288125/28.  
DR P-PSDB; ABU60671.  
XX  
PT New novel human polynucleotides encoding proteins sharing sequence  
PT similarity with animal kinases, useful for diagnosing or treating  
PT disorders -  
XX  
PS Disclosure; Page 62-63; 78pp; English.

CC The invention discloses isolated nucleic acids, and the protein that they  
CC encode, of novel human kinases. Kinases mediate the phosphorylation of a  
CC wide variety of proteins and compounds in the cell and are involved in a  
CC range of regulatory pathways. The novel human polynucleotides, encoding  
CC proteins sharing sequence similarity with animal kinases, are useful for  
CC diagnosing or treating (e.g. gene therapy) disorders. The sequence  
CC presented is a cDNA encoding a human kinase.

SQ Sequence 2875 BP; 531 A; 983 C; 905 G; 453 T; 3 other;

Query Match 15.1%; Score 38; DB 25; Length 2875;  
Best Local Similarity 50.3%; Pred. No. 14;  
Matches 89; Conservative 1; Mismatches 87; Indels 0; Gaps 0;

OY 36 TCCTGCGCGCTTCACCTCCCGAGGCGGAGAGGCGCCCGAGAGAGCCCGAGTCCCGA 95  
DB 61 YCGCTGCGCGCGCGCTGCGCGCGAGAGATCGGCGCGCGCGCGCGAGATCGCGG 120  
OY 96 CGTTGCCAGCGTCTGGGATTCAGAGGAGGAGACCGAGGAGCCAGAACTGCGCGCGCG 155  
DB 121 TCGGAGAGCGCGCGCGCGCGGAGGAGCGGATCCCAACCGCGACTAGCGCGCGCG 180  
OY 156 CCCCTGCGCGCGCGAGGAGAGCTCCCTACCGAGGAGAGCTCCCTCACCGCGCG 212  
DB 181 CCGCGCGCGCGCGCGCGGAGATCGCGCGCGCGCGCGAGCTGCTGCTCGCGCGCGCG 237

## RESULT 17

AAK34648/C  
ID AAK34648 standard; DNA; 4890 BP.

AC AAK34648;

DT 05-JUL-1999 (first entry)

DE Promoter containing sequence of SBE 1.

KW Starch biosynthetic pathway; cereal plant; enzyme; SBE; SSS; DBE; GBS;

KW starch branching enzyme; starch soluble synthase; debanching enzyme;

KW endosperm; wheat; barley; granule-bound synthase; glucanin; starch;

KW grain softness protein I; bacterial isoamylase; glycogen synthase;

OS Triticum tauschii.

PN WO9914314-A1.

PD 25-MAR-1999.

PF 11-SEP-1998; 98WO-AU00743.

PR 20-MAR-1998; 98AU-0002509.

PR 12-SEP-1997; 97AU-0009108.

PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.

PA (GOOD-) GOODMAN FIELDER LTD.

PA (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.

PA (AUSU ) UNIV AUSTRALIAN NAT.

PI Li Z, Morell M, Rahman S;

DR WPI; 1999-229525/19.

XX New isolated cereal plant enzyme genes used for, e.g. expression of

PT antisense sequences of granule bound synthase  
XX  
PS Claim 17; Page 63-65; 171pp; English.  
XX  
CC The invention relates to a novel enzyme of starch biosynthetic pathway  
CC in a cereal plant, where the enzyme is selected from starch branching  
CC enzyme (SBE) I, SBE II, starch soluble synthase (SSS) I, and debranching  
CC enzyme (DBE), with the proviso that the enzyme is not SSS I of rice, or  
CC SBE I of rice or maize. The methods and products can be used for  
CC targeting expression specifically to the endosperm of the seeds of cereal  
CC plants such as wheat or barley. They can be used for the expression of  
CC 6g. wt. glutelin, grain softness protein I, bacterial isomylase, low  
CC molecular weight glycogen synthase, and wheat high mol. wt. glutelin Bx17. They  
CC can be used for modifying the characteristics of starch produced by a  
CC plant. The present sequence represents the wheat SBE I promoter  
CC containing sequence.  
XX  
SQ Sequence 4890 BP; 1403 A; 1067 C; 1035 G; 1385 T; 0 other;  
Query Match 15.1%; Score 38; DB 20; Length 4890;  
Best Local Similarity 51.5%; Pred. No. 14;  
Matches 86; Conservative 0; Mismatches 81; Indels 0; Gaps 0;  
XX  
QY 24 GAGGCTGATCTCTCTGCGCTTCCACCTCCAGCGCCAGAAAGCGCCCAAGAGACC 83  
Db 173 GGGCCCTGTCTCGACCCGAGACCTCAGCTGCGCGGCTTTAAAGCCGACGCCGTGCCC 114  
QY 84 CCCAGTGGCCGACGTTGCCACGGCTGGAGATCAGAGGACGAGGAGCCAGAGAACT 143  
Db 113 GCGCTCAGCCCAAGTGGCGCGCGCGCGGAAACCTTAGCGCGCGCCGCCGCCGCCG 54  
QY 144 GCG 190  
Db 53 GCG 7  
RESULT 18  
ABK99879  
ID ABK99879 standard; cDNA; 1947 BP.  
XX  
AC ABK99879;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human cDNA encoding a novel kinase protein #6.  
XX  
KW Human; ss; kinase; gene; noctropic; gene therapy; novel human protein;  
KW NHP; serine-threonine kinase; casein kinase; mitogen activated kinase;  
KW calcium/calmodulin-dependent protein kinase; chromosome 6;  
KW mental disorder.  
XX  
OS Homo sapiens.  
XX  
PN WO200248333-A2.  
XX  
PD 20-JUN-2002.  
XX  
PF 12-DEC-2001; 2001WO-US49068.  
XX  
PR 12-DEC-2000; 2000US-255103P.  
PR 08-MAY-2001; 2001US-289422P.  
XX  
PA (LEXI-) LEXICON GENETICS INC.  
XX  
PI Turner CA, Mathur B, Friddle CJ;  
XX  
DR WPI, 2002-583505/62.  
DR P-PDB; ABG69455.  
XX  
XX Novel polynucleotides encoding human proteins that are structurally  
PT related to animal kinases, useful for drug screening, diagnosis and in  
PT gene therapy of biological disorders

XX  
PS Disclosure; Page 50-51; 94pp; English.  
XX  
CC The invention relates to an isolated nucleic acid molecule comprising a  
CC nucleotide sequence encoding a novel human protein (NHP) appearing  
CC as ABG69450-ABG69469, that share structural similarity with animal  
CC kinases, including serine-threonine kinases, casein kinases,  
CC calcium/calmodulin-dependent protein kinases, and mitogen activated  
CC kinases. NHP oligonucleotides are useful as hybridization probes for  
CC screening libraries and assessing gene expression patterns. NHP  
CC sequences are useful to identify mutations associated with a particular  
CC disease and also as a diagnostic or prognostic assay, and also in the  
CC molecular mutagenesis/evolution of proteins that are at least partially  
CC encoded by the NHP boundaries. Sequences derived from regions adjacent  
CC to the intron/exon boundaries of NHP gene can be used to design primers  
CC for use in amplification assays to detect mutations within the exons,  
CC splice sites, introns that can be used in diagnostics and  
CC pharmacogenomics. NHP sequences are utilized in microarrays or other  
CC assay formats, to screen collections of genetic material from patients  
CC who have a particular medical condition. NHP nucleotide sequences are  
CC useful for drug screening effective in the treatment of symptomatic or  
CC phenotypic manifestations of perturbing the normal function of NHP in the  
CC body, and nucleotide constructs encoding NHP products are used to  
CC genetically engineer host cells to express NHP products in vivo. These  
CC delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion  
CC protein to the body. Nucleotide constructs encoding NHP products are also  
CC useful in gene therapy for modulating NHP expression. The encoded NHP  
CC polypeptides are useful for generating antibodies, as reagents in  
CC diagnostic assays, for identifying other cellular gene products related  
CC to NHP and as reagents in assays for screening for compounds that are  
CC useful in the treatment of mental, biological or medical disorders and  
CC diseases. The gene for the NHP is located on human chromosome 6.  
XX  
SQ Sequence 1947 BP; 395 A; 586 C; 658 G; 306 T; 2 other;  
Query Match 15.0%; Score 37.8; DB 24; Length 1947;  
Best Local Similarity 50.6%; Pred. No. 16;  
Matches 90; Conservative 0; Mismatches 88; Indels 0; Gaps 0;  
XX  
QY 35 GTCCCTGGCGCTTCCACCTTCCAGCGCGCAAGAGCGCCCAAGAGACCCCAAGTCCCG 94  
Db 41 GCGCTGTCTCGACCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 100  
QY 95 ACGTTGCCACGGTCTGGATCAGAGCGAGGACCAAGAGCCAGAACTCGCGCGCGCC 154  
Db 101 GTCGAGAGCG 160  
QY 155 GCGCCTGCGCTTGGCGCGCGAGGAGTCTCCTCACCAGGAGGAGTCTCCTCACCAGC 212  
Db 161 GCG 218  
RESULT 19  
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ID ABX90541 standard; cDNA; 1947 BP.  
XX  
AC ABX90541;  
XX  
DT 02-MAY-2003 (first entry)  
XX  
DE Human kinase cDNA #6.  
XX  
KW Human; gene; ss; kinase; phosphorylation; regulatory pathway;  
KW gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN US2002161213-A1.  
XX  
PD 31-OCT-2002.



AC ABX90540;  
 XX 02-MAY-2003 (first entry)  
 XX Human kinase cDNA #5.  
 XX Human kinase cDNA #5.  
 XX Human, gene; ss; kinase; phosphorylation; regulatory pathway;  
 XX gene therapy.  
 XX Homo sapiens.  
 XX US2002161213-A1.  
 XX 31-OCT-2002.  
 XX 12-DEC-2001; 2001US-0020079.  
 XX 12-DEC-2000; 2000US-255103P.  
 XX 08-MAY-2001; 2001US-289422P.  
 XX (TURN/) TURNER C A.  
 XX (MATH/) MATHUR B.  
 XX (FRID/) FRIDDLE C J.  
 XX Turner CA, Mathur B, Friddle CJ;  
 XX WPI; 2003-288125/28.  
 XX P-PSDB; ABU60559.  
 XX New novel human polynucleotides encoding proteins sharing sequence  
 PT similarity with animal kinases, useful for diagnosing or treating  
 PT disorders -  
 XX disclosure; Page 23-24; 78pp; English.  
 XX The invention discloses isolated nucleic acids, and the protein that they  
 CC encode, of novel human kinases. Kinases mediate the phosphorylation of a  
 CC wide variety of proteins and compounds in the cell and are involved in a  
 CC range of regulatory pathways. The novel human polynucleotides, encoding  
 CC proteins sharing sequence similarity with animal kinases, are useful for  
 CC diagnosing or treating (e.g. gene therapy) disorders. The sequence  
 CC presented is a cDNA encoding a human kinase.  
 XX Sequence 1965 BP; 397 A; 589 C; 666 G; 311 T; 2 other;  
 SQ  
 Query Match 15.0%; Score 37.8; DB 25; Length 1965;  
 Best Local Similarity 50.6%; Pred. No. 16;  
 Matches 90; Conservative 0; Mismatches 88; Indels 0; Gaps 0;  
 QY 35 GTCCTGCGGCTCCCACTCCCGAGGCGGAGAGGCGCCCGGAGGAGCCCGGAGTCCCG 94  
 DB 59 GCGGCTGCGGCGGCGGCTCCCGAGGAGGAGTCCCGGCGGCGGCGGAGTCCCG 118  
 QY 95 AGCTGCGGAGGAGTCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 154  
 DB 119 GTCGGAAGGCGGCGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 178  
 QY 155 GCGGCTGCGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 212  
 DB 179 GCGGCTGCGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 236

KW Leukaemia; immune disorder; lymphoma; melanoma; developmental disorder;  
 KW acquired immunodeficiency syndrome; AIDS; allergy; anaemia; hypertension;  
 KW asthma; Crohn's disease; rheumatoid arthritis; buritis; atherosclerosis;  
 KW cirrhosis; hepatitis; psoriasis; Cushing's syndrome; cytostatic; cancer;  
 KW cholesterol; cardiac; cardiovascular disorder; Niemann-Pick's disease;  
 KW lipid disorder; fatty liver; Gaucher's disease; myocardial infarction;  
 KW drug screening; transgenic animal; anti-inflammatory; hepatotropic;  
 KW hypotensive; anti-HIV; enzyme; ss.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 XX CDS 1..2226  
 XX /tag=a  
 XX /product="Human PKIN-4"  
 XX sig\_peptide 1..57  
 XX /tag=b  
 XX mat\_peptide 58..2223  
 XX /tag=c  
 XX /product="Mature human PKIN-4"  
 XX WO200208399-A2.  
 XX 31-JAN-2002.  
 XX 20-JUL-2001; 2001WO-US23092.  
 XX 21-JUL-2000; 2000US-220038P.  
 XX 28-JUL-2000; 2000US-222112P.  
 XX 04-AUG-2000; 2000US-222831P.  
 XX 11-AUG-2000; 2000US-224729P.  
 XX (INCY-) INCYTE GENOMICS INC.  
 XX (THOR/) THORNTON M.  
 XX Thornton M, Yue H, Khan FA, Gurusajan R, Hafalia AJA, Walla NK;  
 XX Patterson C, Rakhumay J, Gandhi AR, Policky JL, Baughn MK;  
 XX Tribouley CM, Bandman O, Nguyen DB, Lu Y, Burford N, Lai P;  
 XX Ding L, Yao MG, Elliott VS, Reipon SA, Kearney L, Lu DM;  
 XX Greenwald SR, Yang YT, Xu Y, Walsh RT, Gietzen KU, Yang J;  
 XX Hillman JL;  
 XX WPI; 2002-206083/26.  
 XX P-PSDB; AME19146.  
 XX New human kinase polypeptide, useful in diagnosis, prevention and  
 PT treatment of cancer, immune disorder, growth and developmental  
 PT disorder, cardiovascular disorder and lipid disorder -  
 XX Claim 5; Page 177-178; 196pp; English.  
 XX The present invention relates to an isolated human kinase polypeptide  
 CC (PKIN) or a biologically active/immunogenic fragment of PKIN. PKIN is  
 CC useful for diagnosing, treating and preventing cancer (e.g., leukaemia,  
 CC lymphoma, melanoma), an immune disorder (e.g., acquired immunodeficiency  
 CC syndrome (AIDS), Addison's disease, allergy, anaemia, asthma, Crohn's  
 CC disease, rheumatoid arthritis), a growth and developmental disorder (e.g.,  
 CC buritis, cirrhosis, hepatitis, psoriasis, Cushing's syndrome), a  
 CC cardiovascular disorder (e.g., atherosclerosis, hypertension, myocardial  
 CC infarction), and a lipid disorder (e.g., fatty liver, cholesterol,  
 CC Gaucher's disease, Niemann-Pick's disease). PKIN is useful in a number of  
 CC drug screening techniques and to analyse the proteome of a tissue or cell  
 CC type. PKIN is useful for creating knock-in humanised animals or transgenic  
 CC animals to model human diseases, in somatic or germ-line gene therapy, to  
 CC generate a transcript image of a tissue or cell type, for detecting  
 CC differences in the chromosomal location due to translocation, inversion,  
 CC etc., among normal, carrier or affected individuals, and as hybridisation  
 CC probes for mapping naturally occurring genomic sequences. PKIN is useful  
 CC in southern or northern analysis, dot blot or other membrane-based  
 CC technologies, in PCR technologies, in dipstick, pin, multiformat enzyme  
 CC linked immunosorbent (ELISA)-like assays and in microarrays utilising  
 CC fluids or tissues from patients to detect altered PKIN expression. The  
 CC present sequence is human PKIN-4 cDNA.







XX	PS	Disclosure, Page 13-14; 78pp; English.
XX	CC	The invention discloses isolated nucleic acids, and the protein that they
XX	CC	encode, of novel human kinases. Kinases mediate the phosphorylation of a
XX	CC	wide variety of proteins and compounds in the cell and are involved in a
XX	CC	range of regulatory pathways. The novel human polynucleotides, encoding
XX	CC	proteins sharing sequence similarity with animal kinases, are useful for
XX	CC	diagnosing or creating (e.g. gene therapy) disorders. The sequence
XX	CC	presented is a cDNA encoding a human kinase.
XX	SQ	Sequence 2595 BP; 498 A; 865 C; 845 G; 385 T; 2 other;
QY	Query Match	15.0%; Score 37.8; DB 25; Length 2595;
Db	Best Local Similarity	50.6%; Pred. No. 16;
Matches	90; Conservative	0; Mismatches 88; Indels 0; Gaps 0;
QY	35	GTCCCTGAGCGCCTCCACCTCCCGACGCGCAGAGGCGCCACGAGACCCCGATGCCG 94
Db	41	GCCGCTGCGCGCCGCGCCCTCCGCCAAGAGAGATCGGAGCGCGGCGCGGATGATCCGG 100
QY	95	ACGTTGCCACGCGTGTGGATTCAGAGCGAGGACAGAGGAGCAGAGAACTCGCGCGCCC 154
Db	101	GTGCGAAGGCGCGCGCGCGCGCGAGGAGCGGATCACCAAGCGCGCACTAGCGCGCCCC 160
QY	155	GCCCTGCGCCTGAGCGGAGGAGGAGTCCCTCACCGAGGAGGAGTCCCTCAACCGCGC 212
Db	161	GCCCGCGCGCGCGCGCGCGCGGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 218
RESULT 25		
ABK99874		
ID	ABK99874	standard; cDNA; 2613 BP.
AC	ABK99874;	
XX	XX	21-OCT-2002 (first entry).
DE	XX	Human cDNA encoding a novel kinase protein #1.
XX	KX	Human; 88; kinase; gene; noctropic; gene therapy; novel human protein;
KW	KW	NBP; serine-threonine kinase; casein kinase; mitogen activated kinase;
KW	KW	calcium/calmodulin-dependent protein kinase; chromosome 6; SNP;
XX	KW	mental disorder; single nucleotide polymorphism.
OS	XX	Homo sapiens.
XX	XX	
FH	FH	Key Location/Qualifiers
FT	FT	variation replace (2166,C)
FT	FT	/tag_a
XX	XX	/standard_name="Single nucleotide polymorphism"
PN	XX	MO20024833-A2.
XX	XX	20-JUN-2002.
XX	XX	12-DEC-2001; 2001WO-US49068.
XX	XX	12-DEC-2000; 2000US-255103P.
PR	XX	08-MAY-2001; 2001US-289422P.
XX	XX	(LEXI-) LEXICON GENETICS INC.
PI	XX	Turner CA, Matchur B, Fiddle CJ;
DR	XX	WPI; 2002-583505/62.
DR	XX	P-PSDB; ABG69450.
XX	XX	Novel polynucleotides encoding human proteins that are structurally
XX	XX	related to animal kinases, useful for drug screening, diagnosis and in
XX	XX	gene therapy of biological disorders
XX	XX	Claim 2; Page 36-37; 94pp; English.

XX	The invention relates to an isolated nucleic acid molecule comprising a nucleotide sequence encoding a novel human protein (NHP) appearing as AB695950-AB695969, that share structural similarity with animal kinases, including serine-threonine kinases, casein kinases, calmodulin-dependent protein kinases, and mitogen activated kinases. NHP oligonucleotides are useful as hybridization probes for screening libraries and assessing gene expression patterns. NHP sequences are useful to identify mutations associated with a particular disease and also as a diagnostic or prognostic assay, and also in the molecular mutagenesis/evolution of proteins that are at least partially encoded by the NHP sequences. Sequences derived from regions adjacent to the intron/exon boundaries of NHP gene can be used to design primers for use in amplification assays to detect mutations within the exons, splice sites, introns that can be used in diagnostics and pharmacogenomics. NHP sequences are utilized in microarrays or other assay formats, to screen collections of genetic material from patients who have a particular medical condition. NHP nucleotide sequences are useful for drug screening effective in the treatment of symptomatic or phenotypic manifestations of perturbing the normal function of NHP in the body, and nucleotide constructs encoding NHP products are used to genetically engineer host cells to express NHP products in vivo. These constructs are continuous supply of a NHP, a NHP peptide, or a NHP fusion protein to the body. Nucleotide constructs encoding NHP products are also useful in gene therapy for modulating NHP expression. The encoded NHP polypeptides are useful for generating antibodies, as reagents in diagnostic assays, for identifying other cellular gene products related to NHP and as reagents in assays for screening for compounds that are useful in the treatment of mental, biological or medical disorders and diseases. The gene for the NHPs is located on human chromosome 6.
XX	The present sequence encodes an NHP of the invention.
XX	Sequence 2613 BP, 500 A; 868 C; 853 G; 390 T; 2 other;
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Query Match	15.0%; Score 37.8; DB 24; Length 2613;
Best Local Similarity	50.6%; Fred. No. 16;
Matches	90; Conservative 0; Mismatches 88; Indels 0; Gaps 0
Dy	35 GTCCCTGCGCCTCACTCCCGAGCGCGACGAAGCGGCCACGAGAGCCCCAGTGC CGG 94
Db	59 GCCGTGCGCGCGCGCTGCCCGCCAGAGAGATCGGGCGCGGCGCGAGTAGATCCGG 118
Dy	95 ACCTTGCCACGGCTCTGGAGATAGAGGACGAGGACCAGGAAGTGCAGCGCGCGCC 154
Db	119 GTCCGAGAGCGCGCGCGCGCCCGCCGAGAGAGCGGGGTCAACCAAGCGCGCATGAGCGCGCCC 178
Dy	155 GCCTTCGCGCTTGCGCGAGGAACTCCCTCACAGGAGAACTCCCTCACCGCGCG 212
Db	179 GCCCGCGCGCGCGCGCGGGGAGTGC CGCGCCCGAAGCTGCTGCTCGCGCGCGCGC 236
RESULT 26	
ABX90536	
DD	ABX90536 standard; cDNA; 2613 BP.
XX	
AC	ABX90536;
XX	
DT	02-MAY-2003 (first entry)
XX	
DE	Human kinase cDNA #1.
XX	
KW	Human; gene; ss; kinase; phosphorylation; regulatory pathway;
KM	gene therapy; single nucleotide polymorphism; SNP; chromosome 6.
XX	
OS	Homo sapiens.
XX	
FT	Key Location/Qualifiers
FT	misc_feature 2186
FT	/tag= a
FN	/standard_name= "Single nucleotide polymorphism"
NN	US2002161213-A1.

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XX 31-OCT-2002.
PD 12-DEC-2001; 2001US-0020079.
XX
XX 12-DEC-2001; 2000US-255103P.
XX
XX 08-MAY-2001; 2001US-289422P.
XX
XX (TURNER) TURNER C A.
XX (MATH) MATHUR B.
XX (FRID) FRIDDLE C J.
XX
XX Turner CA, Mathur B, Friddle CJ,
XX
XX WPI; 2003-288125/28.
XX
XX P-PSDB; AB060655.
XX
XX New novel human polynucleotides encoding proteins sharing sequence
XX similarity with animal kinases, useful for diagnosing or treating
XX disorders -
XX
XX Claim 2; Page 9-11; 78bp; English.
XX
XX The invention discloses isolated nucleic acids, and the protein that they
XX encode, of novel human kinases. Kinases mediate the phosphorylation of a
XX wide variety of proteins and compounds in the cell and are involved in a
XX range of regulatory pathways. The novel human polynucleotides, encoding a
XX proteins sharing sequence similarity with animal kinases, are useful for
XX diagnosing or treating (e.g. gene therapy) disorders. The sequence
XX presented is a cDNA encoding a human kinase, the gene for which is
XX located on chromosome 6.
XX
XX Sequence 2613 BP; 500 A; 868 C; 853 G; 390 T; 2 other;
XX
XX Query Match 15.0%; Score 37.8; DB 25; Length 2613;
XX Best Local Similarity 50.6%; Pred. No. 16;
XX Matches 90; Conservative 0; Mismatches 88; Indels 0; Gaps 0;
XX
XX 35 GTCCTGGGCGCTTCACCTCCCGAGGCGCCACAGAGAGACCCCAAGTCCCG 94
XX 59 GCGCGTGGCGCGCTTCACCTCCCGAGGCGCCAGAGAGATCGGGCGCGGATGATCCGG 118
XX
XX 95 ACCTTCCACGCTGTGAGATCAAGAGCAGAGACCAAGAGGACCAAGAACTGCCCGCCCC 154
XX
XX 119 GTCGGAAGAGCGCGCGCGCGAGAGAGCGGTCAACCCAGCCGCACTGAGACTCCCGCC 178
XX
XX 155 GCGCCCTGCGCTTCGCGCGAGAGAGAGCTCCCTCAACGAGAGAAAGTCCCTCAACCGCG 212
XX
XX 179 GCGCCGCGCGCGCGCGCGCGAGAGTGCAGCCCGCCGAGCTGCTGCTCCGCGCGCGCG 236
XX
XX
XX RESULT 27
XX ABR99883
XX ID ABR99883 standard; cDNA; 2670 BP.
XX
XX ABR99883;
XX
XX 21-OCT-2002 (first entry)
XX
XX Human cDNA encoding a novel kinase protein #10.
XX
XX Human; as; kinase; gene; noctropic; gene therapy; novel human protein;
XX NHP; serine/threonine kinase; casein kinase; mitogen activated kinase;
XX calcium/calmodulin-dependent protein kinase; chromosome 6;
XX mental disorder.
XX
XX Homo sapiens.
XX
XX WO200248333-A2.
XX
XX 20-JUN-2002.
XX
XX 12-DEC-2001; 2001WO-US49068.
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XX 12-DEC-2000; 2000US-255103P.
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XX 08-MAY-2001; 2001US-289422P.
XX
XX (LEXT-) LEXICON GENETICS INC.
XX
XX Turner CA, Mathur B, Friddle CJ;
XX
XX WPI; 2002-583505/62.
XX
XX P-PSDB; ABG69459.
XX
XX Novel polynucleotides encoding human proteins that are structurally
XX related to animal kinases, useful for drug screening, diagnosis and in
XX gene therapy of biological disorders -
XX
XX Disclosure; Page 60-61; 94bp; English.
XX
XX The invention relates to an isolated nucleic acid molecule comprising a
XX nucleotide sequence encoding a novel human protein (NHP) appearing
XX as ABG69450-ABG69469, that share structural similarity with animal
XX kinases, including serine/threonine kinases, casein kinases,
XX calcium/calmodulin-dependent protein kinases and mitogen activated
XX kinases. NHP oligonucleotides are useful as hybridisation probes for
XX screening libraries and assessing gene expression patterns. NHP
XX sequences are useful to identify mutations associated with a particular
XX disease and also as a diagnostic or prognostic assay, and also in the
XX molecular mutagenesis/evolution of proteins that are at least partially
XX encoded by the NHP sequences. Sequences derived from regions adjacent
XX to the intron/exon boundaries of NHP gene can be used to design primers
XX for use in amplification assays to detect mutations within the exons,
XX splice sites, introns that can be used in microarrays or other
XX pharmacogenomics. NHP sequences are utilised in microarrays or other
XX assay formats, to screen collections of genetic material from patients
XX who have a particular medical condition. NHP nucleotide sequences are
XX useful for drug screening effective in the treatment of symptomatic or
XX phenotypic manifestations of perturbing the normal function of NHP in the
XX body, and nucleotide constructs encoding NHP products are used to
XX genetically engineer host cells to express NHP products in vivo. These
XX constructs are useful for screening and identifying NHP products that
XX deliver a continuous supply of a NHP, a NHP peptide, or a NHP fusion
XX protein to the body. Nucleotide constructs encoding NHP products are also
XX useful in gene therapy for modulating NHP expression. The encoded NHP
XX polypeptides are useful for generating antibodies, as reagents in
XX diagnostic assays, for identifying other cellular gene products related
XX to NHP and as reagents in assays for screening for compounds that are
XX useful in the treatment of mental, biological or medical disorders and
XX diseases. The gene for the NHPs is located on human chromosome 6.
XX
XX The present sequence encodes an NHP of the invention.
XX
XX Sequence 2670 BP; 538 A; 846 C; 863 G; 421 T; 2 other;
XX
XX Query Match 15.0%; Score 37.8; DB 24; Length 2670;
XX Best Local Similarity 50.6%; Pred. No. 16;
XX Matches 90; Conservative 0; Mismatches 88; Indels 0; Gaps 0;
XX
XX 35 GTCCTGGGCGCTTCACCTCCCGAGGCGCCACAGAGAGACCCCAAGTCCCG 94
XX 41 GCGCGTGGCGCGCTTCACCTCCCGAGGAGATCGGGCGCGGCGCGGATGATCCGG 100
XX
XX 95 ACCTTCCACGCTGTGAGATCAAGAGCAGAGACCAAGAGGACCAAGAACTGCCCGCCCC 154
XX
XX 101 GTCGGAAGAGCGCGCGCGCGAGAGAGCGGTCAACCAAGCCGCACTGAGACTCCCGCC 160
XX
XX 155 GCGCCCTGCGCTTCGCGCGAGAGAGAGCTCCCTCAACGAGAGAAAGTCCCTCAACCGCG 212
XX
XX 161 GCGCCGCGCGCGCGCGCGAGAGTGCAGCCCGCCGAGCTGCTGCTCCGCGCGCGCG 218
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XX RESULT 28
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XX ID ABR90545 standard; cDNA; 2670 BP.
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XX ABR90545;
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XX 02-MAY-2003 (first entry)  
 XX Human kinase cDNA #10.  
 DE Human; gene; ss; kinase; phosphorylation; regulatory pathway;  
 KW gene therapy.  
 XX Homo sapiens.  
 OS  
 PN US2002161213-A1.  
 XX  
 PD 31-OCT-2002.  
 XX  
 PF 12-DEC-2001; 2001US-0020079.  
 XX  
 PR 12-DEC-2000; 2000US-255103P.  
 PR 08-MAY-2001; 2001US-289422P.  
 XX  
 PA (TURN/) TURNER C A.  
 PA (MATH/) MATHUR B.  
 PA (FRID/) FRIDDLE C J.  
 XX  
 PI Turner CA, Mathur B, Friddle CJ;  
 XX  
 DR WPI; 2003-288125/28.  
 DR P-PSDB; ABU60664.  
 XX  
 PT New novel human polynucleotides encoding proteins sharing sequence  
 PT similarity with animal kinases, useful for diagnosing or treating  
 PT disorders -  
 XX  
 PS Disclosure; Page 37-38; 78pp; English.  
 CC The invention discloses isolated nucleic acids, and the protein that they  
 CC encode, of novel human kinases. Kinases mediate the phosphorylation of a  
 CC wide variety of proteins and compounds in the cell and are involved in a  
 CC range of regulatory pathways. The novel human polynucleotides, encoding  
 CC proteins sharing sequence similarity with animal kinases, are useful for  
 CC diagnosing or treating (e.g. gene therapy) disorders. The sequence  
 CC presented is a cDNA encoding a human kinase.  
 XX  
 SQ Sequence 2670 BP; 538 A; 846 C; 863 G; 421 T; 2 other;  
 Query Match 15.0%; Score 37.8; DB 25; Length 2670;  
 Best Local Similarity 50.6%; Pred. No. 16;  
 Matches 90; Conservative 0; Mismatches 88; Indels 0; Gaps 0;  
 QY 35 GTCCCTGCGCCCTCCACCTCCAGGCGCAGAGGCGCCACGAGAGCCCGAGTGCCTG 94  
 DB 41 GCGGCTGCGCCCGCCGTCGCCCAAGAGATCGGGGCGGGCCGGGATGATCCGG 100  
 QY 95 ACGTTGCCACGATCTGGGATCAGAGCGAGGAGCCAGAGAGCCAGAACTGCGCGCCCG 154  
 DB 101 GTCGGAAGCGCGCGCGCGCGGAGGAGCGGATCAACCAAGCGCGCATGAGCGCGCCCG 160  
 QY 155 GCGCCTGCGCGCGCGAGGAGAGCTCCCTCACGAGGAGGAGCTCCCTCAACCGCGGC 212  
 DB 161 GCCCGCGCGCGCGCGCGGAGATGCGCGCCCGCGAGCTGCTGCTCGCGCGCGCGCG 218

RESULT 29  
 ABK99882  
 ID ABK99882 standard; cDNA; 2688 BP.  
 XX  
 AC ABK99882;  
 XX  
 DT 21-OCT-2002 (first entry)  
 XX  
 DE Human cDNA encoding a novel kinase protein #9.  
 XX  
 KW Human; ss; kinase; gene; noctropic; gene therapy; novel human protein;  
 KW NHF; serine-threonine kinase; casein kinase; mitogen activated kinase;

KW calcium/calmodulin-dependent protein kinase; chromosome 6;  
 KW mental disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200248333-A2.  
 XX  
 PD 20-JUN-2002.  
 XX  
 PF 12-DEC-2001; 2001WO-US49068.  
 XX  
 PR 12-DEC-2000; 2000US-255103P.  
 PR 08-MAY-2001; 2001US-289422P.  
 XX  
 PA (LEXI-) LEXICON GENETICS INC.  
 XX  
 PI Turner CA, Mathur B, Friddle CJ;  
 XX  
 DR WPI; 2002-583505/62.  
 DR P-PSDB; ABG69458.  
 XX  
 PT Novel polynucleotides encoding human proteins that are structurally  
 PT related to animal kinases, useful for drug screening, diagnosis and in  
 PT gene therapy of biological disorders -  
 XX  
 PS Disclosure; Page 57; 94pp; English.  
 CC The invention relates to an isolated nucleic acid molecule comprising a  
 CC nucleotide sequence encoding a novel human protein (NHP) appearing  
 CC as ABG69450-ABG69469, that share structural similarity with animal  
 CC kinases, including serine-threonine kinases, casein kinases,  
 CC calcium/calmodulin-dependent protein kinases, and mitogen activated  
 CC kinases. NHP oligonucleotides are useful as hybridization probes for  
 CC screening libraries and assessing gene expression patterns. NHP  
 CC sequences are useful to identify mutations associated with a particular  
 CC disease and also as a diagnostic or prognostic assay, and also in the  
 CC molecular mutagenesis/evolution of proteins that are at least partially  
 CC encoded by the NHP sequences. Sequences derived from regions adjacent  
 CC to the intron/exon boundaries of NHP gene can be used to design primers  
 CC for use in amplification assays to detect mutations within the exons,  
 CC splice sites, introns that can be used in diagnostics and  
 CC pharmacogenomics. NHP sequences are utilized in microarrays or other  
 CC assay formats, to screen collections of genetic material from patients  
 CC who have a particular medical condition. NHP nucleotide sequences are  
 CC useful for drug screening effective in the treatment of symptomatic or  
 CC phenotypic manifestations of perturbing the normal function of NHP in the  
 CC body, and nucleotide constructs encoding NHP products are used to  
 CC genetically engineer host cells to express NHP products in vivo. These  
 CC delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion  
 CC protein to the body. Nucleotide constructs encoding NHP products are also  
 CC useful in gene therapy for modulating NHP expression. The encoded NHP  
 CC polypeptides are useful for generating antibodies, as reagents in  
 CC diagnostic assays, for identifying other cellular gene products related  
 CC to NHP and as reagents in assays for screening for compounds that are  
 CC useful in the treatment of mental, biological or medical disorders and  
 CC diseases. The gene for the NHPs is located on human chromosome 6.  
 CC  
 XX The present sequence encodes an NHP of the invention.  
 SQ Sequence 2688 BP; 540 A; 849 C; 871 G; 426 T; 2 other;  
 Query Match 15.0%; Score 37.8; DB 24; Length 2688;  
 Best Local Similarity 50.6%; Pred. No. 15;  
 Matches 90; Conservative 0; Mismatches 88; Indels 0; Gaps 0;  
 QY 35 GTCCCTGCGCCCTCCACCTCCAGGCGCAGAGGCGCCACGAGAGCCCGAGTGCCTG 94  
 DB 59 GCGGCTGCGCGCGCGTCGCCCAAGAGATCGGGGCGGGCCGGGATGATCCGG 118  
 QY 95 ACGTTGCCACGATCTGGGATCAGAGCGAGGAGCCAGAGAGCCAGAACTGCGCGCCCG 154  
 DB 119 GTCGGAAGCGCGCGCGCGGAGGAGCGGATCAACCAAGCGCGCATGAGCGCGCCCG 178



CC	The present sequence encodes an NHP of the invention.
SQ	Sequence 2856: BP; 529 A; 980 C; 897 G; 448 T; 2 other;
Query Match	15.0%; Score 37.8; DB 24; Length 2856;
Best Local Similarity	50.6%; Pred. No. 15;
Matches	90; Conservative 0; Mismatches 88; Indels 0; Gaps 0
OY	35 GTCCCTGGGCGCCTTCACATCTGCCAGAGCCGCACAGAACCCCAGTCCCG 94
DB	41 GCCGCTCCGCCGCCCTCCGCAAGAAGATCGGGGCGGAGGTGAATCCGG 100
OY	95 ACCTTGCCACAGCTGTGGAGATCAAGAGCACAGGACCGAAGAACTGCGCCGCC 154
DB	101 GTCGAAGAGCGCGCGCGCGCGGAGAGGAGGTCAACCAGCGCATAGCGGCCCC 160
OY	155 GCCCTTCGCTTGCGCGGAGAGGAGACTTCCTCAACGAGGAGAGTCCCTCAACCCGAGC 212
DB	161 GCCCGCGCGCGCGCGCGGAGATGCGCGCGCGCGAGCTGCTGCTCGCGCGCGCGC 218
RESULT 32	
ID	ABX90553 standard; cDNA; 2856 BP.
XX	ABX90553
XX	ABX90553;
DT	02-MAY-2003 (first entry)
DE	Human kinase cDNA #18.
KW	Human; kinase; ser; kinase; phosphorylation; regulatory pathway;
OS	gene therapy.
PN	Homo sapiens.
UN	US2002161213-A1.
XX	31-OCT-2002.
PE	12-DEC-2001; 2001US-0020079.
PR	12-DEC-2000; 2000US-255103P.
FR	08-MAY-2001; 2001US-289422P.
XX	(TURN/) TURNER C A.
PA	(MATH/) MATHUR B.
PA	(FRID/) FRIDDLE C J.
PI	Turner CA, Mathur B, Friddle CJ;
DR	WPI; 2003-288125/28.
DR	P-PSDB; ABU60672.
PT	New novel human polynucleotides encoding proteins sharing sequence
PT	similarity with animal kinases, useful for diagnosing or treating
PT	disorders -
PS	Dialecture; Page 66-67; 78pp; English.
XX	
CC	The invention discloses isolated nucleic acids, and the protein that they
CC	encode, of novel human kinases. Kinases mediate the phosphorylation of a
CC	wide variety of proteins and compounds in the cell and are involved in a
CC	range of regulatory pathways. The novel human polynucleotides, encoding
CC	proteins sharing sequence similarity with animal kinases, are useful for
CC	diagnosing or treating (e.g. gene therapy) disorders. The sequence
CC	presented is a cDNA encoding a human kinase.
SO	Sequence 2856 BP; 529 A; 980 C; 897 G; 448 T; 2 other;
Query Match	15.0%; Score 37.8; DB 25; Length 2856;
Best Local Similarity	50.6%; Pred. No. 15;
Matches	90; Conservative 0; Mismatches 88; Indels 0; Gaps 0

QY	35	GTCCCTGAGCGCCTTCACACTCCCGCAGGCGCAGAAAGCGCCGACAGAGAACCCCACTGCGCCG	94
Db	41	GGCGCTCCGCGCCCGCTCCGCCCAAGAGAGATCGGGGCGGGGCGGGATGATCCGG	100
QY	95	ACGTTGCGCAGGCTGAGATCAAGGCACAGGACACAGGAGCGAGAACTGGCGCGCCG	154
Db	101	GTCGGAAGCGCGCGCGCGCGGAGAGAGCGGATCCCAACGCCGCACTGAGCGCCGCC	166
QY	155	GGCCCTGCGCCCTGGCGCGGAGGAAAGCTCCCTCACACAGAGAAAGTCCCTTCACCGCGG	212
Db	161	GCCCCGCGCGCGCGCGCGGAGATCGCGCCCGCCCAAGCTCTGCTCTCCGCGCGCGC	218
<p>RESULT 33</p> <p>ID ABR99890 standard, cDNA, 2874 BP.</p> <p>ABR99890;</p> <p>21-OCT-2002 (first entry)</p> <p>Human cDNA encoding a novel kinase protein #17.</p> <p>Human, ss; kinase, gene; noctropic; gene therapy, novel human protein; NHP, serine-threonine kinase; casein kinase; mitogen activated kinase; calcium/calmodulin-dependent protein kinase; chromosome 6; mental disorder.</p> <p>Homo sapiens.</p> <p>WO200248333-A2.</p> <p>20-JUN-2002.</p> <p>12-DEC-2001; 2001WO-US49068.</p> <p>12-DEC-2000; 2000US-255103P.</p> <p>08-MAY-2001; 2001US-289422P.</p> <p>(LEXI-) LEXICON GENETICS INC.</p> <p>Turner CA, Mathur B, Fiddle CJ;</p> <p>WPI; 2002-58305/62.</p> <p>P-PSDB; ABR99466.</p> <p>Novel polynucleotides encoding human proteins that are structurally related to animal kinases, useful for drug screening, diagnosis and in gene therapy of biological disorders</p> <p>Disclosure; Page 82; 94pp; English.</p>			
CC	PS	The invention relates to an isolated nucleic acid molecule comprising a nucleotide sequence encoding a novel human protein (NHP) spearing as ABG69450-ABG69469, that share structural similarity with animal kinases, including serine-threonine kinases, casein kinase, calcium/calmodulin-dependent protein kinases, and nitrogen activated kinases. NHP oligonucleotides are useful as hybridization probes for screening libraries and assessing gene expression patterns. NHP sequences are useful to identify mutations associated with a particular disease and also as a diagnostic or prognostic assay, and also in the molecular mutagenesis/evolution of proteins that are at least partially encoded by the NHP boundaries. Sequences derived from regions adjacent to the intron/exon boundaries of NHP gene can be used to design primers for use in amplification assays to detect mutations within the exons, splice sites, introns that can be used in diagnostics and pharmaco-genomics. NHP sequences are utilized in microarrays or other assay formats, to screen collections of genetic material from patients who have a particular medical condition. NHP nucleotide sequences are useful for drug screening effective in the treatment of symptomatic or phenotypic manifestations of perturbing the normal function of NHP in the body, and nucleotide constructs encoding NHP products are used to	



PA (MATH/) MATHUR B.  
 XX (FRID/) FRIDDLE C J.  
 XX PI Turner CA, Mathur B, Friddle CJ;  
 XX DR WPI: 2003-288125/28.  
 XX DR P-PSDB; AB060668.  
 PT New novel human polynucleotides encoding proteins sharing sequence  
 PT similarity with animal kinases, useful for diagnosing or treating  
 PT disorders -  
 XX Disclosure; Page 51-52; 78pp; English.  
 XX The invention discloses isolated nucleic acids, and the protein that they  
 CC encode, of novel human kinases. Kinases mediate the phosphorylation of a  
 CC wide variety of proteins and compounds in the cell and are involved in a  
 CC range of regulatory pathways. The novel human polynucleotides, encoding  
 CC proteins sharing sequence similarity with animal kinases, are useful for  
 CC diagnosing or treating (e.g. gene therapy) disorders. The sequence  
 CC presented is a cDNA encoding a human kinase.  
 XX  
 SQ Sequence 2931 BP; 569 A; 961 C; 915 G; 484 T; 2 other;  
 Query Match 15.0%; Score 37.8; DB 25; Length 2931;  
 Best Local Similarity 50.6%; Pred. No. 15;  
 Matches 90; Conservative 0; Mismatches 88; Indels 0; Gaps 0;  
 OY 35 GTCCCTGGCGCTCCACCTCCCGAGAGCGCGCCACGAGAACCCCGAGTCCCG 94  
 DB 41 GCCCGTGGCGCGCTCCCGAGAGCGCGCCACGAGAACCCCGAGTCCCG 100  
 OY 95 ACGTTGCCAGCGTCTGGATGATGAGAGCGAGAGCGAGAGCGAGAGTCCCGCGCCG 154  
 DB 101 GTCCGAGAGCGCGCGCGCGCGAGAGCGCGGTACCCACGCGCGCACTGAGCGCGCCG 160  
 OY 155 GCCCCTGGCGCGCGCGAGAGTCCCTCACGAGAGAACTCCCTACCGCGCG 212  
 DB 161 GCCCGCGCGCGCGCGCGAGATGCGCGCCCGAGCTGCTGCTCCGCGCGCGCG 218

RESULT 36  
 ABK99886  
 ID ABK99886 standard; cDNA; 2949 BP.  
 XX  
 XX ABR99886;  
 XX  
 DT 21-OCT-2002 (first entry)  
 XX  
 DE Human cDNA encoding a novel kinase protein #13.  
 XX  
 KW Human; ss; kinase; gene; nootropic; gene therapy; novel human protein;  
 KW NHP; serine-threonine kinase; casein kinase; mitogen activated kinase;  
 KW calcium/calmodulin-dependent protein kinase; chromosome 6;  
 KW mental disorder.  
 XX  
 OS Homo sapiens.  
 OS  
 FN WO200248333-A2.  
 XX  
 PD 20-JUN-2002.  
 XX  
 PF 12-DEC-2001; 2001WO-US49068.  
 XX  
 PR 12-DEC-2000; 2000US-255103P.  
 PR 08-MAY-2001; 2001US-289422P.  
 XX  
 PA (LEXI-) LEXICON GENETICS INC.  
 XX  
 PI Turner CA, Mathur B, Friddle CJ;  
 XX  
 DR WPI: 2002-583505/62.  
 DR P-PSDB; ABG69462.

XX  
 PT Novel polynucleotides encoding human proteins that are structurally  
 PT related to animal kinases, useful for drug screening, diagnosis and in  
 PT gene therapy of biological disorders -  
 XX Disclosure; Page 69; 94pp; English.  
 XX The invention relates to an isolated nucleic acid molecule comprising a  
 CC nucleotide sequence encoding a novel human protein (NHP) appearing  
 CC as ABG69450-ABG69469, that share structural similarity with animal  
 CC kinases, including serine-threonine kinases, casein kinases,  
 CC calcium/calmodulin-dependent protein kinases and mitogen activated  
 CC kinases. NHP oligonucleotides are useful as hybridisation probes for  
 CC screening libraries and assessing gene expression patterns. NHP  
 CC sequences are useful to identify mutations associated with a particular  
 CC disease and also as a diagnostic or prognostic assay, and also in the  
 CC molecular mutagenesis/evolution of proteins that are at least partially  
 CC encoded by the NHP sequences. Sequences derived from regions adjacent  
 CC to the intron/exon boundaries of NHP gene can be used to design primers  
 CC for use in amplification assays to detect mutations within the exons,  
 CC splice sites, introns that can be used in diagnostics and  
 CC pharmacogenomics. NHP sequences are utilised in microarrays or other  
 CC assay formats, to screen collections of genetic material from patients  
 CC who have a particular medical condition. NHP nucleotide sequences are  
 CC useful for drug screening effective in the treatment of symptomatic or  
 CC phenotypic manifestations of perturbing the normal function of NHP in the  
 CC body, and nucleotide constructs encoding NHP products are used to  
 CC genetically engineer host cells to express NHP products in vivo. These  
 CC delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion  
 CC protein to the body. Nucleotide constructs encoding NHP products are also  
 CC useful in gene therapy for modulating NHP expression. The encoded NHP  
 CC polypeptide are useful for generating antibodies, as reagents in  
 CC diagnostic assays, for identifying other cellular gene products related  
 CC to NHP and as reagents in assays for screening for compounds that are  
 CC useful in the treatment of mental, biological or medical disorders and  
 CC diseases. The gene for the NHPs is located on human chromosome 6.  
 CC  
 XX The present sequence encodes an NHP of the invention.  
 XX  
 SQ Sequence 2949 BP; 571 A; 964 C; 923 G; 489 T; 2 other;  
 Query Match 15.0%; Score 37.8; DB 24; Length 2949;  
 Best Local Similarity 50.6%; Pred. No. 15;  
 Matches 90; Conservative 0; Mismatches 88; Indels 0; Gaps 0;  
 OY 35 GTCCCTGGCGCTCCACCTCCCGAGAGCGCGCCACGAGAACCCCGAGTCCCG 94  
 DB 59 GCCCGTGGCGCGCGCGCTCCCGAGAGAGTGGCGCGCGCGCGAGATGTCGG 118  
 OY 95 ACGTTGCCAGCGTCTGGATGATGAGAGCGAGAGCGAGAGCGAGAGTCCCGCGCCG 154  
 DB 119 GTCCGAGAGCGCGCGCGCGAGAGCGAGCGGTACCCACGCGCGCACTGAGCGCGCCG 178  
 OY 155 GCCCCTGGCGCGCGCGAGAGTCCCTCACGAGAGAACTCCCTACCGCGCG 212  
 DB 179 GCCCGCGCGCGCGCGCGAGATGCGCGCCCGAGCTGCTGCTCCGCGCGCGCG 236

RESULT 37  
 ABK90548  
 ID ABK90548 standard; cDNA; 2949 BP.  
 XX  
 XX ABX90548;  
 XX  
 DT 02-MAY-2003 (first entry)  
 XX  
 DE Human kinase cDNA #13.  
 XX  
 KW Human; gene; ss; kinase; phosphorylation; regulatory pathway;  
 KW gene therapy.  
 XX  
 OS Homo sapiens.  
 OS  
 FN  
 XX  
 PD  
 XX  
 PF  
 XX  
 PR  
 XX  
 PA  
 XX  
 PI  
 XX  
 DR  
 XX



PN US2002161213-A1.  
 XX  
 PD 31-OCT-2002.  
 XX  
 PF 12-DEC-2001; 2001US-0020079.  
 XX  
 PR 12-DEC-2000; 2000US-255103P.  
 XX 08-MAY-2001; 2001US-289422P.  
 XX  
 PA (TURN/) TURNER C A.  
 PA (MATH/) MATHUR B.  
 PA (FRID/) FRIDDLE C J.  
 XX  
 PI Turner CA, Mathur B, Friddle CJ;  
 XX  
 DR WPI; 2003-288125/28.  
 DR P-PSDB; ABU60667.  
 XX  
 PT New novel human polynucleotides encoding proteins sharing sequence  
 PT similarity with animal kinases, useful for diagnosing or treating  
 PT disorders -  
 XX  
 PS Disclosure; Page 47-48; 78pp; English.  
 CC The invention discloses isolated nucleic acids, and the protein that they  
 CC encode, of novel human kinases. Kinases mediate the phosphorylation of a  
 CC wide variety of proteins and compounds in the cell and are involved in a  
 CC range of regulatory pathways. The novel human polynucleotides, encoding  
 CC proteins sharing sequence similarity with animal kinases, are useful for  
 CC diagnosing or treating (e.g. gene therapy) disorders. The sequence  
 CC presented is a cDNA encoding a human kinase.  
 XX  
 SQ Sequence 2949 BP; 571 A; 964 C; 923 G; 489 T; 2 other;  
 Query Match 15.0%; Score 37.8; DB 25; Length 2949;  
 Best Local Similarity 50.6%; Pred. No. 15;  
 Matches 90; Conservative 0; Mismatches 88; Indels 0; Gaps 0;  
 OY 35 GTCCCTGCGCCTCCACCTCCCGAGGCGCAGAGGCGCCCGCAGAGACCCCGAGTCCCG 94  
 DB 59 GCCGCTGCG 118  
 OY 95 ACGTTGCCAGCGATCGGATCAGAGGCGAGGAGCCAGGAGCCAGAACTGCGCGCGCCCG 154  
 DB 119 GTCCGAGGCG 178  
 OY 155 GCCCCTGCG 212  
 DB 179 GCCCG 236  
 RESULT 38  
 AAT94191/C  
 ID AAT94191 standard; DNA; 5418 BP.  
 XX  
 AC AAT94191;  
 XX  
 DT 22-MAY-1998 (first entry)  
 XX  
 DE Promoter region of pig complement inhibitor DNA.  
 XX  
 KM Promoter region; pig complement inhibitor DNA; thrombomodulin;  
 KM transgenic pig; hyperacute rejection; organ transplant;  
 KM tissue transplant; ds.  
 XX  
 OS Sus scrofa.  
 XX  
 FH Key Location/Qualifiers  
 FT 3797..5418  
 FT /tag= a  
 FT /note= "preferred 1.7 kb fragment of claim 3"  
 XX  
 PN WO9744449-A1.

XX 27-NOV-1997.  
 XX  
 XX 19-MAY-1997; 97MO-JP01677.  
 XX  
 XX 17-MAY-1996; 96JP-0148335.  
 XX  
 PA (NIME-) NIPPON MEAT PACKERS INC.  
 XX  
 PI Fujimura T, Murakami H, Shigenisa T, Toyomura K;  
 XX  
 DR WPI; 1998-018504/02.  
 XX  
 PT Pig complement inhibitor promoter sequence - allows human complement  
 PT inhibitor to be expressed efficiently in transgenic pigs  
 XX  
 PS Claim 1; Pages 13-16; 27pp; Japanese.  
 CC The present sequence is the promoter region of pig complement  
 CC inhibitor DNA. It allows human complement inhibitors or other  
 CC thrombus formation inhibiting factors (e.g. thrombomodulin) to be  
 CC expressed efficiently in transgenic pigs, when inserted upstream of  
 CC a human DNA sequence. This prevents hyperacute rejection when  
 CC organs or tissue from the transgenic pigs are transplanted into  
 CC humans.  
 XX  
 SQ Sequence 5418 BP; 1578 A; 1261 C; 1109 G; 1409 T; 61 other;  
 Query Match 15.0%; Score 37.8; DB 19; Length 5418;  
 Best Local Similarity 53.8%; Pred. No. 15;  
 Matches 78; Conservative 0; Mismatches 67; Indels 0; Gaps 0;  
 OY 38 CCTGCGCCTCCACCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 97  
 DB 5298 CGTGCGCTGGGCG 5239  
 OY 98 TTGCCACGGTCTGGATCAGAGGCGAGGAGCCAGGAGCCAGAACTGCGCGCGCGCGCG 157  
 DB 5238 GAGCCAAATGGGCGGCG 5179  
 OY 158 CCTGCGCCTGGCG 182  
 DB 5178 GAGAGAGGAGCGCCCTTGTCTCTCC 5154  
 RESULT 39  
 AAV73802  
 ID AAV73802 standard; DNA; 35100 BP.  
 XX  
 AC AAV73802;  
 XX  
 DT 25-FEB-1999 (first entry)  
 XX  
 DE KSHV LTR DNA (nucleotides 1-35,100).  
 XX  
 KM Kaposi's sarcoma; acquired immune deficiency syndrome; AIDS; DHFR; Bcl-2;  
 KM dihydrofolate reductase; LTR; long unique region; vaccine; Prophylaxis;  
 KM diagnosis; treatment; HHV8; complement binding protein; V-CB; SSBP;  
 KM ssDNA binding protein; transport protein; glycoprotein B; pol; vIL-6;  
 KM DNA polymerase; viral interleukin-6; BHV4-IE1 I; thymidylate synthase;  
 KM vMIP-1I; BHV4-IE1 II; vMIP-I; capsid protein I; tegument protein I; ds.  
 XX  
 OS Kaposi's sarcoma-associated herpesvirus.  
 XX  
 PN US5849564-A.  
 XX  
 PD 15-DEC-1998.  
 XX  
 DT 29-NOV-1996; 96US-0770379.  
 XX  
 DE 29-NOV-1996; 96US-0770379.  
 XX  
 PA (UYCO ) UNIV COLUMBIA NEW YORK.









```
RESULT 2
US-09-471-867-1
; Sequence 1, Application US/09471867
; Patent No. 6455289
; GENERAL INFORMATION:
; APPLICANT: Uchimura, Kenji
; APPLICANT: Muramatsu, Hideki
; APPLICANT: Kadomatsu, Kenji
; APPLICANT: Kanagaki, Reiji
; APPLICANT: Habuchi, Osamu
; APPLICANT: Muramatsu, Takashi
; TITLE OF INVENTION: POLYPEPTIDE OF N-ACETYLGLUCOSAMINE-6-0-SULFOTRANSFERASE AND
; FILE REFERENCE: TOYAMA1.001AUS
; CURRENT FILING DATE: 1999-12-23
; EARLIER APPLICATION NUMBER: US 09/263,023
; EARLIER FILING DATE: 1999-03-05
; EARLIER APPLICATION NUMBER: JP 10-54007
; EARLIER FILING DATE: 1998-03-05
; EARLIER APPLICATION NUMBER: JP 10-177844
; EARLIER FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2150
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (470) .. (1918)
US-09-471-867-1
Query Match 16.7%; Score 42.2; DB 4; Length 2150;
Best Local Similarity 50.0%; Pred. No. 0.17;
Matches 104; Conservative 0; Mismatches 104; Indels 0; Gaps 0;
QY 28 CCTGATGTCCTCGGCGGCTCCACCTCCCGGAGGAGGCGCCAGAGAGACCCCA 87
DB 143 CCAGGTCCTTCTCGAGCGCGCTGCATGGAGAGCCAGCCCTCGGGCGCGGAGACCA 202
QY 88 GTGCCCGAGCTTGCACGCGTGGATCAGAGCAGGAGCAGGAGCCAGGAAGTGGC 147
DB 203 GCTCTGCGCGCGCGCGCGCGCTCGATCGGCGGCCCGCCAGTCCCGCGCGCGAGCC 262
QY 148 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 207
DB 263 TCGAGGTCCTCTCTGAGGCTGCAGAGCGCGCGCTCTCGCGCGCGCGCGCGCTGTG 322
QY 208 CCGCGCGCGCGCTCGAGGCGGCGCGGTG 235
DB 323 CCTGTGATGAGCGCGAGCTCGCGCGAG 350
RESULT 3
US-09-376-728-1/c
; Sequence 1, Application US/09376728
; Patent No. 6372961
; GENERAL INFORMATION:
; APPLICANT: Tarczyński, Mitchell C.
; APPLICANT: Shen, Bo
; TITLE OF INVENTION: Hemoglobin Genes and Their Use
; FILE REFERENCE: 0873
; CURRENT APPLICATION NUMBER: US/09/376,728
; CURRENT FILING DATE: 1999-08-17
; EARLIER APPLICATION NUMBER: US 60/097,242
; EARLIER FILING DATE: 1998-08-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 840
```

```
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: CDS
LOCATION: (51) ... (623)
US-09-376-728-1
Query Match 15.3%; Score 38.6; DB 4; Length 840;
Best Local Similarity 52.5%; Pred. No. 1.1;
Matches 83; Conservative 0; Mismatches 75; Indels 0; Gaps 0;
QY 51 CCTCCCGAGCGAGAGGCGCCAGAGAGCCCGAGTCCCGAGCTTGCACGAGTCTG 110
DB 465 CTTCTCCCAAGCGCGCTTCATCTCCGGCGTCCACATGTCGGGACCGGATCCTGATG 406
QY 111 GATTCAGAGCAGGAGCAGGAGCCAGAGAACTGGCGCGCGCGCGCGCGCTGGCGGC 170
DB 405 TGTCCAGCAGCGCGCTTGTAGACACTCGAATGCGCGTGGGAGCGCCGCTTGGCT 346
QY 171 GAGGAACTTCCTCAGCAGAGAGAGAGTCTCCCTAC 208
DB 345 GCGTCGCGCCAGCGCGCTTCAGGATGAGCTTCTCTAC 308
RESULT 4
US-09-679-279-25/c
; Sequence 25, Application US/09679279
; Patent No. 6524841
; GENERAL INFORMATION:
; APPLICANT: McDaniel, Robert
; APPLICANT: Volchegursky, Yanina
; TITLE OF INVENTION: Recombinant Megalomicin Biosynthetic
; FILE REFERENCE: 300622004700
; CURRENT APPLICATION NUMBER: US/09/679,279
; CURRENT FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/158,305
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: US 60/190,024
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 528
; TYPE: DNA
; ORGANISM: Micromonospora megalomicea
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1) ... (528)
; OTHER INFORMATION: Sequence with codon changes as described in the
; Patent No. 6524841
; OTHER INFORMATION: specification at page 99, line 22 thru page 101, line 23
US-09-679-279-25
Query Match 15.2%; Score 38.2; DB 4; Length 528;
Best Local Similarity 48.2%; Pred. No. 1.3;
Matches 106; Conservative 0; Mismatches 114; Indels 0; Gaps 0;
QY 14 GCGCGGAGTGAAGCTGATGCTGCTGCGCGCTCCACCTCCCGAGCGCGAGAGCGCC 73
DB 300 GGCCTTGACCTCTCCAGACGACCGGCGCGAGCGCGCGCGCGAGCGCTTACGTGCC 241
QY 74 CACGAGAGCCCGAGCGCGCGAGCTTGCACGCTGTGGATCAGAGGCGAGGACAGGGA 133
DB 240 CAGAGAGGCGCGCAGCTTCAGCGGATCCCGAGGCGGCGGCGGCGGTGGCGCTCGAC 181
QY 134 GCGAGAACTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 193
DB 180 GACTCGAGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 121
QY 194 GAGCTTCCTCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 233
DB 120 CTGGCGAGCGCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 81
```

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RESULT 5
US-09-039-609-1
; Sequence 1, Application US/09039609
; Patent No. 6107473
; GENERAL INFORMATION:
; APPLICANT: ALBONE, EARL
; APPLICANT: KIKLY, KRISTINE
; TITLE OF INVENTION: A KRINGLE-RELATED CLONE,
; TITLE OF INVENTION: HTHE247
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestlia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/039,609
; FILING DATE: 16-MAR-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/060,623
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestlia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GP-70275
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1875 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-039-609-1

Query Match      15.1%; Score 38; DB 3; Length 1875;
Best Local Similarity 49.2%; Pred. No. 1.5;
Matches 98; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

QY      52 CTCGCCAGGCGCAAGAGCGGCCCAAGAGAACCCCGCAGTGGCGTGTGG 111
DB      1 CTCGCCCTGTCTCCCATGCGCGCCCGCTCCCGCGCTGCCCCCTTTACCCCGGCGCG 60

QY      112 GATCAGAGGAGGAGGAGCCAGGAGAACTGGCGCGCCCGCCCGCCCTGCTGGCGCG 171
DB      61 GCCCGCGGCGCCGCACTGACGCGCCCATGCGCGCGCCAGCGCCCGCTGCGCTGCT 120

QY      172 AGGGAACCTCCCTACCCGAGGAGGAGAGCTCCCTACCCGCGCGCCCTCGAGGGGGGCG 231
DB      121 CCGCGCGGCGGCTCAGCTGAGCGCGCCCGCGCGCTTACCCCGCGCTGCGCGCGGAC 180

QY      232 CGTGGGGTCAAGACCGGAAA 250
DB      181 CCGAGTGTTCACAGCCAA 199

RESULT 6
US-09-180-939-2/C
; Sequence 2, Application US/09180939A
; Patent No. 6255474
```

```
; GENERAL INFORMATION:
; APPLICANT: TOTOMURA, KOJI
; APPLICANT: FUJIMURA, Tatsuya
; APPLICANT: MORAKAMI, Hiroshi
; APPLICANT: SHIGEMISA, Tamotsu
; TITLE OF INVENTION: A Promoter Gene for a Porcine Complement Inhibitor
; FILE REFERENCE: 2520-0116P
; CURRENT APPLICATION NUMBER: US/09/180,939A
; EARLIER FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: PCT/JP97/01677
; EARLIER FILING DATE: 1997-05-19
; EARLIER APPLICATION NUMBER: 148335/1996 JAPAN
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1622
; TYPE: DNA
; ORGANISM: Porcine sp.
; US-09-180-939-2

Query Match      15.0%; Score 37.8; DB 3; Length 1622;
Best Local Similarity 53.8%; Pred. No. 1.6;
Matches 78; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY      38 CTGGCGCTTCACTCCCGAGCGCGCAGAGCGCCACAGAGACCCCGAGTGGCGGAGC 97
DB      1502 CGTGGCTGGGCCCCCGCTGGGCGGAGTGTCTTAAGGAGTGACTCCAGGCGCGGCG 1443

QY      98 TTGCCACGGTCTGGAGATCAGAGGAGGAGCCAGGAGCCAGGAACTGCGCGCCCGCGCC 157
DB      1442 GAGCCATATGGCGGCGCGGCGGAGCGGCGCTGAGGCGCGGCGCGGCGCGGCGCTCGCGCC 1383

QY      158 CCTGCCCTGGCGCGCAGGAGGAGCTCC 182
DB      1382 GAGAGAGGAGCGCCCTTGTCTCC 1358

RESULT 7
US-10-020-079-11
; Sequence 11, Application US/10020079
; Patent No. 6579710
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Friedle, Carl Johan
; TITLE OF INVENTION: No. 6579710e1 Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0281-USA
; CURRENT APPLICATION NUMBER: US/10/020,079
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255,103
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/289,422
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 1947
; TYPE: DNA
; ORGANISM: homo sapiens
; US-10-020-079-11

Query Match      15.0%; Score 37.8; DB 4; Length 1947;
Best Local Similarity 50.6%; Pred. No. 1.6;
Matches 90; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY      35 GTGCCCTGGGCGCTTCACTCCCGAGGAGCGCGCCAGAGAGACCCCGAGTGGCGCG 94
DB      41 GCCGCTGCGCGCGCCCTGCTCCCAAGAGAGATCGGGGCGCGCGCGCGAGTATCCGG 100

QY      95 ACCTTGCCACGGTCTGGAGATCAGAGGAGGAGACGAGAGCCAGAACTGGCGCGCGCGCC 154
DB      101 GTCCGAGAGCGCGCGCGCGCGGAGGAGGCGGATCACCCAGCCCGCACTGAGCGCGCGCC 160
```

QY 155 GCCCCTGCGCTGCGGCGGAGGAGTCCCTCCACGAGGAGGAGTCCCTCCACCCCGG 212  
DB 161 GCCCGCGCGCGCGCGCGGCGGAGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 218

## RESULT 8

US-10-020-079-9  
; Sequence 9, Application US/10020079  
; Patent No. 6579710  
; GENERAL INFORMATION:  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Mathur, Brian  
; APPLICANT: Friddle, Carl Johan  
; TITLE OF INVENTION: No. 6579710e1 Human Kinases and Polynucleotides Encoding the Same  
; FILE REFERENCE: LEX-0281-USA  
; CURRENT APPLICATION NUMBER: US/10/020,079  
; PRIOR FILING DATE: 2001-12-12  
; PRIOR APPLICATION NUMBER: US 60/255,103  
; PRIOR FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: US 60/289,422  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 1965  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-10-020-079-9

Query Match 15.0%; Score 37.8; DB 4; Length 1965;  
Best Local Similarity 50.6%; Pred. No. 1.6;  
Matches 90; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 35 GTCCTGCGCTGCGCTGCGGCGGAGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCG 94  
DB 59 GCCGCTGCG 118  
QY 95 ACGTTGCCACGGTCTGAGATCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 154  
DB 119 GTCGGAAGCG 178  
QY 155 GCCCCTGCGCTGCGGCGGAGGAGGAGTCCCTCCACGAGGAGGAGGAGGAGGAGGAGGAG 212  
DB 179 GCCCG 236

## RESULT 9

US-10-020-079-3  
; Sequence 3, Application US/10020079  
; Patent No. 6579710  
; GENERAL INFORMATION:  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Mathur, Brian  
; APPLICANT: Friddle, Carl Johan  
; TITLE OF INVENTION: No. 6579710e1 Human Kinases and Polynucleotides Encoding the Same  
; FILE REFERENCE: LEX-0281-USA  
; CURRENT APPLICATION NUMBER: US/10/020,079  
; PRIOR FILING DATE: 2001-12-12  
; PRIOR APPLICATION NUMBER: US 60/255,103  
; PRIOR FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: US 60/289,422  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 2595  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-10-020-079-3

Query Match 15.0%; Score 37.8; DB 4; Length 2595;  
Best Local Similarity 50.6%; Pred. No. 1.7;

Matches 90; Conservative 0; Mismatches 88; Indels 0; Gaps 0;  
QY 35 GTCCTGCGCTGCGCTGCGGCGGAGGAGTCCCTCCACGAGGAGGAGGAGGAGGAGGAGGAGGAG 94  
DB 41 GCCGCTGCG 100  
QY 95 ACGTTGCCACGGTCTGAGATCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 154  
DB 101 GTCGGAAGCG 160  
QY 155 GCCCCTGCGCTGCGGCGGAGGAGGAGTCCCTCCACGAGGAGGAGGAGGAGGAGGAGGAGGAG 212  
DB 161 GCCCG 218

## RESULT 10

US-10-020-079-1  
; Sequence 1, Application US/10020079  
; Patent No. 6579710  
; GENERAL INFORMATION:  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Mathur, Brian  
; APPLICANT: Friddle, Carl Johan  
; TITLE OF INVENTION: No. 6579710e1 Human Kinases and Polynucleotides Encoding the Same  
; FILE REFERENCE: LEX-0281-USA  
; CURRENT APPLICATION NUMBER: US/10/020,079  
; PRIOR FILING DATE: 2001-12-12  
; PRIOR APPLICATION NUMBER: US 60/255,103  
; PRIOR FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: US 60/289,422  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 2613  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-10-020-079-1

Query Match 15.0%; Score 37.8; DB 4; Length 2613;  
Best Local Similarity 50.6%; Pred. No. 1.7;  
Matches 90; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 35 GTCCTGCGCTGCGCTGCGGCGGAGGAGGAGTCCCTCCACGAGGAGGAGGAGGAGGAGGAGGAGGAG 94  
DB 59 GCCGCTGCG 118  
QY 95 ACGTTGCCACGGTCTGAGATCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 154  
DB 119 GTCGGAAGCG 178  
QY 155 GCCCCTGCGCTGCGGCGGAGGAGGAGTCCCTCCACGAGGAGGAGGAGGAGGAGGAGGAGGAG 212  
DB 179 GCCCG 236

## RESULT 11

US-10-020-079-19  
; Sequence 19, Application US/10020079  
; Patent No. 6579710  
; GENERAL INFORMATION:  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Mathur, Brian  
; APPLICANT: Friddle, Carl Johan  
; TITLE OF INVENTION: No. 6579710e1 Human Kinases and Polynucleotides Encoding the Same  
; FILE REFERENCE: LEX-0281-USA  
; CURRENT APPLICATION NUMBER: US/10/020,079  
; PRIOR FILING DATE: 2001-12-12  
; PRIOR APPLICATION NUMBER: US 60/255,103  
; PRIOR FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: US 60/289,422  
; NUMBER OF SEQ ID NOS: 40

```

: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 19
: LENGTH: 2670
: TYPE: DNA
: ORGANISM: homo sapiens
US-10-020-079-19

```

Query Match	15.0%;	Score 37.8;	DB 4;	Length 2670;
Best Local Similarity	50.6%;	Pred. No.1.7;		
Matches 90;	Conservative 0;	Mismatches 88;	Indels 0;	Gaps 0;

QY 35 GTGCTCTGAGGCGCTTCCACCTCTCCCAAGGCCAAGAAGGCGCCACAGAGAACCCCTCAGTCCCG 94

Db 41 GCCGCTGCGCGCCGCTCGCCCAAGAGAAATCGGGGCGGGGCGGGGCGGAGATGATCCGG 100

QY 95 ACCTGTGCACGCTCTGGATTCAGAGGCAAGGAGCCAGGAGCCAGAATCTGCGCGGCCCC 154

Db 101 GTGCGAAGGCGCGCGCGCGCGGAGGAGGCGGTTACCCCAACCGCGCATGTAGCGCGCCCC 160

QY 155 GCCCTGCGCCTGCGCGGAGGAAAGTCTCTACACNAGAGGAAGTCTCCCTCAACCGGC 212

Db 161 GCCCGCGCGCGCGCGGGGAGATGCGCGCGCCCGACAGCTGTGCTTCGCGCGCGCGCCG 218

```

RESULT 12
US-10-020-079-17
: Sequence 17, Application US/10020079
: Patent No. 6579710
: GENERAL INFORMATION:
: APPLICANT: Turner, C. Alexander Jr.
: APPLICANT: Mathur, Brian
: APPLICANT: Friddie, Carl Johan
: TITLE OF INVENTION: No. 6579710el Human Kinases and Polynucleotides Encoding the Same
: PTE REFERENCE: tex-0281-USA

```

```

1 CURRENT APPLICATION NUMBER: US/10/020,079
2 CURRENT FILING DATE: 2001-12-12
3 PRIOR APPLICATION NUMBER: US 60/255,103
4 PRIOR FILING DATE: 2000-12-12
5 PRIOR APPLICATION NUMBER: US 60/289,422
6 PRIOR FILING DATE: 2001-05-08
7 NUMBER OF SEQ ID NOS: 40
8 SOFTWARE: fastseq for windows version 4.0
9 SEQ ID NO 17
10 LENGTH: 2688
11 TYPE: DNA
12 ORGANISM: homo sapiens
13 US-10-020-079-17

```

Query Match	15.0%	Score 37.8	DB 4	Length 2688
Best Local Similarity	50.6%	Pred. No. 1.7		
Matches	90	Mismatches	88	Indels 0
				Gaps 0
QY	35	GTCTCTGGGGCTTCACTCTCCACGCGCAGAGGCGCCACGAGACCCCCAGTCCCG	94	
Db	59	GCCGCTGCCCGCCCTCGCCCGCAGAGATCGGGCGGGCGGGCGGAGATGATCCGG	118	
QY	95	ACGTTGCCACGGTCTGGGATTCAGAGCGAGGACCGAGAGTCAGAACTGCGCCGCCCC	154	
Db	119	GTGGAAGGCGCGCGCGCGCGGAGGAGCGGGATCCCAAGCGCCGACGTAGCGCGCCCC	178	
QY	155	GCCCTCTGCTTGGCGGAGGAGAGCTCCTTCAACGAGGAGAGTCCCTCTACCCGCGC	212	
Db	179	GCCCCCGCCCGCGCGGGGAGTGGCGCGCCCGACAGCTGTGCTTCTCGCGCGCGCGC	236	

RESULT 13  
US-10-020-079-35  
; Sequence 35, Application US/10020079  
; Patent No. 6579710  
; GENERAL INFORMATION:  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Mathur, Brian  
; APPLICANT: Fiddle, Carl Johan

```

: TITLE OF INVENTION: No. 6579710e1 Human Kinases and Polynucleotides Encoding the Same
: FILE REFERENCE: LEX-0281-USA
: CURRENT APPLICATION NUMBER: US/10/020,079
: CURRENT FILING DATE: 2001-12-12
: PRIOR APPLICATION NUMBER: US 60/255,103
: PRIOR FILING DATE: 2000-12-12
: PRIOR APPLICATION NUMBER: US 60/289,422
: PRIOR FILING DATE: 2001-05-06
: NUMBER OF SEQ. ID NOS: 40
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ. ID NO. 35
: LENGTH: 2856
: TYPE: DNA
: ORGANISM: homo sapiens
: US-10-020-079--35

```

Query Match	15.0%	Score 37.8	DB 4	Length 2856
Best Local Similarity	50.6%	Pred. No. 17	88	Indels 0
Matches	90	Conservative	0	Mismatches
				Gaps
QY	35	GTCCCTGGGGCCCTTCACCTCCCCAGAGCGCCGACAGAGAGCCCCCATGTGCGG	94	
Db	41	GCCCGCTCCCGCCCGCCCTCCGCCAAGAGATGGGGCGCGGCGCGCGGAGATATCCGG	100	
QY	95	ACGTTGCCACGCGTCTGGATTCAGAGACAGAGACACAGAGAACTGGCGCGCGCC	154	
Db	101	GTGGGAAGCGCGCGCGCGCGGAGAGCGGATCACCAAGCCGACATGAGCGCGCC	160	
QY	155	GCCCCCTGCTCTGGCGCGGAGGGAAGCTCCCTCAACGAGAGGAAGTTCCTCACCGCGG	212	
Db	161	GCCCCCGCGCGCGCGGAGATGGCGCGCGCCCGGACGTCTGTCTTCGCGCGCGCGCG	218	

```

RESULT 14
US-10-020-079-33
; Sequence 33, Application US/10020079
; Patent No. 6579710
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Fiddie, Carl Johan
; TITLE OF INVENTION: No. 6579710el Human Kinases and Polynucleotides Encoding the Same

```

```

CURRENT APPLICATION NUMBER: US/10/020, 079
CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 60/255,103
PRIOR FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: US 60/289,422
PRIOR FILING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 33
LENGTH: 2874
TYPE: DNA
ORGANISM: homo sapiens
US-10-020-079-33

```

Query Match	Similarity	Score	DB	Length
Best Local	50.8%	Pred. No. 1.7	88	Indels 0
Matches	90	Mismatches	0	Gaps 0
QY	35	GTCTCTGGGGCTTCACCTCTCCCAAGCCGAGAGCCGCCACAGAGATCCCAATGCTCCG	94	
DB	59	GCCGCTGCGCGCCGCTCCGCCAAGAGATGCGGCGCGCGCGCGGAGATATCCGG	118	
QY	95	ACGTTGCACAGCTTGGGATTCAGAGGCAAGGACCGSAGGTCAGAACTGGCGCCGCC	154	
DB	119	GTGGAAGGCGCGCCGCGCGAGGAGACCGGATCACCCACGCGCGCACTAGCGCGCCCC	178	
QY	155	GCCCTTGCCTTGGCGCGAGGAGAGCTCTCCCTACCGAGGAGAGCTCTCTCATCCCGCG	212	
DB	179	GCCCGCGCGCGCGCGCGGAGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	236	











Db 1957 GCGCCGCTCTCCCGGGGGGGCG 1981

## RESULT 25

US-09-259-821A-1  
Sequence 1, Application US/09259821A  
Patent No. 6210926  
GENERAL INFORMATION:  
APPLICANT: LEOPARDI, ROSARIO  
TITLE OF INVENTION: HERPES SIMPLEX VIRUS ICP4 IS AN INHIBITOR OF APOPTOSIS  
FILE REFERENCE: AKD317  
CURRENT FILING DATE: US/09/259, 821A  
PRIOR APPLICATION NUMBER: 1999-03-01  
PRIOR FILING DATE: 1996-07-26  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 1  
LENGTH: 4257  
TYPE: DNA  
ORGANISM: HERPES VIRUS, TYPE 1  
US-09-259-821A-1

## Query Match

14.9%; Score 37.6; DB 3; Length 4257;  
Best Local Similarity 48.8%; Pred. No. 1.9;  
Matches 100; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

Qy 27 GCGGATCGTCCCTGCGGCTCCACCTCCCGAGGCGAGAGGCGCCGACGAGACCCCG 86  
Db 1777 GCTACGCGCCCTGTTGGCGCGAGAGACGCGCGCTGACGCGGGCGCCGCGAGCCCC 1836  
Qy 87 AGTCCCGACGTTGCCAGGCTGGGATCGAGAGGAGGACGAGGACGAGAACTGGG 146  
Db 1837 GCGCGCGCGCAATATACGAGGGGCTGCGCCGCTGCGCCCGCCGACCGGAGAGCC 1896  
Qy 147 CCGCGCGCGCGCGCGCGCGCGCGCGCGAGGAGGAGTCTCTACCGAGGAGAACTCCCTTA 206  
Db 1897 GCGGTGCGCGCGCGGTACGCGCGCGCGCGGAGATCTGCGCGCTGCGGCGCTGTCGC 1956  
Qy 207 CCGCGCGCGAGCGCTGCGAGGGGGCG 231  
Db 1957 GCGCGCGCTCTCCCGCGGGGGCG 1981

## RESULT 26

US-08-843-659-1  
Sequence 1, Application US/08843659  
Patent No. 6218103  
GENERAL INFORMATION:  
APPLICANT: LEOPARDI, ROSARIO  
TITLE OF INVENTION: HERPES SIMPLEX VIRUS US3 AND ICP4 AS  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: United States  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/843,659  
FILING DATE: Concurrently Herewith  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:

NAME: Highlander, Steven L.  
REGISTRATION NUMBER: 37,642  
REFERENCE/DOCKET NUMBER: ARSB.519  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 474-7577  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4257 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

## US-08-843-659-1

## Query Match

14.9%; Score 37.6; DB 3; Length 4257;  
Best Local Similarity 48.8%; Pred. No. 1.9;  
Matches 100; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

Qy 27 GCGGATCGTCCCTGCGGCTCCACCTCCCGAGGCGAGAGGCGCCGACGAGACCCCG 86  
Db 1777 GCTACGCGCCCTGTTGGCGCGAGAGACGCGCGCTGACGCGGGCGCGGAGACCCC 1836  
Qy 87 AGTCCCGACGTTGCCAGGCTGGGATCGAGAGGAGGACGAGGACGAGAACTGGG 146  
Db 1837 GCGCGCGCGCAATATACGAGGGGCTGCGCCGCTGCGCCCGCCGACCGGAGAGCC 1896  
Qy 147 CCGCGCGCGCGCGCGCGCGCGCGCGAGGAGGAGTCTCTACCGAGGAGAACTCCCTTA 206  
Db 1897 GCGGTGCGCGCGGTACGCGCGCGCGCGGAGATCTGCGCGCTGCGGCGCTGTCGC 1956  
Qy 207 CCGCGCGCGAGCGCTGCGAGGGGGCG 231  
Db 1957 GCGCGCGCTCTCCCGCGGGGGCG 1981

## RESULT 27

US-09-103-840A-2  
Sequence 2, Application US/09103840A  
Patent No. 6294328  
GENERAL INFORMATION:  
APPLICANT: FLEISCHMAN, Robert D.  
APPLICANT: WHITE, Owen R.  
APPLICANT: FRASER, Clalre M.  
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
FILE REFERENCE: TUBERCULOSIS  
CURRENT FILING DATE: US/09/103,840A  
CURRENT FILING DATE: 1998-06-24  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 2  
LENGTH: 4403765  
TYPE: DNA  
ORGANISM: Mycobacterium tuberculosis  
FEATURE:  
OTHER INFORMATION: CDC 1551  
OTHER INFORMATION: "n" bases at various positions throughout the sequence  
OTHER INFORMATION: represent a, t, c or g  
US-09-103-840A-2

Query Match 14.8%; Score 37.4; DB 3; Length 4403765;  
Best Local Similarity 46.8%; Pred. No. 2.4;  
Matches 116; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

Qy 1 CCGCGCGGAGGCGCGCGGAGTGAAGCTGATGCTGCGCGCTTCACTCCCGAGG 60  
Db 1218214 CCGCGGCGTGGGCGGCGTTCATTCGCTCCCGCTGAACGAGGCGGCGAGCG 1218273  
Qy 61 CGAGAGGCGCGCGAGAGACCCCGAGTCCCGAGCTTCCAGCGTCTGGAGTACAGG 120  
Db 1218274 TGGGACGCGCGGTAACTGCTCCCGCGCGGCTGTATGCAATGAGGCGCGCGG 1218333



Db 1171 TGGCAGAGCCTCGGTCCGCCAGCTCCGTGCGCAGGCGCTCCAGGTCGCGCCCTAGCC 1112  
Qy 134 GCCAGAACTGCGCCGCCGCCCTGCTGCGCGGAGGAAGCTCCCTCAGCNGAG 193  
Db 1111 CTGGCTCCGTCGCGGCGAGCGGCTCCCGCTGCTCGGCGCGCGCGCAGCGCAGACA 1052  
Qy 194 GAAGCTCCCTCAGCCGCGCGGCGGCTGCGAGGGGGGCGG 233  
Db 1051 CGGCTCCGCGCACTGCGCGCTGCTGCTGCGAGCTCGG 1012

## RESULT 31

US-09-186-277-4/c  
; Sequence 4, Application US/09186277  
; Patent No. 6171841  
; GENERAL INFORMATION:  
; APPLICANT: AKIRA, SHIZUO  
; TITLE OF INVENTION: DNA CODING FOR SERINE/THREONINE KINASE  
; FILE REFERENCE: 081356/0128  
; CURRENT APPLICATION NUMBER: US/09/186,277  
; CURRENT FILING DATE: 1998-11-05  
; EARLIER APPLICATION NUMBER: JP97/261589  
; EARLIER FILING DATE: 1997-09-26  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 1429  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (10)..(1353)  
US-09-186-277-4

Query Match 14.5%; Score 36.6; DB 3; Length 1429;  
Best Local Similarity 47.7%; Pred. No. 3;  
Matches 105; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

Qy 14 GGGCGGAGTGAAGCTGATGTCCTGCGGCTCCACCTCCCGAGCGCAGAGGCGCC 73  
Db 1231 GGGAGCGCTTCAGGCCCCCGGCAACCAAGCGCGCCGCTCTGCGCGCGCG 1172  
Qy 74 CAGAGAGCCCCAGTCCCGAGCTGCGCGGCTGAGATCAGAGGAGCAGAGGA 133  
Db 1171 TGGCGAGAGCTCGGTGCGCGCCAGCTCCGTGCGCAGGCGTGCAGGTGCGCGCTAGCC 1112  
Qy 134 GCCAGAACTGCGCCGCCGCCCTGCTGCGCGGAGGAAGCTCCCTCAGCNGAG 193  
Db 1111 CTGGCTCCGTCGCGGCGAGCGGCTCCCGCTGCTCGGCGCGCGCGCAGCGCAGACA 1052  
Qy 194 GAAGCTCCCTCAGCCGCGCGGCGGCTGCGAGGGGGGCGG 233  
Db 1051 CGGCTCCGCGCACTGCGCGCTGCTGCTGCGAGCTCGG 1012

## RESULT 32

US-09-741-154-3  
; Sequence 3, Application US/09741154  
; Patent No. 6437110  
; GENERAL INFORMATION:  
; APPLICANT: BEASLEY, Ellen M. et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEIN, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; FILE REFERENCE: CL001061  
; CURRENT APPLICATION NUMBER: US/09/741,154  
; CURRENT FILING DATE: 2000-12-21  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 16389  
; TYPE: DNA

; ORGANISM: Human  
US-09-741-154-3

Query Match 14.5%; Score 36.6; DB 4; Length 16389;  
Best Local Similarity 48.1%; Pred. No. 3.2;  
Matches 102; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

Qy 2 GGGCGGAGGAGCGCGCGGAGTGAAGCTGATGCTCCCTGAGGCTCCACCTCCAGGC 61  
Db 12683 GGTGTGGGACCGTGTGAGCGGGGGGGTCCAGGCTGCTCCCTCAAGCCACCGGCC 12742  
Qy 62 GCAGAGGCGCCGCGAGAGAGCCCGAGTGGCGGACGTTGCGCAGGCTGAGTCAAGAGC 121  
Db 12743 CCAGGAAGATGCACAGAGAACCTGTGCTCTCTGCGCGGATCTGACACAGGCG 12802  
Qy 122 AGGAGCAGAGGAGCGAGAGTGCAGCGCGCCCGCGCTGCGCGGAGGAGCTC 181  
Db 12803 TGTACATTGTCTAGAGACATGACAGAGTGGGCGGGGCCAGGCGGAGGGGCC 12862  
Qy 182 CCTACCGAGGAGAGCTCCCTCAGCCGCGC 213  
Db 12863 AGGAGGAGAGCAGCCCAACATCCGCGGC 12894

## RESULT 33

US-09-252-991A-310/c  
; Sequence 310, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 310  
; LENGTH: 606  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-310

Query Match 14.4%; Score 36.4; DB 4; Length 606;  
Best Local Similarity 49.2%; Pred. No. 3.3;  
Matches 94; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

Qy 62 GCGAAGAGGCGCCAGAGAGCGCCGAGTGGCGGAGTGCAGCGCTGAGTCAAGAGC 121  
Db 553 GCGGAACCGCCGAGAGAGCAGCGCATGACCCGATGACACAGATGAGATCCGCCGC 494  
Qy 122 AGGAGCAGAGGAGCGAGAGTGGCGCGCCCGCGCCCTGCGCGGAGGAGCTC 181  
Db 493 GAGCGGAGGAGCAGCTCGGCTACGCGCAGCCGAGGCTGCGCGGAGATGCCATCC 434  
Qy 182 CTTACCGAGGAGAGTCCCTCAGCCGCGGAGCTGCGAGGGGGGCGCTGAGCTCA 241  
Db 433 TCGTGTGCGGAGTCAAGCGCGCGCTGCGCGGCTGCGCGGCGCGGCTTCAGAGG 374  
Qy 242 GACCGCAAGC 252  
Db 373 GACATCCAGC 363

## RESULT 34

US-09-252-991A-344  
; Sequence 344, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.

;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
;; FILE REFERENCE: 107196.136  
;; CURRENT APPLICATION NUMBER: US/09/252,991A  
;; PRIOR FILING DATE: 1999-02-18  
;; PRIOR APPLICATION NUMBER: US 60/074,788  
;; PRIOR FILING DATE: 1998-02-18  
;; PRIOR APPLICATION NUMBER: US 60/094,190  
;; PRIOR FILING DATE: 1998-07-27  
;; NUMBER OF SEQ ID NOS: 33142  
;; SEQ ID NO 344  
;; LENGTH: 795  
;; TYPE: DNA  
;; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-344

Query Match 14.4%; Score 36.4; DB 4; Length 795;  
Best Local Similarity 49.2%; Pred. No. 3.3;  
Matches 94; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 62 GCAGAGGCGCCGACGAGGAGCCCGCAGTCCGACGTTGCCAGCTGTGGATCAGAGGC 121  
DB 310 GCGGAAACCCCGAGAGGACGCGCATGACCCGATCAGACGGAATCGAGTCCGCCGC 369  
QY 122 AGGAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 181  
DB 370 GAGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 429  
QY 182 CCTCACCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 241  
DB 430 TCGTCGTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 489  
QY 242 GACCGCAAGC 252  
DB 490 GACATCCAGC 500

RESULT 35  
US-09-252-991A-336  
; Sequence 336, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 336  
; LENGTH: 1350  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-336

Query Match 14.4%; Score 36.4; DB 4; Length 1350;  
Best Local Similarity 49.2%; Pred. No. 3.4;  
Matches 94; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 62 GCAGAGGCGCCGACGAGGAGCCCGCAGTCCGACGTTGCCAGCTGTGGATCAGAGGC 121  
DB 776 GCGGAAACCCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 835  
QY 122 AGGAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 181  
DB 836 GAGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 895  
QY 182 CCTCACCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 241

DB 896 TCGTCGTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 955  
QY 242 GACCGCAAGC 252  
DB 956 GACATCCAGC 966

RESULT 36  
US-09-252-991A-908  
; Sequence 908, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 908  
; LENGTH: 903  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-908

Query Match 14.4%; Score 36.2; DB 4; Length 903;  
Best Local Similarity 50.3%; Pred. No. 3.7;  
Matches 89; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 3 GCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 62  
DB 710 GCGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 769  
QY 63 GAGAGGCGCCGACGAGGAGCCCGCAGTCCGACGTTGCCAGCTGTGGATCAGAGGC 122  
DB 770 GCGGAAACCCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 829  
QY 123 GCGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 179  
DB 830 GCGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 886

RESULT 37  
US-09-030-613-1/C  
; Sequence 1, Application US/09030613  
; Patent No. 6083706  
; GENERAL INFORMATION:  
; APPLICANT: Floorkiewicz, Robert Z.  
; TITLE OF INVENTION: INHIBITORS OF LEADERLESS PROTEIN EXPORT  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: SEED AND BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/030,613  
; FILING DATE: 25-FEB-1998  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 6083706tenburg Ph.D., Carol

REGISTRATION NUMBER: 39,317  
REFERENCE/DOCKET NUMBER: 760100.418C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1120 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-030-613-1

Query Match 14.2%; Score 35.8; DB 3; Length 1120;  
Best Local Similarity 47.0%; Pred. No. 4.6;  
Matches 109; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

QY 2 GGGCGGGAGAGCGCGGAGTGAAGGCTGATGTCCTCGGCGCTCCACCTCCCGAGGC 61  
DB 452 GGTCTTGAAGTGGCGGGGGGAGACCTCGCTGCGCATCTCGGGCCAAAGCGGGC 393  
QY 62 GCAGAAAGCGCGCCACAGAGACCCCGAGTGGCGGAGTGGCGATCGAGAGGC 121  
DB 392 AGCGTGTATGCTCCCGCTGCTCATGTCTCGGGGGCCCGCGGGATCCGAGGC 333  
QY 122 AGGAGACAGAGAGCCAGAACTGCGCGCGCGCGCGCGCTGCGCGGAGAGAACTC 181  
DB 332 GCTGAGAGCGCGCGGGAGCGCCGTCCTCCCGCGCGCGCGCTCCGACCCGCTC 273  
QY 182 CCTCACGAGAGAGAACTCCCTCACCGCGCGCGCGCGCGCGCGCGCGCGCG 223  
DB 272 CGGGGACAGCG 221

RESULT 38  
US-09-451-905-1/c  
Sequence 1, Application US/09451905  
Patent No. 6306613  
GENERAL INFORMATION:  
APPLICANT: Robert Z. Florkiewicz  
APPLICANT: Andrew Balid  
TITLE OF INVENTION: MODULATORS OF LEADERLESS PROTEIN EXPORT  
FILE REFERENCE: 200124.402C4  
CURRENT APPLICATION NUMBER: US/09/451,905  
CURRENT FILING DATE: 1999-12-01  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 1120  
TYPE: DNA  
ORGANISM: Homo sapien  
US-09-451-905-1

Query Match 14.2%; Score 35.8; DB 4; Length 1120;  
Best Local Similarity 47.0%; Pred. No. 4.6;  
Matches 109; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

QY 2 GGGCGGGAGAGCGCGGAGTGAAGGCTGATGTCCTCGGCGCTCCACCTCCCGAGGC 61  
DB 452 GGTCTTGAAGTGGCGGGGGGAGACCTCGCTGCGCATCTCGGGCCAAAGCGGGC 393  
QY 62 GCAGAAAGCGCGCCACAGAGACCCCGAGTGGCGGAGTGGCGATCGAGAGGC 121  
DB 392 AGCGTGTATGCTCCCGCTGCTCATGTCTCGGGGGCCCGCGGGATCCGAGGC 333  
QY 122 AGGAGACAGAGAGCCAGAACTGCGCGCGCGCGCGCGCTGCGCGGAGAGAACTC 181  
DB 332 GCTGAGAGCGCGCGGGAGCGCCGTCCTCCCGCGCGCGCGCTCCGACCCGCTC 273  
QY 182 CCTCACGAGAGAGAACTCCCTCACCGCGCGCGCGCGCGCGCGCGCGCGCG 223

DB 272 CGGGGACAGCG 221

RESULT 39  
US-09-595-549-1/c  
Sequence 1, Application US/09595549  
Patent No. 6511827  
GENERAL INFORMATION:  
APPLICANT: Howard, Andrew D.  
APPLICANT: Casclieri, Margaret A.  
APPLICANT: Smith, Roy G.  
APPLICANT: Sullivan, Kathleen A.  
APPLICANT: Tan, Carina  
APPLICANT: Van der Ploeg, Leonardus H. T.  
TITLE OF INVENTION: GALANIN RECEPTOR GALR3 AND NUCLEOTIDES  
FILE REFERENCE: 20148PCA  
CURRENT APPLICATION NUMBER: US/09/595,549  
CURRENT FILING DATE: 2000-06-16  
PRIOR APPLICATION NUMBER: US98/26812  
PRIOR FILING DATE: 1998-12-17  
PRIOR APPLICATION NUMBER: 60/069,725  
PRIOR FILING DATE: 1997-12-17  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 2263  
TYPE: DNA  
ORGANISM: human  
US-09-595-549-1

Query Match 14.1%; Score 35.6; DB 4; Length 2263;  
Best Local Similarity 49.7%; Pred. No. 5.2;  
Matches 83; Conservative 2; Mismatches 82; Indels 0; Gaps 0;

QY 37 CCTGCGGCTCCACCTCCCGAGCGCGAGAGCGCGCCAGAGACCCCGAGTCCCGAC 96  
DB 1731 CTTGGGCG 1672  
QY 97 GTGCCAGCGTCTGGATGATGAGAGCGAGAGCGAGAGCGAGAACTGCGCGCGCGCG 156  
DB 1671 CGTAGGCGAGGCTCACACRGGCCAGCGGCGAGGATGCGGACGAGAGTGGCCAGT 1612  
QY 157 CCTGCGGCTCCCGAGAGAGCTCCCTCACCGAGAGAGAGTCCCG 203  
DB 1611 CAGGGGCGCGCGCGCGCGCGCGCGCTCCAGGCGGGGACGAGAGCTCC 1565

RESULT 40  
US-09-103-840A-1/c  
Sequence 1, Application US/09103840A  
Patent No. 6294328  
GENERAL INFORMATION:  
APPLICANT: FLEISCHMAN, Robert D.  
APPLICANT: WHITE, Owen R.  
APPLICANT: FRASER, Claire M.  
APPLICANT: VENTER, John C.  
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
FILE REFERENCE: 24366-20007.00  
CURRENT APPLICATION NUMBER: US/09/103,840A  
CURRENT FILING DATE: 1998-06-24  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 4411529  
TYPE: DNA  
ORGANISM: Mycobacterium tuberculosis  
OTHER INFORMATION: H37Rv  
US-09-103-840A-1

Query Match 14.1%; Score 35.6; DB 3; Length 4411529;  
Best Local Similarity 49.7%; Pred. No. 5.2;  
Matches 83; Conservative 2; Mismatches 82; Indels 0; Gaps 0;





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Db 61 CGCAGAAAGGCGCCACGAGAGACCCCGACGTCGTCGATGATCAAGG 120  
Qy 121 CAGGAGACGAGGAGCCGAGAACTGCGCGCGCCCGCTGCGCGGAGGAAAGCT 180  
Db 121 CAGGAGACGAGGAGCCGAGAACTGCGCGCGCCCGCTGCGCGGAGGAAAGCT 177  
Qy 181 CCCCTCACGCGAGGAGGAGTCCCTCTCACCGCGCGCGCGCGCGCGCGCTGCGGTC 240  
Db 178 CCCCTCACGCGAGGAGGAGTCCCTCTCACCGCGCGCGCGCGCGCGCGCTGCGGTC 236  
Qy 241 AGACCGGAAAGC 252  
Db 237 AGACCGGAAAGC 248

RESULT 2  
US-10-027-632-196114/C  
; Sequence 196114, Application US/10027632  
; Publication No. US20030204075A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827,129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; PRIOR FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 196114  
; LENGTH: 533  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-196114

Query Match 57.0%; Score 143.6; DB 12; Length 533;  
Best Local Similarity 94.8%; Pred. No. 4.1e-26;  
Matches 181; Conservative 0; Mismatches 5; Indels 5; Gaps 3;  
Qy 1 CGGCGGAGGAGCGCGCGGAGTGAAGCTGATCTGCTGCGCGCTTCCACCTCCCCAGG 60  
Db 189 CGGCGGAGGAGCGCGCGGAGTGAAGCTGATCTGCTGCGCGCTTCCACCTCCCCAGG 130  
Qy 61 CGCAGAGGCGCCACGAGAGACCCCGAGTCCCGAGCTTGCACAGGTCGATCAGAGG 120  
Db 129 CGCAGAGGCGCCACGAGAGACCCCGAGTCCCGAGCTTGCACAGGTCGATCAGAGG 70  
Qy 121 CA-GGAGCAGAGGAGCAGAGAACTGCGCGCGCGCGCGCGCGCTGCGCGGAGGAAAGC 179  
Db 69 CAGGAGACGAGGAGGAGGAGAACTGCGCGCGCGCGCGCGCGCTGCGCGGAGGAAAGC 14  
Qy 180 TCCTCTACCGG 190  
Db 13 TCCTCTACCGG 3

RESULT 3  
US-10-027-632-196114/C  
; Sequence 196114, Application US/10027632  
; GENERAL INFORMATION:

APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827,129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; PRIOR FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 196114  
; LENGTH: 533  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-196114

Query Match 57.0%; Score 143.6; DB 13; Length 533;  
Best Local Similarity 94.8%; Pred. No. 4.1e-26;  
Matches 181; Conservative 0; Mismatches 5; Indels 5; Gaps 3;  
Qy 1 CGGCGGAGGAGCGCGCGGAGTGAAGCTGATCTGCTGCGCGCTTCCACCTCCCCAGG 60  
Db 189 CGGCGGAGGAGCGCGCGGAGTGAAGCTGATCTGCTGCGCGCTTCCACCTCCCCAGG 130  
Qy 61 CGCAGAGGCGCCACGAGAGACCCCGAGTCCCGAGCTTGCACAGGTCGATCAGAGG 120  
Db 129 CGCAGAGGCGCCACGAGAGACCCCGAGTCCCGAGCTTGCACAGGTCGATCAGAGG 70  
Qy 121 CA-GGAGCAGAGGAGCAGAGAACTGCGCGCGCGCGCGCGCGCTGCGCGGAGGAAAGC 179  
Db 69 CAGGAGACGAGGAGGAGGAGAACTGCGCGCGCGCGCGCGCGCTGCGCGGAGGAAAGC 14  
Qy 180 TCCTCTACCGG 190  
Db 13 TCCTCTACCGG 3

RESULT 4  
US-10-059-579-120  
; Sequence 120, Application US/10059579  
; Publication No. US20030138783A1  
; GENERAL INFORMATION:  
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE  
; APPLICANT: SUKUMAR, Saraswati  
; APPLICANT: EVRON, Ella  
; APPLICANT: DOOLEY, William C.  
; APPLICANT: DAVIDSON, Nancy  
; APPLICANT: PACKER, Mary Jo.  
; TITLE OF INVENTION: ABERRANTLY METHYLATED GENES AS MARKERS OF BREAST MALIGNANCY  
; FILE REFERENCE: JHU1630-1  
; CURRENT APPLICATION NUMBER: US/10/059,579  
; PRIOR FILING DATE: 2003-02-03  
; PRIOR APPLICATION NUMBER: US 09/771,357  
; PRIOR FILING DATE: 2001-01-26  
; NUMBER OF SEQ ID NOS: 136  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 120  
; LENGTH: 1794  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:



QY 148 CGGCCCCGGCCCTGGCCCTGCGGAGAGGAGAGGCTCCCTCAACGAGAGGAGAGAGAGTCCCTCAC 207  
Db 263 TGCAGCGTCCCTCCCTCGGGCTGACAGGCGCCGCTCCGCGCGCGCGGCCCCGACTGTG 322  
QY 208 CCGGCCCCAGCCCTGACAGAGGAGGCGGTG 235  
Db 323 CCTGTATGAGCGCGAGCTGCGGCGAG 350

RESULT 7  
US-10-156-761-1  
; Sequence 1, Application US/10156761  
; Publication No US20030119018A1

```

GENERAL INFORMATION:=====
APPLICANT: OMTURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 1
LENGTH: 9025608
TYPE: DNA
ORGANISM: Streptomyces avermitilis
FEATURE:
NAME/KEY: misc_feature
LOCATION: (4187715)
OTHER INFORMATION: a, b, c, g, other or unknown
US-10-156-761-1

```

	Query	Best Match	Similarity	Score	DB	Length
			59.2%	42.2	14	9025608
				Pred. 0.012		
				Mismatches 43		
				Indels 0		
				Gaps 0		
Qy	117	GAGCGAGGAGCCAGGAGCCAGGAATCTCCGCCGCCGCCCTCTGCGCGAGGGA	176			
Db	2369913	GAGCGTGGCTGAGAGGGGCCGCCGAGCCCGCGGTCTCAAGGCTCAAGCCCGGCGGACAGC	2369972			
Qy	177	AGCTCCCTCAACGAGGAGAGCTCCCTCAACCCCGGCGAGCCCTTCAGAGGGGGCGCGTGG	236			
Db	2369973	AGCCCTCACACCGGCGGGCGCGTGGCTCGCTCGTCCCGCGCGCGGTGAACGGAGGCGCGTGG	2370032			

```

RESULT 8
US-10-101-510-497
; Sequence 497, Application US/10101510
; Publication No. US20030148295A1
GENERAL INFORMATION:
APPLICANT: MAN, JACKSON
APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
FILE REFERENCE: 15117.0012
CURRENT APPLICATION NUMBER: US/10/101,510
CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: 60/276,947
PRIOR FILING DATE: 2001-03-20
NUMBER OF SEQ ID NOS: 805
SOFTWARE: Patentn Ver. 2.1
SEQ ID NO 497
LENGTH: 2666
TYPE: DNA
ORGANISM: Homo sapiens
US-10-101-510-497

```

Query Match	16.2%	Score 40.8;	DB 12;	Length 2666;
Best Local Similarity	49.3%	Pred. No. 0.18;		
Matches 105; Conservative	0;	Mismatches 108;	Indels 0;	Gaps 0;

Qy 1 CGCGCGGGGAGCGCGCGCGGATGAGCGCTTATGTCTCTGCGGCTTCACACTCTCCAGG 60  
 Db 28 CACCGCGGATCGGGGCGGGGAGGAGAGCCAGACGGCGCCCGCTCTCTGCCGAGAGC 87  
 Qy 61 CGGAGAGGCGCGCCACAGAGAGCCCGCATGTGCGGACGTTCAGTCTGGATTCAGAG 120  
 Db 88 CGCGGCGCGCGCACACTCTCGCCCCCGCGCCCCCGGCTCACTGCACTACACCCGGGC 147  
 Qy 121 CAGGAGCCAGGAGCGCAGAGAACTGTGGCGCGCGCGCGCGCGCTCTGTGGCGCGAGAGAACT 180  
 Db 148 GCAGGAGGCGGGGCGGCGCCGAGCCCGACCGAGCGCGCCCATGAGAGCGCCCGACGACGGGGCG 207  
 Qy 181 CCTCATCCAGAGGAAGCTCCCTCTACCGCGGC 213  
 Db 208 CTGAGACCCCCCGGTGCTGCTCCCAAGCCGAGTCC 240

RESULT 9  
US-10-156-761-1/c  
; Sequence 1, Application US/10156761  
; Publication No. 102002011001831

FULLTEXTLENGTH: 022005011901681  
 GENERAL INFORMATION:  
 APPLICANT: OMURA, SATOSHI  
 APPLICANT: IKEDA, HARUO  
 APPLICANT: ISHIKAWA, JUN  
 APPLICANT: HORIKAWA, HIROSHI  
 APPLICANT: SHIBA, TADAYOSHI  
 APPLICANT: SAKAKI, YOSHIYUKI  
 APPLICANT: HATTORI, MASAHIRA  
 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
 FILE REFERENCE: 249-262  
 CURRENT APPLICATION NUMBER: US/10/156,761  
 CURRENT FILING DATE: 2002-05-29  
 PRIOR APPLICATION NUMBER: JP 2001-204089  
 PRIOR FILING DATE: 2001-05-30  
 PRIOR APPLICATION NUMBER: JP 2001-272697  
 PRIOR FILING DATE: 2001-08-02  
 NUMBER OF SEQ ID NOS: 15109  
 SEQ ID NO: 1  
 LENGTH: 9025608  
 TYPE: DNA  
 ORGANISM: Streptomyces avermitilis  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (4187715)  
 OTHER INFORMATION: a, t, c, g, other or unknown  
 IS-10-156-761-1

[illegible]



Db 7676 CGGCGGAGGAGCGCGCGCGCGCGAGAGCTCGGAGCGGAGCGCGCGCGCGCGCG 7617  
QY 61 CGCAGAGAGCG 120  
Db 7616 GCG 7557  
QY 121 CAGGAGACGAGGAGCG 180  
Db 7556 TCGCCG 7497  
QY 181 CCTACACGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 217  
Db 7496 CCG 7460

RESULT 12  
US-09-836-911A-17/c  
; Sequence 17, Application US/09936911A  
; Publication No. US2003003617A1

GENERAL INFORMATION:  
APPLICANT: Hadlaczky, Gyula

TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF  
AND METHODS FOR PREPARING ARTIFICIAL CHROMOSOMES

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESSES:  
ADDRESS: Heller Erman White & McAllister  
STREET: 4350 La Jolla Village Drive, 6th Floor  
CITY: San Diego  
STATE: CA  
COUNTRY: USA

ZIP: 92122

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ Version 1.5

CURRENT APPLICATION NUMBER: US/09/836,911A

APPLICATION NUMBER: 17-APR-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/835,682

FILING DATE: 10-APR-1997

APPLICATION NUMBER: 08/695,191

FILING DATE: 07-AUG-1996

APPLICATION NUMBER: 08/682,080

FILING DATE: 15-JUL-1996

APPLICATION NUMBER: 08/629,822

FILING DATE: 10-APR-1996

ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779

REFERENCE/DOCKET NUMBER: 24601-4021

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 858-450-8403

TELEFAX: 858-587-5360

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:  
LENGTH: 4299 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
HYPOETHERICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: <Unknown>

ORIGINAL SOURCE:  
SEQUENCE DESCRIPTION: SEQ ID NO: 17:

US-09-836-911A-17

Query Match 15.2%; Score 38.4; DB 11; Length 42999;

Best Local Similarity 48.4%; Pred. No. 0.35;  
Matches 105; Conservative 0; Mismatches 112; Indels 0; Gaps 0;  
QY 1 CGGCGGAGGAGCGCGCGCGCGCGAGAGCTCGGAGCGGAGCGCGCGCGCGCGCG 60  
Db 7676 CGGCGGAGGAGCG 7617  
QY 61 CGCAGAGAGCG 120  
Db 7616 GCG 7557  
QY 121 CAGGAGACGAGGAGCG 180  
Db 7556 TCGCCG 7497  
QY 181 CCTACACGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 217  
Db 7496 CCG 7460

RESULT 13  
US-09-738-630-73/c  
; Sequence 73, Application US/09738630  
; Publication No. US2003016231A1

GENERAL INFORMATION:  
APPLICANT: Greenpan, Ralph J.

TITLE OF INVENTION: Methods For Identifying Compounds That  
Modulate Disorders Related To Nitric Oxide/CGMP-Dependent

TITLE OF INVENTION: Protein Kinase Signaling

FILE REFERENCE: P-NI 3906

CURRENT APPLICATION NUMBER: US/09/738,630

NUMBER OF SEQ ID NOS: 105

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 73

LENGTH: 42999

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:  
NAME/KEY: misc\_feature

LOCATION: (1) .. (42999)

OTHER INFORMATION: n = A,T,C or G

US-09-738-630-73

Query Match 15.2%; Score 38.4; DB 12; Length 42999;

Best Local Similarity 48.4%; Pred. No. 0.35;

Matches 105; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

QY 1 CGGCGGAGGAGCGCGCGCGCGCGAGAGCTCGGAGCGGAGCGCGCGCGCGCGCG 60  
Db 7676 CGGCGGAGGAGCG 7617  
QY 61 CGCAGAGAGCG 120  
Db 7616 GCG 7557  
QY 121 CAGGAGACGAGGAGCG 180  
Db 7556 TCGCCG 7497  
QY 181 CCTACACGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 217  
Db 7496 CCG 7460

RESULT 14  
US-10-125-767-17/c  
; Sequence 17, Application US/10125767  
; Publication No. US20020160410A1

GENERAL INFORMATION:  
APPLICANT: Hadlaczky, Gyula  
TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF AND



METHODS  
FOR PREPARING ARTIFICIAL CHROMOSOMES

NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Heller Ehrman White & McCauliffe LLP  
STREET: 4350 La Jolla Village Drive, 7th Floor  
CITY: San Diego  
STATE: CA  
COUNTRY: USA  
ZIP: 92122

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/125,767  
FILING DATE: 17-Apr-2002

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/724,693  
FILING DATE: 28-NOV-2000  
APPLICATION NUMBER: 08/835,682  
FILING DATE: 10-APR-1997  
APPLICATION NUMBER: 08/695,191  
FILING DATE: 07-AUG-1996  
APPLICATION NUMBER: 08/682,080  
FILING DATE: 15-JUL-1996  
APPLICATION NUMBER: 08/629,822  
FILING DATE: 10-APR-1996

ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 24601-402J  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 858-450-8403  
TELEFAX: 858-587-5360  
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 42999 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: <Unknown>  
ORIGINAL SOURCE:  
SEQUENCE DESCRIPTION: SEQ ID NO: 17:  
US-10-125-767-17

Query Match 15.2%; Score 38.4; DB 13; Length 42999;  
Best Local Similarity 48.4%; Pred. No. 0.35;  
Matches 105; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

QY 1 CGGCGGAGAGGCGCGGAGGAGTGGCTGATCGTCCTGCGGCGCTCCACCTCCCGCAGG 60  
DB 7676 CGGCGGAGAGGCGCGGAGGAGTGGCTGATCGTCCTGCGGCGCTCCCGGCGCGG 7617

QY 61 CGCAGAGAGGCGCCACAGAGACCCCGCAGTGCCTGCGGCGCTGCGATCGATCAGAGG 120  
DB 7616 GCGCGGCGCGGAGCGCGAGCGCGGCGCGGCGCGACACACCGCGGCTCCCGCGG 7557

QY 121 CAGGAGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180  
DB 7556 TCGCGCGGCGGAGCAGCGAGACCGCGGCGCTCGCGGCGACGCGGCGCGCGCGGCT 7497

QY 181 CCGTCACGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 217  
DB 7496 CCGCGCGCGCGCGAGCGCGCGCGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 7460

RESULT 15

US-10-151-081-17/C  
Sequence 17, Application US/10151081  
Publication No. US20030083293A1  
GENERAL INFORMATION:  
APPLICANT: Hadjicakky, Gynia  
TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF  
AND METHODS FOR PREPARING ARTIFICIAL CHROMOSOMES

NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Heller Ehrman White & McCauliffe  
STREET: 4250 Executive Square, 7th Floor  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/151,081  
FILING DATE: 16-May-2002  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/799,462  
FILING DATE: HEREWITH 05-MAR-2001  
APPLICATION NUMBER: 09/724,693  
FILING DATE: HEREWITH 28-NOV-2000  
APPLICATION NUMBER: 08/835,682  
FILING DATE: 10-APR-1997  
APPLICATION NUMBER: 08/695,191  
FILING DATE: 07-AUG-1996  
APPLICATION NUMBER: 08/682,080  
FILING DATE: 15-JUL-1996  
APPLICATION NUMBER: 08/629,822  
FILING DATE: 10-APR-1996

ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 24601-402L  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 858-450-8403  
TELEFAX: 858-587-5360  
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 42999 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: <Unknown>  
ORIGINAL SOURCE:  
SEQUENCE DESCRIPTION: SEQ ID NO: 17:  
US-10-151-081-17

Query Match 15.2%; Score 38.4; DB 14; Length 42999;  
Best Local Similarity 48.4%; Pred. No. 0.35;  
Matches 105; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

QY 1 CGGCGGAGAGGCGCGGAGGAGTGGCTGATCGTCCTGCGGCGCTCCACCTCCCGCAGG 60  
DB 7676 CGGCGGAGAGGCGCGGAGGAGTGGCTGATCGTCCTGCGGCGCTCCCGGCGCGG 7617

QY 61 CGCAGAGAGGCGCCACAGAGACCCCGCAGTGCCTGCGGCGCTGCGATCGATCAGAGG 120  
DB 7616 GCGCGGCGCGGAGCGCGAGCGCGGCGCGGCGCGACACACCGCGGCTCCCGCGG 7557

QY 121 CAGGAGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180



Query Match 15.2%; Score 38.4; DB 14; Length 42999;  
Best Local Similarity 48.4%; Pred. No. 0.35; Mismatches 112; Indels 0; Gaps 0;  
Matches 105; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

QY 1 CGGCGGAGAGCGCGCGGAGTGAAGCTGATCGTCCCTGCGCTCTCACTCCCGAG 60  
DB 7676 CGGCGGAGAGCGCGCGCGGAGTGAAGCTGATCGTCCCTGCGCTCTCACTCCCGAG 7617  
QY 61 CGGAGAGGCGCGCGCGGAGTGAAGCTGATCGTCCCTGCGCTCTCACTCCCGAG 120  
DB 7616 GCGCGGCGCGCGCGCGGAGTGAAGCTGATCGTCCCTGCGCTCTCACTCCCGAG 7557  
QY 121 CAGGAGCAGAGGAGGAGGAGTGAAGCTGATCGTCCCTGCGCTCTCACTCCCGAG 180  
DB 7556 TCGCGCGCGCGCGCGGAGTGAAGCTGATCGTCCCTGCGCTCTCACTCCCGAG 7497  
QY 181 CCTCAGCAGAGGAGGAGTGAAGCTGATCGTCCCTGCGCTCTCACTCCCGAG 217  
DB 7496 CCGCGCGCGCGCGCGGAGTGAAGCTGATCGTCCCTGCGCTCTCACTCCCGAG 7460

RESULT 18  
US-10-125-815-4/c  
; Sequence 4; Application US/10125815  
; Publication No. US20020173008A1  
; GENERAL INFORMATION:  
; APPLICANT: Hu, Zhiluo  
; APPLICANT: McDaniel, Robert  
; APPLICANT: Santl, Daniel V.  
; TITLE OF INVENTION: RECOMBINANT POLYKETIDE SYNTHASE GENES  
; FILE REFERENCE: 3062204720  
; CURRENT APPLICATION NUMBER: US/10/125,815  
; PRIOR FILING DATE: 2002-07-25  
; PRIOR APPLICATION NUMBER: 09/679,279  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: 60/190,024  
; PRIOR FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: 60/158,305  
; PRIOR FILING DATE: 1999-10-08  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 615  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: megks6  
US-10-125-815-4

Query Match 15.2%; Score 38.2; DB 13; Length 615;  
Best Local Similarity 48.2%; Pred. No. 1.1; Mismatches 114; Indels 0; Gaps 0;  
Matches 106; Conservative 0; Mismatches 114; Indels 0; Gaps 0;

QY 14 GGGCGGAGTGAAGCTGATCGTCCCTGCGCTCTCACTCCCGAGGAGGAGGCGG 73  
DB 299 GGGCTTGAAGCTGATCGTCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240  
QY 74 CAGGAGAGCGCGCGCGGAGTGAAGCTGATCGTCCCTGCGCTCTCACTCCCGAG 133  
DB 239 CAGGAGAGCGCGCGCGGAGTGAAGCTGATCGTCCCTGCGCTCTCACTCCCGAG 180  
QY 134 CAGGAGAGTGAAGCTGATCGTCCCTGCGCTCTCACTCCCGAGGAGGAGGAGG 193  
DB 179 GATCGGAGTGAAGCTGATCGTCCCTGCGCTCTCACTCCCGAGGAGGAGGAGG 120  
QY 194 GAGGAGTGAAGCTGATCGTCCCTGCGCTCTCACTCCCGAGGAGGAGGAGG 233  
DB 119 CTGCGGAGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 80

RESULT 19  
US-10-156-761-6400/c  
; Sequence 6400; Application US/10156761

Publication No. US20030119018A1  
; GENERAL INFORMATION:  
; APPLICANT: OMURA, SATOSHI  
; APPLICANT: ISEDA, HARUO  
; APPLICANT: ISHIZAWA, YUN  
; APPLICANT: HORIKAWA, HIROSHI  
; APPLICANT: SHIBA, TADAYOSHI  
; APPLICANT: SAKAKI, YOSHIYUKI  
; APPLICANT: HATTORI, MASAHIRA  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-262  
; CURRENT APPLICATION NUMBER: US/10/156,761  
; PRIOR FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: JP 2001-204089  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: JP 2001-272697  
; PRIOR FILING DATE: 2001-08-02  
; NUMBER OF SEQ ID NOS: 15109  
; SEQ ID NO 6400  
; LENGTH: 1365  
; TYPE: DNA  
; ORGANISM: Streptomyces avermitilis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1365)  
US-10-156-761-6400

Query Match 15.2%; Score 38.2; DB 14; Length 1365;  
Best Local Similarity 47.8%; Pred. No. 0.91; Mismatches 119; Indels 0; Gaps 0;  
Matches 109; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

QY 1 CGGCGGAGAGCGCGCGGAGTGAAGCTGATCGTCCCTGCGCTCTCACTCCCGAG 60  
DB 244 CGGAGAGGAGTGAAGCTGATCGTCCCTGCGCTCTCACTCCCGAGGAGGAGGAGG 185  
QY 61 CGGAGAGGAGTGAAGCTGATCGTCCCTGCGCTCTCACTCCCGAGGAGGAGGAGG 120  
DB 184 CGGAGAGGAGTGAAGCTGATCGTCCCTGCGCTCTCACTCCCGAGGAGGAGGAGG 125  
QY 121 CAGGAGCAGAGGAGGAGGAGTGAAGCTGATCGTCCCTGCGCTCTCACTCCCGAG 180  
DB 124 CGGCGGAGGAGGAGGAGGAGTGAAGCTGATCGTCCCTGCGCTCTCACTCCCGAG 65  
QY 181 CCTCAGCAGAGGAGGAGTGAAGCTGATCGTCCCTGCGCTCTCACTCCCGAGGAGG 228  
DB 64 CCGCGGAGGAGGAGGAGGAGTGAAGCTGATCGTCCCTGCGCTCTCACTCCCGAGG 17

RESULT 20  
US-10-020-079-11  
; Sequence 11; Application US/10020079  
; Publication No. US20020161213A1  
; GENERAL INFORMATION:  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Mathur, Brian  
; APPLICANT: Fridtle, Carl Johan  
; TITLE OF INVENTION: NO US20020161213A1 Human Kinases and Polynucleotides Encoding  
; FILE REFERENCE: LEX-0281-USA  
; CURRENT APPLICATION NUMBER: US/10/020,079  
; PRIOR FILING DATE: 2001-12-12  
; PRIOR APPLICATION NUMBER: US 60/255,103  
; PRIOR FILING DATE: 2001-05-08  
; PRIOR APPLICATION NUMBER: US 60/289,422  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 1947  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-10-020-079-11

Query Match 15.0%; Score 37.8; DB 13; Length 1947;





```
Db 59 GCCGCTGCGCGCGCTGCGCCCAAGAGATCGGGGCGGGCGCGCGCGGATGATCCGG 118
Qy 95 AGCTTGCCACGGTCTGGGATCAGAGGACCAAGGAGCCAGGAATGCGCGCGCC 154
Db 119 GTGCGAAGGCGCGCGCGCGCGGAGGAGCGGTGTCACCCAAACCGCATGAGCCCGCC 178
Qy 155 GCCCTGCGCGCGCGCGGAGGAGGAGTCTCTCAACGAGGAGGAGTCTCTCAACCGCG 212
Db 179 GCCCGCGCGCGCGCGCGGAGGAGTGCAGCGCGCGCGCGCGCGCGCGCGCGCG 236

RESULT 28
US-10-020-079-27
; Sequence 27, Application US/10020079
; Publication No. US20020161213A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Fiddle, Carl Johan
; TITLE OF INVENTION: NO. US20020161213A1 Human Kinases and Polynucleotides Encoding
; FILE REFERENCE: LEX-0281-USA
; CURRENT APPLICATION NUMBER: US/10/020,079
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255,103
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/289,422
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 2931
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-020-079-27

Query Match 15.0%; Score 37.8; DB 13; Length 2931;
Best Local Similarity 50.6%; Pred. No. 0.95;
Matches 90; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

Qy 35 GTCCCGGCGCGCTCCACCTCCCGAGAGGCGCCACAGAGACCCCGAGCGCG 94
Db 41 GCGGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 100
Qy 95 AGCTTGCCACGGTCTGGGATCAGAGGACCAAGGAGCCAGGAATGCGCGCGCC 154
Db 101 GTGCGAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 160
Qy 155 GCCCTGCGCGCGCGCGGAGGAGTCTCTCAACGAGGAGGAGTCTCTCAACCGCG 212
Db 161 GCCCGCGCGCGCGCGCGGAGGAGTGCAGCGCGCGCGCGCGCGCGCGCGCG 218

RESULT 29
US-10-020-079-25
; Sequence 25, Application US/10020079
; Publication No. US20020161213A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Fiddle, Carl Johan
; TITLE OF INVENTION: NO. US20020161213A1 Human Kinases and Polynucleotides Encoding
; FILE REFERENCE: LEX-0281-USA
; CURRENT APPLICATION NUMBER: US/10/020,079
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255,103
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/289,422
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 2949
; TYPE: DNA
```

```
; ORGANISM: homo sapiens
US-10-020-079-25

Query Match 15.0%; Score 37.8; DB 13; Length 2949;
Best Local Similarity 50.6%; Pred. No. 0.94;
Matches 90; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

Qy 35 GTCCCTGCGCGCTCCACCTCCCGAGGCGCGAGAGGCGCCACAGAGACCCCGAGTCCCG 94
Db 59 GCCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 118
Qy 95 AGCTTGCCACGGTCTGGGATCAGAGGACCAAGGAGCCAGGAATGCGCGCGCC 154
Db 119 GTGCGAAGGCGCGCGCGCGCGGAGGAGCGGTGTCACCCAAACCGCATGAGCGCGCC 178
Qy 155 GCCCTGCGCGCGCGCGGAGGAGTCTCTCAACGAGGAGGAGTCTCTCAACCGCG 212
Db 179 GCCCGCGCGCGCGCGCGGAGGAGTGCAGCGCGCGCGCGCGCGCGCGCGCG 236

RESULT 30
US-09-825-288A-1
; Sequence 1, Application US/09825288A
; Publication No. US20020192822A1
; GENERAL INFORMATION:
; APPLICANT: LEOPARDI, ROSARIO
; APPLICANT: ROIZMAN, BERNARD
; FILE REFERENCE: ARCD:317USC1
; TITLE OF INVENTION: HERPES SIMPLEX VIRUS ICP4 IS AN INHIBITOR OF APOPTOSIS
; CURRENT APPLICATION NUMBER: US/09/825,288A
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 09/259,821
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: 08/690,473
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4257
; TYPE: DNA
; ORGANISM: HERPES VIRUS, TYPE 1
US-09-825-288A-1

Query Match 14.9%; Score 37.6; DB 10; Length 4257;
Best Local Similarity 48.8%; Pred. No. 0.97;
Matches 100; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

Qy 27 GCTGATGCTGCTGCGCGCTTCCACTCCCGAGGCGCGAGAGCGCCCGACGAGACCCCG 86
Db 1777 GCTTACGCGCGCTCTGTTGGCGCGAGAAAGCGCGCGCTGACGAGGCGCGCGCGCG 1836
Qy 87 AGTCCCGACGTTGCCAGGATCTGGGATCAGAGGAGGAGGAGGAGGAGGAGGAGGAG 146
Db 1837 GAGCGCGCGCGCGAGATGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1896
Qy 147 CGCGCGCGCGCGCGCTGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 206
Db 1897 GCGGTGCGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1956
Qy 207 CCGGCGCGCGCGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 231
Db 1957 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1981

RESULT 31
US-10-156-761-4416
; Sequence 4416, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: IKEDA, HARUO
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
```

APPLICANT: SHIBA, TADAYOSHI  
 APPLICANT: SAKAKI, YOSHIYUKI  
 APPLICANT: HATTORI, MASAHIRA  
 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
 FILE REFERENCE: 249-262  
 CURRENT APPLICATION NUMBER: US/10/156,761  
 CURRENT FILING DATE: 2002-05-29  
 PRIOR APPLICATION NUMBER: JP 2001-204089  
 PRIOR FILING DATE: 2001-05-30  
 PRIOR APPLICATION NUMBER: JP 2001-272697  
 PRIOR FILING DATE: 2001-08-02  
 NUMBER OF SEQ ID NOS: 15109  
 SEQ ID NO 4416  
 LENGTH: 2316  
 TYPE: DNA  
 ORGANISM: Streptomyces avermitilis  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (1)..(2316)  
 US-10-156-761-4416

Query Match 14.8%; Score 37.4; DB 14; Length 2316;  
 Best Local Similarity 50.3%; Pred. No. 1.3;  
 Matches 89; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY 14 GGCCGGAGTGAAGCTGATCTCCTGCGCCTCCACCTCCAGCCGAGAGGCGCC 73  
 DB 1174 GGCCCTGACACACAGCTGCGGAGTGTGAGAGCCGACAGCCGCGCGGTCCGCGCGCC 1233  
 QY 74 CACGAGAGCCCGAGTGCAGCTTGCAGCGGTGTGGATCAGAGGACGAGGAGGA 133  
 DB 1234 CTCGAGAGACACACAGGATCCCGGTGCGCTTGCACACCTGCGCGGAGGAGGAG 1293  
 QY 134 GCGAGGAGTGCAGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCC 188  
 DB 1294 CTGTGTGTCTGCC 1348

## RESULT 32

US-09-918-995-27197/c  
 Sequence 27197, Application US/09918995  
 Publication No. US20030073623A1  
 GENERAL INFORMATION:  
 APPLICANT: Hyseq, Inc.  
 TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
 FROM VARIOUS CDNA LIBRARIES  
 FILE REFERENCE: 20411-756  
 CURRENT APPLICATION NUMBER: US/09/918,995  
 CURRENT FILING DATE: 2001-07-30  
 PRIOR APPLICATION NUMBER: US/09/235,076  
 PRIOR FILING DATE: 1999-01-20  
 NUMBER OF SEQ ID NOS: 38054  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 27197  
 LENGTH: 528  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: (1)..(528)  
 OTHER INFORMATION: n = A,T,C or G  
 US-09-918-995-27197

Query Match 14.8%; Score 37.2; DB 11; Length 528;  
 Best Local Similarity 50.3%; Pred. No. 2;  
 Matches 90; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

QY 69 GCGCCGAGGAGCCCGGAGTGCAGCTTGCAGCGGTGTGGATCAGAGGAGGAGC 128  
 DB 385 GCGCCGAGGAGCCCGGAGTGCAGCTTGCAGCGGTGTGGATCAGAGGAGGAGC 326  
 QY 129 AGGAGGAGGAGTGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCC 188

DB 325 GAAGCCGAGGAGCCCTGCGGCTGCGCCGACCTCTCTGCGAGGAGCCCTGAC 266  
 QY 189 NGAGGAGAGTCCCTTACCCGAGCCGAGCCGAGGAGGAGGAGGAGGAGGAGC 247  
 DB 265 AAGCCGAGGAGTCCGAGTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGC 207

## RESULT 33

US-10-029-386-7001  
 Sequence 7001, Application US/10029386  
 Publication No. US20030194704A1  
 GENERAL INFORMATION:

APPLICANT: Penn, Sharon G.  
 APPLICANT: Rank, David R.  
 APPLICANT: Hanzel, David K.  
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G  
 FILE REFERENCE: AEWICA-X-2  
 CURRENT APPLICATION NUMBER: US/10/029,386  
 CURRENT FILING DATE: 2001-12-20  
 NUMBER OF SEQ ID NOS: 34288  
 SOFTWARE: Annonax Sequence Listing Engine vers. 1.1  
 SEQ ID NO 7001  
 LENGTH: 526  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:

OTHER INFORMATION: MAP TO AC004080.1, SIGNAL = 3.4  
 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.9  
 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5  
 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4  
 OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 1.8  
 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.8  
 OTHER INFORMATION: NT HIT: US2827.1, EVALUATE 0.006+00  
 OTHER INFORMATION: SWISSPROT HIT: P31271, EVALUATE 3.006-23  
 OTHER INFORMATION: EST\_HUMAN HIT: AA160421.1, EVALUATE 8.006-41  
 US-10-029-386-7001

Query Match 14.7%; Score 37; DB 12; Length 526;  
 Best Local Similarity 51.9%; Pred. No. 2.2;  
 Matches 82; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 88 GTGCCGAGCTTGCAGCGTCTTGGATTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGC 147  
 DB 120 GTGTCAGGAGGAGTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGC 179  
 QY 148 CGCCCGGAGGAGTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGC 207  
 DB 180 AAGCCAGGAGGAGTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGC 239  
 QY 208 CCGGCGGAGGAGTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGC 245  
 DB 240 CCGAGGAGGAGGAGTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGC 277

## RESULT 34

US-10-156-761-4189  
 Sequence 4189, Application US/10156761  
 Publication No. US20030119018A1  
 GENERAL INFORMATION:

APPLICANT: OMURA, SATOSHI  
 APPLICANT: IKEDA, HARUO  
 APPLICANT: ISHIKAWA, JUN  
 APPLICANT: HORIKAWA, HIROSHI  
 APPLICANT: SHIBA, TADAYOSHI  
 APPLICANT: SAKAKI, YOSHIYUKI  
 APPLICANT: HATTORI, MASAHIRA  
 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
 FILE REFERENCE: 249-262  
 CURRENT APPLICATION NUMBER: US/10/156,761  
 CURRENT FILING DATE: 2002-05-29  
 PRIOR APPLICATION NUMBER: JP 2001-204089

PRIOR FILING DATE: 2001-05-30  
PRIOR APPLICATION NUMBER: JP 2001-272697  
PRIOR FILING DATE: 2001-08-02  
NUMBER OF SEQ ID NOS: 15109  
SEQ ID NO 4189  
LENGTH: 4437  
TYPE: DNA  
ORGANISM: Streptomyces avermitilis  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(4437)  
US-10-156-761-4189

Query Match 14.5%; Score 36.6; DB 14; Length 4437;  
Best Local Similarity 51.2%; Pred. No. 1.7; Mismatches 80; Indels 0; Gaps 0;  
Matches 84; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 84 CCCAGTCCCGACGTTGCGACGCTCTGGATCAGAGGACGAGCCAGGAGCTTCC 143  
DB 3428 CCCAGACGCGACGCTCTGCGACGACGAGCCGAGGAGGAGGAGGAGGAGGAGG 3487  
QY 144 GCGCGCCCGCCGCTCTGCGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 203  
DB 3488 GCGACGCTCTGCGACGCGCGCGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3547  
QY 204 TCACCGCGCGCGCGCTCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 247  
DB 3548 CCGCGCGAGTCCCGCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3591

RESULT 35  
US-09-769-734-49/c  
Sequence 49, Application US/09769734  
Publication No.: US20030143666A1  
GENERAL INFORMATION:  
APPLICANT: Ecopila Biosciences Inc.  
TITLE OF INVENTION: Genetic locus for Evernimolcin Biosynthesis  
FILE REFERENCE: PA 005-US  
CURRENT APPLICATION NUMBER: US/09/769,734  
CURRENT FILING DATE: 2001-01-26  
NUMBER OF SEQ ID NOS: 58  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 49  
LENGTH: 11115  
TYPE: DNA  
ORGANISM: M. carbonacei  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (8)..(1207)  
OTHER INFORMATION: ORF 41 (positive strandedness)  
OTHER INFORMATION: Incomplete: C-terminus only  
NAME/KEY: misc\_feature  
LOCATION: (1213)..(2331)  
OTHER INFORMATION: ORF 42 (positive strandedness)  
NAME/KEY: misc\_feature  
LOCATION: (2364)..(3611)  
OTHER INFORMATION: ORF 43 (positive strandedness)  
NAME/KEY: misc\_feature  
LOCATION: (3623)..(4243)  
OTHER INFORMATION: ORF 44 (positive strandedness)  
NAME/KEY: misc\_feature  
LOCATION: (4145)..(5177)  
OTHER INFORMATION: ORF 45 (positive strandedness)  
NAME/KEY: misc\_feature  
LOCATION: (5177)..(6094)  
OTHER INFORMATION: ORF 46 (negative strandedness)  
NAME/KEY: misc\_feature  
LOCATION: (6271)..(7824)  
OTHER INFORMATION: ORF 47 (negative strandedness)  
NAME/KEY: misc\_feature  
LOCATION: (7903)..(8760)  
OTHER INFORMATION: ORF 48 (negative strandedness)  
NAME/KEY: misc\_feature

LOCATION: (8781)..(9800)  
OTHER INFORMATION: ORF 49 (negative strandedness)  
US-09-769-734-49

Query Match 14.5%; Score 36.6; DB 12; Length 11115;  
Best Local Similarity 50.3%; Pred. No. 1.3; Mismatches 89; Indels 0; Gaps 0;  
Matches 90; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

QY 1 CGGCGCGGAGCGCGCGCGGAGTGAAGCTGATGCTCTGCGGCGCTCCACCTCCCGAG 60  
DB 8173 CGGCTGAGAGTGGCGCAGGAGGAGCTGGGCTCTGGCGGTCCCGCGAGCCTGAGCATGTCTCG 8114  
QY 61 CGCAGAGCGCGCCACAGAGACCCCGATGCGCGGAGCGTTCGACAGCTTGAGTCAAG 120  
DB 8113 CTGGAGCAGCTTCAGCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCA 8054  
QY 121 CAGGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 179  
DB 8053 CGTGACGAGTTCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 7995

RESULT 36  
US-10-187-900-3  
Sequence 3, Application US/10187900  
Publication No.: US20030166221A1  
GENERAL INFORMATION:  
APPLICANT: BEASLEY, Ellen M. et al  
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
FILE REFERENCE: CL001061  
CURRENT APPLICATION NUMBER: US/10/187,900  
CURRENT FILING DATE: 2002-07-03  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 16389  
TYPE: DNA  
ORGANISM: Human  
US-10-187-900-3

Query Match 14.5%; Score 36.6; DB 12; Length 16389;  
Best Local Similarity 48.1%; Pred. No. 1.2; Mismatches 110; Indels 0; Gaps 0;  
Matches 102; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

QY 2 GCGCGGAGGAGCGCGCGGAGTGAAGCTGATGCTCTGCGGCTTCCACTTCCAGGC 61  
DB 12683 GAGTGGGAGCCGTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 12742  
QY 62 GCAGAGCGCGCCACGAGAGACCCCTCAGTGGCGGAGCTTGCAGAGTGTGGATCAGAGGC 121  
DB 12743 CCAGAGAGATGCAACAGAGACCTGATGCTCTCTGAGCTGATCTGCACAGAGGC 12802  
QY 122 AGGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 181  
DB 12803 TGTACATTTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 12862  
QY 182 CCTACGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 213  
DB 12863 ACGCAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 12894

RESULT 37  
US-10-027-632-9421/c  
Sequence 9421, Application US/10027632  
Publication No.: US20030204075A9  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
TITLE OF INVENTION: Polymorphisms in the Human Genome  
FILE REFERENCE: 108927.129  
CURRENT APPLICATION NUMBER: US/10/027,632  
CURRENT FILING DATE: 2002-04-30



```
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 9421
; LENGTH: 1114
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-9421
```

```
Query Match
Best Local Similarity 14.4%; Score 36.4; DB 12; Length 1114;
Matches 91; Conservative 1; Mismatches 93; Indels 0; Gaps 0;
```

```
QY 16 CCGGAGTGAAGGCTGATGCTCCCTGCGCTTCACCTCCCAAGCGCGAAGGCGCCCA 75
DB 862 CTGCGGCTGTGAGTCTCTCCACAGGGGGCTTCTGAGACGAGGAGGTAGTCTCC 803
QY 76 CGAGGACCCCAAGTCCGCAAGTTCAGAGTGGATCAGAGGAGGAGGAGGAGC 135
DB 802 CGTCTCCAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 743
QY 136 CAGGAAGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 195
DB 742 CGGGAATTTGGCTTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 683
QY 196 AGCTC 200
DB 682 TCCTC 678
```

```
RESULT 38
US-10-027-632-9422/c
; Sequence 9422, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 9422
; LENGTH: 1114
; TYPE: DNA
```

```
; ORGANISM: Human
US-10-027-632-9422
Query Match
Best Local Similarity 14.4%; Score 36.4; DB 12; Length 1114;
Matches 91; Conservative 1; Mismatches 93; Indels 0; Gaps 0;
```

```
QY 16 CCGGAGTGAAGGCTGATGCTCCCTGCGCTTCACCTCCCAAGCGCGAAGGCGCCCA 75
DB 862 CTGCGGCTGTGAGTCTCTCCACAGGGGGCTTCTGAGACGAGGAGGTAGTCTCC 803
QY 76 CGAGGACCCCAAGTCCGCAAGTTCAGAGTGGATCAGAGGAGGAGGAGGAGGAGC 135
DB 802 CGTCTCCAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 743
QY 136 CAGGAAGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 195
DB 742 CGGGAATTTGGCTTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 683
QY 196 AGCTC 200
DB 682 TCCTC 678
```

```
RESULT 39
US-10-027-632-9421/c
; Sequence 9421, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 9421
; LENGTH: 1114
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-9421
```

```
Query Match
Best Local Similarity 14.4%; Score 36.4; DB 13; Length 1114;
Matches 91; Conservative 1; Mismatches 93; Indels 0; Gaps 0;
```

```
QY 16 CCGGAGTGAAGGCTGATGCTCCCTGCGCTTCACCTCCCAAGCGCGAAGGCGCCCA 75
DB 862 CTGCGGCTGTGAGTCTCTCCACAGGGGGCTTCTGAGACGAGGAGGTAGTCTCC 803
QY 76 CGAGGACCCCAAGTCCGCAAGTTCAGAGTGGATCAGAGGAGGAGGAGGAGGAGC 135
DB 802 CGTCTCCAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 743
QY 136 CAGGAAGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 195
DB 742 CGGGAATTTGGCTTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 683
QY 196 AGCTC 200
```

Fri Nov 7 08:10:00 2003

us-10-081-817a-19\_copy\_1\_252.rmpb

Page 16

Db 682 TCCTC 678

```
RESULT 40
US-10-027-632-9422/c
; Sequence 9422 Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 10827.139
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9422
; LENGTH: 1114
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-9422
```

Query Match 14.4% Score 36.4; DB 13; Length 1114;  
Best Local Similarity 49.2%; Pred No. 2.6; Mismatches 93; Indels 0; Gaps 0;  
Matches 91; Conservative 1;

```
QY 16 CCGGAGTGAAGCTGATGCTCCCTGCGCTTCCAGGCGGAGGAGGCGCCCA 75
Db 862 CTGCGGCTCTGCTCTCTCCCAAGGGGCTTCTGAGAGCGAGGCGAGGTATCCC 803
QY 76 CAGAGACCCCGAAGTCCCGAGTTGCCAGGTCGTGGATCAGAGGAGCCAGGAGC 135
Db 802 CGTCTCCAGCCAGCCAGGCGCGCCAGAGAGGGATCTCCCAATCTGCCCCGTACG 743
QY 136 CAGGAACTGGCGCGCCCGCCCTGAGCGCGAGGAGAACTTCCCTCACCAGAGGA 195
Db 742 CCGGAATTGCTTACGCGCCCGCGGCTCTCCGAAAGAGAGCTCTCCACCTTTAGGC 683
QY 196 AGCTC 200
Db 682 TCCTC 678
```

Search completed: November 6, 2003, 10:39:32  
Job time : 212.322 secs



/mol\_type="mRNA"  
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/clone="CS0DF027YD08"  
/issue\_type="FETAL BRAIN"  
/dev\_stage="fetal"  
/clone\_id="Homo sapiens FETAL BRAIN"  
/note="Organ: brain; Vector: PCWVSPT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the PCWVSPT 6 vector. Library was not normalized."  
76 a 322 c 351 g 32 t 143 others

Query Match 22.2%; Score 56; DB 13; Length 924;  
Best Local Similarity 41.2%; Pred. No. 0.14; Mismatches 89; Conservative 35; Indels 0; Gaps 0;

14 GGGCGGAGTGGCTGATGCTGCTGCGGCTCCCACTCCAGCGGAGAGGCGC 73  
Db 609 GCGCGGG 668  
Qy 74 CACAGAGACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 133  
Db 669 GCGCGGG 728  
Qy 134 GCGGAGAACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 193  
Db 729 GCGGG 788  
Qy 194 GAAGCTCCCTCACTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 229  
Db 789 GCGCGGG 824

RESULT 2  
BX425797 828 bp mRNA linear EST 15-MAY-2003  
LOCUS BX425797 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone  
DEFINITION CLOBB0302E01 3-PRIME, mRNA sequence.  
ACCESSION BX425797  
VERSION BX425797.1 GI:30784485  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 828)  
L.I.W.B., Gruber, C., Jesses, V. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished  
Contact: Centre National de Sequencage  
Genoscope - Centre National de Sequencage  
BP 191 91006 Evry cedex - France  
Email: seqref@genoscope.cns.fr Web: www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 8556.f For  
more information about this cluster, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CLOBB0302E01P1&cluster=8556.f. Contact :  
Feng Liang Email: fliang@life.com URL: http://fulllength.invitrogen.com/Invitrogen Corporation 1600  
Paradey Avenue Genoscope sequence ID : CLOBB0302E01P1.

FEATURES  
Source  
1..828  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CLOBB0302E01"  
/issue\_type="NEUROBLASTOMA"  
/clone\_id="Homo sapiens NEUROBLASTOMA"  
/note="Vector: PCWVSPT 6; 1st strand cDNA was primed  
with a NotI-oligo(dT) primer. Five prime end enriched,

double-strand cDNA was digested with Not I and cloned into  
the Not I and EcoRV sites of the PCWVSPT 6 vector.  
Library was not normalized."  
BASE COUNT 88 a 191 c 161 g 181 t 207 others  
ORIGIN

Query Match 22.1%; Score 55.8; DB 13; Length 828;  
Best Local Similarity 36.4%; Pred. No. 0.16; Mismatches 72; Conservative 49; Indels 0; Gaps 0;

Qy 41 GGGCGCTCCACCTCCCGAGCGGAGAGGCGCCACAGAGACCCAGTCCCGACCTTG 100  
Db 341 GGGCGCTCCACCTCCCGAGCGGAGAGGCGCCACAGAGACCCAGTCCCGACCTTG 400  
Qy 101 CCACGCTGCTGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 160  
Db 401 CCGMAAMVSS 460  
Qy 161 GCGCTGCGGAG 220  
Db 461 CCCCCCGGG 520  
Qy 221 GCAGGG 238  
Db 521 GGG 538

RESULT 3  
BX384405/c 559 bp mRNA linear EST 08-MAY-2003  
LOCUS BX384405 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens  
DEFINITION CDNA clone CS0DK009Y1P 3-PRIME, mRNA sequence.  
ACCESSION BX384405  
VERSION BX384405.1 GI:30460453  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 559)  
L.I.W.B., Gruber, C., Jesses, V. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished  
Contact: Centre National de Sequencage  
Genoscope - Centre National de Sequencage  
BP 191 91006 Evry cedex - France  
Email: seqref@genoscope.cns.fr Web: www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 10148.f For  
more information about this cluster, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CS0DK009Y1P1&cluster=10148.f. Contact :  
Feng Liang Email: fliang@life.com URL: http://fulllength.invitrogen.com/Invitrogen Corporation 1600  
Paradey Avenue Genoscope sequence ID : CS0DK009Y1P1.

FEATURES  
Source  
1..559  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0DK009Y1P"  
/issue\_type="HELA CELLS COT 25-NORMALIZED"  
/cell\_line="HELA"  
/clone\_id="Homo sapiens HELA CELLS COT 25-NORMALIZED"  
/note="1st strand cDNA was primed with a NotI-oligo(dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and cloned into the Not I and EcoRV  
sites of the PCWVSPT 6 vector. Library was normalized."  
BASE COUNT 92 a 88 c 106 g 94 t 179 others  
ORIGIN

Query Match 21.8%; Score 55; DB 13; Length 559;  
Best Local Similarity 17.3%; Pred. No. 0.22;

```

Matches 32; Conservative 97; Mismatches 56; Indels 0; Gaps 0;
QY 54 CCCAGCGCAGAGAGCGCCACAGAGACCCCGAGTGCCTGCGACGCTTGGA 113
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 559 SCCGTCACATVAVVACACCCACSSSSSSSSSSSSSSSSSSSSSSSCA 500
QY 114 TCAGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 173
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 499 SASASSSSCVASSSSCCSSSSSSSSSSSSSCAASSSSSSSSSCSSSSSS 440
QY 174 GAGAGCTCCCTGACCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 233
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 439 SSSSSSSSSSCACACCCSSSSSCSSSSSCCCGACCCSSSSSSSCSSSS 380
QY 234 TGGGG 238
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 379 VSSSS 375

RESULT 4
CN80091P/c 925 bp DNA linear GSS 03-JUN-1999
LOCUS DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR19D16 of RPECI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL053013.1 GI:4934461
VERSION GSS.
KEYWORDS Drosophila melanogaster (fruit fly)
SOURCE Drosophila melanogaster
ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 925)
REFERENCE Genoscope.
AUTHORS Direct Submission
TITLE Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE [E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr]
COMMENT Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutyo Osogawa and
Aaron Mamoser in Peter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPECI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
P1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila\_bac.htm.
FEATURES
source
1..925
location/Qualifiers
1..925
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR19D16"
/clone_lib="RPECI-98"
/note="end : TET3"

BASE COUNT 120 a 61 c 172 t 511 others
ORIGIN
Query Match 20.8%; Score 52.4; DB 29; Length 925;
Best Local Similarity 11.8%; Pred. No. 0.73;
Matches 28; Conservative 128; Mismatches 82; Indels 0; Gaps 0;
QY 1 CGGCGGAGGAGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 60
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 875 SSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS 816

Matches 32; Conservative 97; Mismatches 56; Indels 0; Gaps 0;
QY 61 CGCAGAGCGCCACAGAGACCCCGAGTGCCTGCGACGCTTGGA 120
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 815 GAGACRGGGAGGAGASASSSSSSSACBSSSSSSACBSSSSSSSSSSSS 756
QY 121 CAGGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 755 SSSSSSSSSSASASVVSASSSSSSSSSSSSSSSSSSSSSSSSSSSS 696
QY 181 CCTCACCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 238
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 695 ASGASGCGCTGACGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 638

RESULT 5
BX415111/c 982 bp mRNA linear EST 15-MAY-2003
LOCUS DEFINITION BX415111 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP004Y120
5-PRIME, mRNA sequence.
ACCESSION BX415111
VERSION BX415111.1 GI:30765470
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 982)
REFERENCE Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
AUTHORS Full-length cDNA libraries and normalization
TITLE Unpublished
JOURNAL Contact: Genoscope
COMMENT Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : filang@lifestech.com URL :
http://fulllength.invitrogen.com/
Faraday Avenue Genoscope sequence ID : CS0CAP004BE10P1.
FEATURES
source
1..982
location/Qualifiers
1..982
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/db_xref="taxon:9606"
/clone="CS0CAP004Y120"
/issue_type="THYMUS"
/clone_lib="Homo sapiens THYMUS"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

BASE COUNT 177 a 257 c 323 g 18 t 207 others
ORIGIN
Query Match 20.8%; Score 52.4; DB 13; Length 982;
Best Local Similarity 32.0%; Pred. No. 0.73;
Matches 72; Conservative 60; Mismatches 93; Indels 0; Gaps 0;
QY 8 GAGGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 67
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 547 GGGGGGGSSGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 488
QY 68 GGGCGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 127
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 487 CCCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 428
QY 128 CAGGAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 187
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 427 CCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 368
QY 188 CAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 232
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 367 SSGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 323

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Fri NOV 7 08:10:01 2003

us-10-081-817a-19 copy 1 252.rst

Page 4

[illegible]

ACCESSION	EX403654	GI:30762430	
VERSION	EX403654.1		
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1. (base 1 to 1103)		
AUTHORS	L.A. M.B., Gruber, C., Jesses, J. and Polayes, D.		
TITLE	Full-length cDNA libraries and normalization		
JOURNAL	Unpublished		
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 Evry cedex - France Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr Library was constructed by life technologies, a division of Invitrogen. Contact : Feng Jiang Email : fjiang@lifetech.com URL : http://fulllength.invitrogen.com/Invitroden Corporation 1600 Faraday Avenue Genoscope sequence ID : CLOB40072H12PPI. Location/Qualifiers 1. 1103		
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	/clone="CLOB40072H12"		
	/cissue_type="PLACENTA"		
	/clone_lib="Homo sapiens PLACENTA"		
	/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."		
BASE COUNT	194 a 34 c 310 g 269 t	296 others	
ORIGIN			
Query Match	20.64; Score 51.8; DB 13; Length 1103;		
Best Local Similarity	26.34; Pred. No. 0.95; 71; Indels 0; Gaps 0;		
Matches	51; Conservative 72; Mismatches		
OY	26 GGCCTGATGCTCCCTGCGCGCTTCACCTCCCGAGCGCAGAGAGCGCCACGAGACCC 85		
Db	494 SSSSTSS 435		
OY	86 CAGTGCCTGCGAGCTTGCCAGCGATGAGATCAGAGCGAGGACCGAGGAGCTGAGACTGC 145		
Db	434 SSS 375		
OY	146 GCCGCCCCCGCCCTGCGCTGCGCGAGCGAGGAGAGCTCTCCACGAGGAGAGCTCCCTC 205		
Db	374 CCCCCSS 315		
OY	206 ACCCGAGCCGAGCC 219		
Db	314 CCCCCCCCCCCCC 301		
RESULT 8			
EX415111	982 bp	mRNA	linear
LOCUS	EX415111	Homo sapiens	THYMUS
DEFINITION	5-PRIME mRNA sequence.	Homo sapiens	cDNA clone
ACCESSION	EX415111	GI:30765470	
VERSION	EX415111.1		
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1. (bases 1 to 982)		
AUTHORS	L.A. M.B., Gruber, C., Jesses, J. and Polayes, D.		
TITLE	Full-length cDNA libraries and normalization		
JOURNAL	Unpublished		
COMMENT	Contact: Genoscope		







[illegible][illegible]

QY 186 ACCNAGAGGAGAGCTCCCTCAGCCCGGCGGAGGCGGCGG 231  
Db 295 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 340

## RESULT 15

LOCUS BX462440 Homo sapiens T CELLS (JURKAT CELL LINE) Homo sapiens cDNA  
DEFINITION clone CS0DH002ZH23 3-PRIME, mRNA sequence.  
ACCESSION BX462440.1 GI:31019574  
VERSION EST.  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1, W.B., Gruber, C., Jessee, J. and Polyes, D.  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
1 (bases 1 to 1201)  
Full-length cDNA libraries and normalization  
Unpublished  
JOURNAL  
COMMENT Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 9865.f  
Contact: Feng Liang Email: fliang@lifetech.com URL:  
http://fulllength.invitrogen.com/InvitrogenCorporation 1600  
Faraday Avenue Genoscope sequence ID: CS0DH002CD12NP1.  
Location/Qualifiers

FEATURES  
source 1. 1201  
/organism="Homo sapiens"  
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/clone="CS0DH002ZH23"  
/issue\_type="T CELLS (JURKAT CELL LINE)"  
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/clone\_lib="Homo sapiens T CELLS (JURKAT CELL LINE)"  
/note="Vector: PCWVSPORT 6; 1st strand cDNA was primed  
with a NotI-oligo(dT) primer. Five prime end enriched,  
double-strand cDNA was digested with Not I and cloned into  
the Not I and EcoRV sites of the pCMVSPORT 6 vector.  
Library was not normalized."

BASE COUNT 225 a 332 c 293 g 245 t 106 others  
ORIGIN

Query Match 19.9%; Score 50.2; DB 13; Length 1201;  
Best Local Similarity 40.3%; Pred. No. 2;  
Matches 94; Conservative 35; Mismatches 104; Indels 0; Gaps 0;

QY 6 GGGAGAGCGCGCGGAGTGAAGCTGATGCTCCCTGAGCGCTCAACCTCCCGAGCGGCG 65  
Db 1198 GGTTGTCGCGCGCGGCGGCGGCGGCTTCYGGGKTTTSCSYCCCTCCSTGGGKGGGGGTTK 1139  
QY 66 AAGCGCGCCACGACGAGACCCCGACGTTGCGACGATCTGCGATCAGAGGACAGG 125  
Db 1138 KKGSCCGCGTGGGCGGCTTTCAGAGGCGGCGCCCTGCGGCGGCGGCGGCGGCGG 1079  
QY 126 ACCAGGAGACCGAGACTGCGCGCGCGCGCGCGCGCTGCGCGGAGGAGAGCTCCCTC 185  
Db 1078 GGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1019  
QY 186 ACCNAGAGGAGAGTCCCTCAGCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 238  
Db 1018 SSSBKKGCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 966

RESULT 16  
BX425080/c 1165 bp mRNA 11near EST 15-MAY-2003  
LOCUS BX425080 Homo sapiens PLACENTA Homo sapiens cDNA clone Cl0BA0092FP07  
DEFINITION 3-PRIME, mRNA sequence.

ACCESSION BX425080  
VERSION BX425080.1 GI:30772433  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1, W.B., Gruber, C., Jessee, J. and Polyes, D.  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
1 (bases 1 to 1165)  
Full-length cDNA libraries and normalization  
Unpublished  
JOURNAL  
COMMENT Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 10451.f For  
more information about this cluster, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=Cl0BA0092FP07P1&cluster=10451.f. Contact :  
Feng Liang Email: fliang@lifetech.com URL:  
http://fulllength.invitrogen.com/InvitrogenCorporation 1600  
Faraday Avenue Genoscope sequence ID: Cl0BA0092FP07P1.  
Location/Qualifiers

FEATURES  
source 1. 1165  
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/clone\_lib="Homo sapiens PLACENTA"  
/note="Vector: PCWVSPORT 6; 1st strand cDNA was primed  
with a NotI-oligo(dT) primer. Five prime end enriched,  
double-strand cDNA was digested with Not I and cloned into  
the Not I and EcoRV sites of the pCMVSPORT 6 vector.  
Library was not normalized."

BASE COUNT 270 a 69 c 221 g 273 t 332 others  
ORIGIN

Query Match 19.7%; Score 49.6; DB 13; Length 1165;  
Best Local Similarity 17.1%; Pred. No. 2.6; 75; Indels 0; Gaps 0;  
Matches 35; Conservative 95; Mismatches 75; Indels 0; Gaps 0;

QY 7 GGGAGCGCGCGGAGTGAAGCTGATGCTCCCTGAGCGCTCAACCTCCCGAGCGGCGG 66  
Db 614 SSSSSSSSSSSSSSSSSSSSSSCCTTTTTSSSSSSSSSSSSSSSSSSSSSSSSSSSSS 555  
QY 67 AGCGCGCCACGAGACCCCGAGTGCCTGCGACGTTGCCACGCTGTGAGTCAAGGACG 126  
Db 554 SSSSSSSSSSSSSSSSSSSSSSBTSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS 495  
QY 127 CAGAGGAGCGAGACTGCGCGCGCGCGCGCGCGCGCTGCGCGGAGGAGAGCTCCCTCA 186  
Db 494 CCGSCCG 435  
QY 187 CCNAGAGGAGAGTCCCTCAGCCCGG 211  
Db 434 SSSSBKKGKKTTCCTCCCGCGG 410

RESULT 17  
CNS0200G 879 bp DNA 11near GSS 01-SEP-2000  
LOCUS CNS0200G Tetradodon nigroviridis genome survey sequence T7 end of clone  
DEFINITION 15806 of library G from Tetradodon nigroviridis, genomic survey  
sequence.  
ACCESSION AL209545.1 GI:7868364  
VERSION  
KEYWORDS GSS; genome survey sequence.  
SOURCE Tetradodon nigroviridis  
ORGANISM Tetradodon nigroviridis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

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REFERENCE
AUTHORS      1 Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
               Tetraodontidae; Tetraodontidae; Tetraodon.
TITLE        2 Roest Crolius, H., Jallion, O., Dasilva, C., Bouneau, L., Fisher, C.,
               Bernot, A., Fizes, C., Wincker, P., Broctier, P., Quetier, F.,
               Saurin, W. and Weissenbach, J.
               Estimate of human gene number provided by genome-wide analysis
               using Tetraodon nigroviridis DNA sequence
JOURNAL      20296633
MEDLINE      20296633
PUBMED       10835645
REFERENCE
AUTHORS      2 Roest Crolius, H., Jallion, O., Dasilva, C., Ozouf-Costaz, C.,
               Fizes, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F.,
               Saurin, W., Bernot, A. and Weissenbach, J.
               Characterization and repeat analysis of the compact genome of the
               freshwater pufferfish Tetraodon nigroviridis
JOURNAL      Genome Res. 10 (7), 939-949 (2000)
MEDLINE      10899143
PUBMED       10899143
REFERENCE
AUTHORS      3 (bases 1 to 879)
TITLE        Genoscope.
               Direct Submission
               Submitted (12-Apr-2000) Genoscope - Centre National de Sequencage :
               BP 191 91006 Evry cedex - FRANCE (E-mail : segre@genoscope.cns.fr
               - Web : www.genoscope.cns.fr)
               This sequence is a single read and was generated as part of a large
               scale clone-end sequencing project of the Tetraodon nigroviridis
               genome. For more information, please take a look at
               http://www.genoscope.cns.fr/Tetraodon.
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source       1..879
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               /clone_1ib="G"
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               /note="Genoscope sequence ID : COAG158B031P1-end : 77"
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ORIGIN
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Best Local Similarity 47.1%; Pred. No. 2.8;
Matches 104; Conservative 12; Mismatches 105; Indels 0; Gaps 0;
QY          13 CGCGCGGAGTGAAGCGCTGATGTCCTCGCGCCCTTCACCTCCCGAGCGCCAGAAAGCGC 72
Db          627 CGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 686
QY          73 CCACAGAGACCCCGAGTGGCGACGTTGCCACGATCTGGATCAGAGCGAGACACAGGG 132
Db          687 GCGCGGGGSCCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 746
QY          133 AGCCAGAGAACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 192
Db          747 CGSCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 806
QY          193 GGAAGCTCCCTCACCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 233
Db          807 GCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 847

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REFERENCE
AUTHORS      1 (bases 1 to 1169)
TITLE        NIH-MGC http://mgs.nci.nih.gov/.
               National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished
COMMENT       Contact: Robert Strausberg, Ph.D.
               Email: cgabs-r@mail.nih.gov
               Tissue Procurement: Life Technologies, Inc.
               CDNA Library Preparation: Life Technologies, Inc.
               CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
               DNA Sequencing by: Agencourt Bioscience Corporation
               Clone distribution: MGC clone distribution information can be
               found through the I.M.A.G.E. Consortium/LLNL at:
               http://image.llnl.gov
               Plate: LLAM12769 row: 1 column: 01
               High quality sequence stop: 334.
FEATURES
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               /clone_1ib="IMAGE:5745864"
               /issue_type="leukocyte"
               /lab_host="DH10B"
               /clone_1ib="NIH-MGC_118"
               /note="Vector: pCMV-SPORT6, Site 1: NotI, Site 2: EcoRV
               (destroyed); RNA source: leukocytes from anonymous pool of
               non-activated adult donors. Library is oligo-dT primed
               and directionally cloned (EcoRV site is destroyed upon
               cloning). Average insert size 1.7 kb, insert size range
               1.2-3.3 kb. Library is normalized and enriched for
               full-length clones and was constructed by C. Gruber
               (Invitrogen). Research Genetics tracking code 027. Note:
               this is a NIH MGC Library."
BASE COUNT   78 a 391 c 585 g 65 t 50 others
ORIGIN
Query Match 19.5%; Score 49.2; DB 12; Length 1169;
Best Local Similarity 49.0%; Pred. No. 3.1;
Matches 123; Conservative 0; Mismatches 128; Indels 0; Gaps 0;
QY          2 GCGCGGGGAGGGGGGGGGGGAGTGAAGCGCTGATGTCCTCGGGGCGCTTCACCTCCCGAGCG 61
Db          595 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 654
QY          62 GCGAAGGGCGCCCGACAGACACCCCGAGTGGCGACGTTGCCACGATCTGGATCAGAGGC 121
Db          655 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 714
QY          122 AGGACCAAGAGAGCGAGAACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 181
Db          715 GAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 774
QY          182 CTTACACNAGAGGAGTCTCCCTCACCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 241
Db          775 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 834
QY          242 GACCGCAAGC 252
Db          835 GCNGGGGGGNGC 845

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```

RESULT 19
LOCUS      CNS006XK
DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC #
ACCESSION AL066051
VERSION    AL066051.1 GI:4945019
KEYWORDS   Drosophila melanogaster (fruit fly)
SOURCE     Drosophila melanogaster
ORGANISM   Drosophila melanogaster

```

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
1 (bases 1 to 935)  
Genoscope.  
Direct Submission  
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr - Web : www.genoscope.cns.fr)  
determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).  
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs for further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoko Ohsawa and Aaron Hammoser in Pictet de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's pi and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

## FEATURES

source

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/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7227"  
/clone\_lib="RPCI-98"  
/note="end : T7"  
Location/Qualifiers

BASE COUNT 257 a 170 c 162 g 96 t 250 others  
ORIGIN  
Query Match 19.4%; Score 49; DB 29; Length 935;  
Best Local Similarity 31.7%; Pred. No. 3.3; Mismatches 99; Indels 0; Gaps 0;  
Matches 73; Conservative 58; Mismatches 99; Indels 0; Gaps 0;

QY 3 GCGGGGAGGCGCGGAGTGAAGCTGATGCTGCTGCGGCTCCACCTCCAGGCG 62  
DB 694 GCGGGGAGGCGCGGAGTGAAGCTGATGCTGCTGCGGCTCCACCTCCAGGCG 753  
QY 63 CAGAGGCGCGCGGAGTGAAGCTGATGCTGCTGCGGCTCCACCTCCAGGCG 122  
DB 754 CCGCGCGCGGAGTGAAGCTGATGCTGCTGCGGCTCCACCTCCAGGCG 813  
QY 123 GCGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 182  
DB 814 CCGGGGAGGCGCGGAGTGAAGCTGATGCTGCTGCGGCTCCACCTCCAGGCG 873  
QY 183 CTCACCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 232  
DB 874 SSGGGSSSSGSGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 923

RESULT 20  
CNS0154/c 1203 bp DNA linear GSS 26-JUL-1999  
LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC  
DEFINITION BACN15E10 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.  
ACCESSION AL106054.1 GI:5619805  
VERSION AL106054  
KEYWORDS GSS.  
SOURCE Drosophila melanogaster (fruit fly)  
ORGANISM Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
REFERENCE 1 (bases 1 to 1203)  
AUTHORS Genoscope.  
TITLE Direct Submission

JOURNAL  
COMMENT

Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr - Web : www.genoscope.cns.fr)  
determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - <http://www.edgp.ebi.ac.uk> - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billand at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Rayan. It has been constructed in the vector peloBAC11.

## FEATURES

source

1..1203  
/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7227"  
/clone\_lib="DrosBAC"  
/plasmid="peloBAC11"  
/note="end : T7"  
Location/Qualifiers

BASE COUNT 154 a 274 c 380 g 158 t 237 others  
ORIGIN  
Query Match 19.4%; Score 49; DB 29; Length 1203;  
Best Local Similarity 36.1%; Pred. No. 3.3; Mismatches 87; Conservative 46; Mismatches 108; Indels 0; Gaps 0;

QY 7 GCGAGCGCGCGGAGTGAAGCTGATGCTGCTGCGGCTCCACCTCCAGGCGCAGA 66  
DB 1196 GCGGGGAGGCGCGGAGTGAAGCTGATGCTGCTGCGGCTCCACCTCCAGGCGC 1137  
QY 67 AGCGGCCACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 126  
DB 1136 GCGGGGAGGCGCGGAGTGAAGCTGATGCTGCTGCGGCTCCACCTCCAGGCGC 1077  
QY 127 CAGAGGCGCGGAGTGAAGCTGATGCTGCTGCGGCTCCACCTCCAGGCGCAGA 186  
DB 1076 GCGGGGAGGCGCGGAGTGAAGCTGATGCTGCTGCGGCTCCACCTCCAGGCGC 1017  
QY 187 CCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 246  
DB 1016 CCGGGGAGGCGCGGAGTGAAGCTGATGCTGCTGCGGCTCCACCTCCAGGCGC 957  
QY 247 C 247  
DB 956 C 956

RESULT 21  
CNS00720/c 932 bp DNA linear GSS 03-JUN-1999  
LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC #  
DEFINITION BACR14B09 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.  
ACCESSION AL066742.1 GI:4945205  
VERSION AL066742  
KEYWORDS GSS.  
SOURCE Drosophila melanogaster (fruit fly)  
ORGANISM Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
REFERENCE 1 (bases 1 to 932)  
AUTHORS Genoscope.  
TITLE Direct Submission  
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr - Web : www.genoscope.cns.fr)  
determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).  
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila

melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCL-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw ap, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

## FEATURES

source

1. 932  
/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7227"  
/clone="BACH1AB09"  
/clone\_lib="RPCL-98"  
/note="end : 17"

BASE COUNT 155 a 202 c 241 g 91 t 243 others  
ORIGIN

Query Match 19.4%; Score 48.8; DB 29; Length 932;  
Best Local Similarity 35.0%; Pred. No. 3.6;  
Matches 90; Conservative 62; Mismatches 100; Indels 5; Gaps 1;

QY 1 CGGCGGGAGGCGGCGGAGTGAAGCTGATGCTGCTGCGGCTCCACCTCCCGAG 60  
DB 715 CGGSCGSGCGCGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 656  
QY 61 CCAGAGAGGCGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120  
DB 655 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 596  
QY 121 CAGGAGCAG 175  
DB 595 CAVARAAVAVSCCCGCCMASCCCGCGVSGCGSCGSCGSCGSCGSCGSCGSCG 536  
QY 176 AAGCTCCCTCACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 235  
DB 535 CAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 476  
QY 236 GCGTCGAGCGGAGAGC 252  
DB 475 CCGAGAGCGGAGAGC 459

RESULT 22  
AG074680/c 986 bp DNA linear GSS 03-NOV-2001  
LOCUS AG074680  
DEFINITION Pan troglodytes DNA, clone: PTB-066N16.R, genomic survey sequence.  
ACCESSION AG074680  
VERSION AG074680.1 GI:16626482  
KEYWORDS GSS.  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.  
1 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.  
BAC end sequences of library PTB  
Unpublished  
2 (bases 1 to 986)  
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.  
Direct Submission  
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC), Japan  
1-7-22 Suehiro-chou, Tsukuba, Ibaraki, 305-8565, Japan  
Tel: 81-45-503-9111, Fax: 81-45-503-9110  
E-mail: [chimpesgsc.riken.go.jp](mailto:chimpesgsc.riken.go.jp) URL: <http://hgp.gsc.riken.go.jp/>  
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of

COMMENT

clone tracking errors.

PRIMERS  
Sequencing: M13revLIBRARY  
Vector : pKSI45

R.Site 1 : SacI

R.Site 2 : SacI

Location/Qualifiers

1. 986

/organism="Pan troglodytes"

/mol\_type="genomic DNA"

/db\_xref="taxon:9598"

/clone="PTB-066N16.R"

/sex="male"

/cell\_type="lymphoblast"

/clone\_lib="PTB Chimpanzee Male BAC library"

BASE COUNT 15 a 433 c 495 g 10 t 33 others

ORIGIN

Query Match 19.4%; Score 48.8; DB 29; Length 986;  
Best Local Similarity 50.2%; Pred. No. 3.6;  
Matches 116; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

QY 2 GCGCGGAGGCGGCGGAGTGAAGCTGATGCTGCTGCGGCTCCACCTCCCGAG 61  
DB 414 GCGGCGGCGGCGGCGGAGTGAAGCTGATGCTGCTGCGGCTCCACCTCCCGAG 355  
QY 62 GCAGAGGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 121  
DB 354 GCGGCGGCGGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 295  
QY 122 AGGAGACAG 181  
DB 294 CCGGCGGCGGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 235  
QY 182 CCGGCGGCGGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 232  
DB 234 CCGGCGGCGGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 184

RESULT 23  
B0712096/c 902 bp RNA linear EST 16-JUL-2002  
LOCUS B0712096  
DEFINITION AGENCOURT\_8351502 NIH\_MGC\_113 Homo sapiens CDNA clone IMAGE:8282461  
ACCESSION B0712096  
VERSION B0712096.1 GI:21850995  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 902)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: Dr. Mark Watson  
CDNA Library Preparation: Rubin Laboratory  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LMC2476 row: 0 column: 06  
High quality sequence start: 4  
High quality sequence stop: 526.  
Location/Qualifiers

1. 902  
/organism="Homo sapiens"  
/mol\_type="RNA"  
/db\_xref="taxon:9606"

/clone="IMAGE:6282461"  
/lab host="PH10B (phage-resistant)"  
/clone.lib="NIH\_MGC.113"  
/note="Organ: E. coli; Vector: pOTM7; Site 1: XhoI; Site 2:  
EcoRI; CDNA made by oligo-dT priming. Directionally cloned  
into EcoRI/XhoI sites using the following 5' adaptor:  
GGCAGCAG(G) library constructed by Ling Hong in the  
laboratory of Gerald M. Rubin (University of California,  
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and  
SuperScript II RT (Life Technologies). Note: this is a  
NIH\_MGC library."  
BASE COUNT 85 a 403 c 271 g 123 t 20 others

Query Match 19.3%; Score 48.6; DB 13; Length 902;  
Best Local Similarity 49.4%; Pred. No. 4;  
Matches 114; Conservative 0; Mismatches 117; Indels 0; Gaps 0;  
QY 5 CGGGGAGGCGCGCGGAGTGAAGCTGATGCTCTGCGGCTTCCAGCTCCAGAGCGCA 64  
DB 793 CGGAGAGGCGCGCGCGGAGGAGCCGAGAGAGCGCGCGCGCGCGCGAGAGCGG 734  
QY 65 GAAGCGCGCGCGCGCGGAGAGCGCGCGAGGTTGCGAGGTTGAGTCAAGAGCAG 124  
DB 733 GAAGGCGCGCGCGCGGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGG 674  
QY 125 GACGAGGAGAGCGCGAGAGTCCGCGCGCGCGCGCGCGCGCGCGCGAGAGAGCTCCT 184  
DB 673 GCGCGCGCGCGCGCGGAGAGGAGGCGCGCGCGCGCGCGCGCGCGCGCGAGAGGCGG 614  
QY 185 CACGAGGAGAGAGTCCCTCAAGCGCGCGCGCGCGCGCGCGCGCGCGAGGAGGCGG 235  
DB 613 GGGGCGCGCGCGAGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGGAGG 563

RESULT 24  
BX391246 1061 bp mRNA linear EST 13-MAY-2003  
LOCUS BX391246 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA  
DEFINITION clone:CS0D10081N19.3-PRIME, mRNA sequence.  
ACCESSION BX391246  
VERSION BX391246.1 GI:30615383  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1061)  
L.I.W.B., Gruber, C., Jessee, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr; Web: www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 7394.f. For  
more information about this cluster, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CS0BAH012ZH06NP1&cluster=7394.f. Contact :  
Feng Liang Email: fliang@life.techn.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Faraday Avenue Genoscope sequence ID : CS0BAH012ZH06NP1.  
Location/Qualifiers  
1. 1061  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
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/tissue\_type="PLACENTA COT 25-NORMALIZED"  
/note="1st strand CDNA was primed with a NotI-oligo(dT)  
primer. Five prime end enriched, double-strand CDNA was

digested with Not I and cloned into the Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized."  
BASE COUNT 225 a 153 c 229 g 289 t 165 others

Query Match 19.3%; Score 48.6; DB 13; Length 1061;  
Best Local Similarity 29.9%; Pred. No. 4;  
Matches 64; Conservative 62; Mismatches 88; Indels 0; Gaps 0;  
QY 1 CGGCGGAGGAGCGCGCGGAGTGAAGCTGATGCTCTGCGGCTTCCAGCTCCAGAG 60  
DB 584 CGCCCGGAGGAGCGCGCGGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 525  
QY 61 CGGAGAGGCGCGCGCGGAGAGCGCGCGAGTCCCGAGCTTGCAGGCTTGGAGTCAAG 120  
DB 524 CCGCGCGCGCGCGCGGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGG 465  
QY 121 CAGGAGCAGAGAGCGCGAGAGTGCAGCGCGCGCGCGCGCGCGCGCGCGCGAGAGCT 180  
DB 464 SSSCGSSSSSSSSCGSSCGSSCGSSCGSSCGSSCGSSCGSSCGSSCGSSCGSSCG 405  
QY 181 CCTCAACGAGGAGAGCTCCCTCAAGCGCGCGCGCGCGCGCGCGCGCGCGAGGCT 214  
DB 404 CCGCGCGCGCGCGCGGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGG 371

RESULT 25  
AL514261 1201 bp mRNA linear EST 08-MAY-2003  
LOCUS AL514261 Homo sapiens NEUROBLASTOMA Homo sapiens CDNA clone  
DEFINITION AL514261 Homo sapiens NEUROBLASTOMA Homo sapiens CDNA clone  
ACCESSION AL514261  
VERSION AL514261.2 GI:30464146  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1201)  
L.I.W.B., Gruber, C., Jessee, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished  
On Feb 13, 2001 this sequence version replaced gi:12777755.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr; Web: www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 9246.r for  
more information about this cluster, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CL0BB007ZG11P1&cluster=9246.r. Contact :  
Feng Liang Email: fliang@life.techn.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Faraday Avenue Genoscope sequence ID : CL0BB007ZG11P1.  
Location/Qualifiers  
1. 1201  
/organism="Homo sapiens"  
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/db\_xref="taxon:9606"  
/clone="CL0BB007ZG11"  
/tissue\_type="NEUROBLASTOMA"  
/note="Vector: pCMVSPORT 6; 1st strand CDNA was primed  
with a NotI-oligo(dT) primer. Five prime end enriched,  
double-strand CDNA was digested with Not I and cloned into  
the Not I and EcoRV sites of the pCMVSPORT 6 vector.  
Library was not normalized."

BASE COUNT 161 a 217 c 183 g 354 t 286 others  
Query Match 19.3%; Score 48.6; DB 9; Length 1201;  
Best Local Similarity 40.4%; Pred. No. 4;

Matches		92;	Conservative	33;	Mismatches	103;	Indels	0;	Gaps	0;
Oy		4	CCGGGAGACGCCCGCAGATGAAGCTCATGTTCCTTGCAGCGCTCACCTCCCCAGCGC		63					
Dd		362	CSSSGGGGGGGGGGGGGGS		CS	CCCCCCCCCC	CCCCCCCCCC	CCCCCCCCCC	CCCCCCCCCC	CCCCCCCCCCS
Oy		64	AGAAGGCCCACAAGAGCAAGCTGCGCCCAAGCTTGACAGGTGTGGAAATCAAAGAGAG		123					
Dd		422	GCGCGCGCCCCCCCCCCCCCCCCA		CCCCCGAGGAGCGGGGGGGCGCCCCCG					481
Oy		124	GGACCAGGAGCCAGAACTGCGCGCGCGCGCGCGCTTCCTCTGTGCGCAGAGGAAGTTCC		183					
Dd		482	VMAAMARRRTGGCGSRMCCCCCBSCCACTVCCCMGABWKRKRGSCCSSMMCCGMHC		541					
Oy		184	TCACCNGAGGAAGTCTCCCTCAGCCCGGCCAGCCCTGCAAGGGGCGC		221					
Dd		542	CCCCCGSGAGGGGKKKB		CCCCCCCCCCCCCKKKRKGQGGG					589
RESULT 26 LOCUS DEFINITION		AL514267	Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone		EST 08-MAY-2003					
ACCESSION		AL514267								
VERSION		ALI514267.2	GI:30464152							
KEYWORDS		EST.								
SOURCE		Homo sapiens (human)								
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.								
REFERENCE		I. M.B., Gruber C., Jessee J., and Polayes D. Li W-B., et al. (1972) Full-length cDNA libraries and normalization Unpublished On Feb 13, 2001 this sequence version replaced gi:12777761.								
AUTHORS		Contact: Genoscope - Centre National de Sequencage BP 191 91006 Evry cedex - France Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr								
TITLE		Llibrary was constructed by life technologies, a division of Invitrogen. This sequence belongs to Sequence cluster 6437.r For more information about this cluster, see http://www.genoscope.cns.fr/cgi-bin/custer.cgi?seq=CL0BB007ZD09FPF&cluster=6437.r. Contact :								
JOURNAL		Feng liang Email : fliang@lifetech.com URL : <a href="http://fulllength.invitrogen.com/">http://fulllength.invitrogen.com/</a> Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CL0BB007ZD09FPF.								
COMMENT		Location/Qualifiers 1..1172 organism="Homo sapiens" mol_type="mRNA"								
FEATURES		/db_xref="taxon:9606" clone="CL0BB007ZD09" tissue_type="NEUROBLASTOMA" clone_lib="Homo sapiens NEUROBLASTOMA" note="Vector: pCMVSORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSORT 6 vector. Library was not normalized."								
SOURCE		Library was not normalized." Location/Qualifiers								
BASE COUNT		35 a         476 c         244 g         241 t                  176 others								
ORIGIN										
Query Match:		19.2% ; Score 48.4 ; DB 9 ; Length 1172 ;								
Best Local Similarity		41.9% ; Pred.No.4,4 ;								
Matches		90 ; Conservative   28 ; Mismatches   97 ; Indels   0 ; Gaps   0 ;								
Oy		13 CGCGCGGAGTAGAGCGCTGATTGTCCCTTGCAGCTTCCAGCGCAGAGGCGC			72					
Dd		311 TBCCCCCGGGGGGGGGGGGS			CCS	CCCCCCCC	CCCCCCCC	CCCCCCCC	CCCCCCCC	CCCCCCCCG
Oy		73 CCACGAGACCCCGAGTCGAGCTTGCACGCTCTGGATCAAGAGCGAGCACGAG			132					

[illegible]



Db	414	CGGNGGCGGAGINTCCCCCGCCCCCCCCCGGCGCCCGCGCGCGTGGCGGGC	473
QY	181	CCCTCAACNAGGAGAGCTCCCTCAACCGGCGCCAGCCCTGCAAGGAGGCGCTGGAGTTC	240
Db	474	CGGCGCGGCGCGCGGCGCGCGCGTCCCCCGCGCGGCGGCGCGCGGCGGCGNAGCT	533
QY	241	AGACCGC 247	
Db	534	CGGCGCG 540	

RESULT 28				
LOCUS	CNS006XK/c			
DEFINITION	CNS006XK Drosophila melanogaster genome survey sequence T7 end of BAC # BAR14A09 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.			
ACCESSION	AL066051	935 bp	DNA	linear
VERSION	AL066051.1	GI:4945019		GSS 03-JUN-1999
KEYWORDS	GSS.			
SOURCE	Drosophila melanogaster (fruit fly)			
ORGANISM	Drosophila melanogaster			
REFERENCE	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Peiryocta; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephyridioidae; Drosophilidae; Drosophila.			
AUTHORS	1 (bases 1 to 935)			
TITLE	Genoscope.			
JOURNAL	Direct Submission			
	Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :			

COMMENT

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the *Drosophila melanogaster* genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP *Drosophila melanogaster* BAC library was prepared by Kazuhiro Oosawa and Aaron Mammocci at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial *EcoRI* digestion of *Drosophila* DNA provided by the BDGP from the isogenic strain *yz<sup>1</sup> cn bw sp*, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

```

FEATURES
  Source
    Location/Qualifiers
      1..935
        /organism="Drosophila melanogaster"
        /mol_type="genomic DNA"
        /db_xref="taxon:7227"
        /clone="BACRI4N09"
        /clone_1fb="RPCI-98"
        /note="end : 17"
  BASE COUNT
    257 a 170 c 162 g 96 t 250 others
  ORIGIN

```

	Query Match	19.0%;	Score 48;	DB 29;	Length 935;
	Best Local Similarity	31.0%;	Pred. No. 5.2;		
	Matches	74;	Conservative 61;	Mismatches 104;	Indels 0; Gaps 0;
Qy	9 GAGGCGCGCGGAGATGTGAGAGCCCTGATCTGCTTCCTGAGGCGCTTCCACTCTCCCAAGCCAGAG	68			
Db	804 GCGCGCGGSGGCGCSGCGSSGCGGSGCGGCGSSCCGSGGKCCGCGCGSSGSSGSG	745			
Qy	69 GCGCCACGAGAGACCCCGCAGTGCCTCGAGATTTGACACGCTGAGATCAGAGCAGGAGACC	128			
Db	744 SCGSGGSGGSSCGSGCGSGGSGGSGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	685			
Qy	129 AGGAGAGCAGAACTGCGCGCGCGCGCGCGCGCGCGCTGCTGAGCGCGAGAGGAGTCTCTTACC	188			
Db	684 GCG	625			

OY	189	NGAGGGAAGCTCCCCCTACCCCGGCCAACCCTTGATGGGGGACGTGGAGGTTCAGACCCG	247
Db	624	CSCGCCGCSCCCTCCGCGAGCSGCMAGVAGSGASRSVVSSGSSSASGCGCGC	566
RESULT 29			
LOCUS	BX422338		
DEFINITION	BX422338 Homo sapiens FRTL Liver Homologous CDNA clone	1201 bp	linear EST J3-MAY-2003
ACCESSION	CSDMD003YL04.5-PRIME, mRNA sequence.		
VERSION	BX422338		
KEYWORDS	BX422338.1 GI:30659284		
SOURCE	EST.		
ORGANISM	Homo sapiens (human)		

REFERENCE	1 (bases 1 to 1201)
AUTHORS	Li, W.B., Gruber, C., Jesses, J. and Polares, D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished
COMMENT	Contact: Genoscope

Genoscope - Centre National de Séquençage  
BP 191 91006 Evry cedex - France  
Email: [seqref@genoscope.cns.fr](mailto:seqref@genoscope.cns.fr), Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
Library was constructed by life technologies, a division of  
Invitrogen. This sequence belongs to sequence Cluster 6006.r For  
more information about this cluster, see  
[http://www.genoscope.cns.fr/  
cg1-bin/cluster.cgi?seq=CS0DM003DF02QPR1&cluster=6006.r](http://www.genoscope.cns.fr/cg1-bin/cluster.cgi?seq=CS0DM003DF02QPR1&cluster=6006.r). Contact :  
Peng Liang Email : [liang@lifetech.com](mailto:liang@lifetech.com) URL :  
<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600  
Paradise Avenue Genoscope sequence ID : CS0DM003DF02QPR1.  
Location/Qualifiers

```

source
1. .1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DM003YL04"
/tissue_type="FETAL LIVER"
/dev_stage="fetal"
/clone_lip="Homo sapiens FETAL LIVER"
/note="Organ: liver; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime and enriched, double-strand cDNA was digested with NotI and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."
BASE COUNT      251 a      334 c      358 g      111 t      147 others
ORIGIN

```

Query Match	19.0%	Score 47.8	DB 13	Length 1201
Best Local Similarity	42.1%	Pred. No. 5.7		
Matches	85	Conservative	28	Mismatches 89; Indels 0; Gaps 0;
Qy	37	CCCTGGGACCTCCACCTCCCCAGACGCCAGAGAGACCCCAATGACCAC	96	
Db	901	CCSGGGGSMCCCCCSCSSGGGGVMMGGGSCMCCCCCSCSCSSMGGGGGCCCC	960	
Qy	97	GTTGCCACGCTGTGGGATCAGAGCAGAGGACAGAGGACCAAGAACTGACCCGCCCCCGC	156	
Db	961	CCGGRGRVYAMRMVMMAMCCCCGGGGGGGGGYMRCGGGGGGGWTMCCCCCCCCCCCCC	1020	
Qy	157	CCCTGCCCTTCGACCGAGAGGAGTCTCTCAACMGAGAGAACTCCCTACCCGGGCCAG	216	
Db	1021	CCCCCCCCCCCCVGGGGGRRVMMCCCCCCCCCGGGGGGGCCCCCSCCCCCCCCCCCCC	1080	
Qy	217	CCCTGCAGGGGGGGCGCTGGGG	238	
Db	1081	CCCMCAARGSGGGGGGGCG	1102	



EX415926/c 1144 bp mRNA linear EST 13-MAY-2003  
 LOCUS BX415926 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP008YH01  
 DEFINITION 5-PRIME. mRNA sequence.  
 ACCESSION BX415926  
 VERSION BX415926.1 GI:30650131  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1. Drees, I. to 1144).  
 AUTHORS Li, W.-B., Gruber, C., Jessee, J. and Polayes, D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished  
 COMMENT Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 Library was constructed by life technologies, a division of  
 Invitrogen. This sequence belongs to sequence cluster 9016.f For  
 more information about this cluster, see  
 http://www.genoscope.cns.fr/  
 cgi-bin/cluster.cgi?seq=CS0CAP008CD01Q1&cluster=9016.f. Contact :  
 Feng Liang Email : fliang@life.com URL :  
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
 Faraday Avenue Genome sequence ID : CS0CAP008CD01Q1.  
 Location/Qualifiers  
 source  
 1. 1144  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="CS0CAP008YH01"  
 /cfeature="THYMUS"  
 /clone\_lib="Homo sapiens THYMUS"  
 /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed  
 with a NotI-oligo(dT) primer. Five prime end enriched,  
 double-strand cDNA was digested with Not I and cloned into  
 the Not I and EcoRV sites of the pCMVSPORT 6 vector.  
 Library was not normalized."  
 BASE COUNT 230 a 297 c 389 g 123 t 105 others  
 ORIGIN  
 Query Match 18.9%; Score 47.6; DB 13; Length 1144;  
 Best Local Similarity 38.3%; Pred. No. 6.3;  
 Matches 80; Conservative 37; Mismatches 92; Indels 0; Gaps 0;  
 Oy 11 GCGGCGCGGAGTGAAGCTGATCGTCCCTGCGCCCTCCACCTCCCGAGCGCAGAAAGC 70  
 Db 1006 GGGGSSGGGCGGCGGSSGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 947  
 Oy 71 GCCACAG 130  
 Db 946 GGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 887  
 Oy 131 GGAGCGAG 190  
 Db 886 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 827  
 Oy 131 AGGGAAGCTCCCTCAACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 219  
 Db 826 CGSSGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 798  
 RESULT 31  
 CDS0163 1201 bp DNA linear GSS 26-JUL-1999  
 LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC  
 DEFINITION BACN15A15 of Drosophila library from Drosophila melanogaster (fruit  
 fly), genomic survey sequence.  
 ACCESSION AL106629  
 VERSION AL106629.1 GI:5622856  
 KEYWORDS GSS.

SOURCE Drosophila melanogaster (fruit fly)  
 ORGANISM Drosophila melanogaster  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Brachyera; Muscomorpha;  
 Ephydroidea; Drosophilidae; Drosophila.  
 REFERENCE 1 (bases 1 to 1201)  
 AUTHORS Direct Submission  
 JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :  
 BP 191 91006 EVRY cedex FRANCE (E-mail : segref@genoscope.cns.fr  
 - web : www.genoscope.cns.fr)  
 COMMENT Determination of this BAC-end sequence was carried out as part of a  
 collaboration with the European Drosophila Genome Project (EDGP) -  
 http://www.edgp.ebi.ac.uk/. This Drosophila melanogaster BAC  
 library (Dros BAC) was made by Alain Billard at CEPH (Centre  
 d'Etude du Polymorphisme Humain) with funding provided by a MRC  
 project grant. The DNA was prepared from embryos by Alain Bucheton  
 and Genevieve Payan. It has been constructed in the vector  
 pBelobAC11.  
 Location/Qualifiers  
 source  
 1. 1201  
 /organism="Drosophila melanogaster"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:7227"  
 /clone="BACN15A15"  
 /clone\_lib="DrosBAC"  
 /plasmid="pBelobAC11"  
 /note="end : T7"  
 BASE COUNT 211 a 300 c 350 g 168 t 172 others  
 ORIGIN  
 Query Match 18.9%; Score 47.6; DB 29; Length 1201;  
 Best Local Similarity 43.6%; Pred. No. 6.3;  
 Matches 72; Conservative 25; Mismatches 68; Indels 0; Gaps 0;  
 Oy 82 CCCCAGTGGCCGAGCTGCGGATCGATCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 141  
 Db 916 CCGCGGSSGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 975  
 Oy 142 CTGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 201  
 Db 976 GSSSSCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1035  
 Oy 202 CCTCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 246  
 Db 1036 CCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1080  
 RESULT 32  
 CDS0436 384 bp DNA linear GSS 01-SEP-2000  
 LOCUS Tetradon nigroviridis genome survey sequence pUC-ori end of clone  
 DEFINITION 07907 of library G from Tetradon nigroviridis, genomic survey  
 sequence.  
 ACCESSION AL272751  
 VERSION AL272751.1 GI:7994989  
 KEYWORDS GSS; genome survey sequence.  
 SOURCE Tetradon nigroviridis  
 ORGANISM Tetradon nigroviridis  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 Acanthomorpha; Acanthopterygii; Perciformes; Tetraodontiformes;  
 Tetraodontidae; Tetraodontidae; Tetraodon.  
 REFERENCE 1. Roest Crollius, H., Dailion, O., Dasilva, C., Bouneau, L., Fisher, C.,  
 Bernot, A., Fzmes, C., Wincker, P., Brothier, P., Quetier, F.,  
 Saurin, W., and Weissenbach, J.  
 TITLE Estimate of human gene number provided by genome-wide analysis  
 using Tetradon nigroviridis DNA sequence.  
 JOURNAL Nat. Genet. 25 (2), 235-238 (2000)  
 MEDLINE 20296633  
 PUBMED 10835645  
 REFERENCE 2

AUTHORS	JOURNAL
TITLE	MEDLINE
PUBMED	10899143
REFERENCE	3 (bases 1 to 384)
AUTHORS	Genoscope.
TITLE	Direct Submision
JOURNAL	Submitted (12-APR-2000) Genoscope - Centre National de Sequencage ; BP 191 91006 EVRY cedex - FRANCE (E-mail : segrete@genoscope.cns.fr
COMMENT	- Web : www.genoscope.cns.fr This sequence is a single read and was generated as part of a large scale clone end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/tetraodon. Location/Qualifiers
FEATURES	1..384
SOURCE	/organism="Tetraodon nigroviridis" /mol_type="genomic DNA" /db_xref="taxon:99883" /clone="079JU07" /clone_11b="G" /note="Genoscope sequence ID : COBG079CE04SP1-end : PUC-Ori"
BASE COUNT	30 a 171 c 78 g 39 t 66 others
ORIGIN	
Query Match	18.8% ; Score 47.4 ; DB 29 ; Length 384 ;
Best Local Similarity	38.2% ; Pred. No. 6.7 ;
Matches	71 ; conservative 38 ; Mismatches 77 ; Indels 0 ; Gaps 0 ;
OY	37 CCGTCGGCCCTTCACCTCCCGAGGCGCAAGAGGCGGCCAGAGAGCCCCAGTGCCCGAC 96
DB	66 CCSSSRCCSSSGSGSGSGSGGGGGSCCCCSCCCSSSSCCSCCCCCSCCCCC 125
OY	97 GTTGCACGCTGTGGATCATGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 156
DB	126 GSSSCSGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 185
OY	157 CCTGCCCCCTGCGCGCAGAGAACTCCCTCACCGNAGAGGAAGCTCCCTTCACCCGCGCCAG 216
DB	186 YCCCCCGGSGGGGGGSGGCGCTCCCGCCGCCCKGSGGGGGGCGGVCSCCSCCS 245
OY	217 CCTGTG 222
DB	246 CCCGSC 251
RESULT 33	
BX424977	515 bp mRNA linear EST 15-MAY-2001
LOCUS	BX424977 Homo sapiens PLACENTA Homo sapiens CDNA clone ClOBA005ZHO0
DEFINITION	3-PRIME. mRNA sequence.
ACCESSION	BX424977
VERSION	BX424977.1 GI:30784421
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria;
TITLE	Li,W.B., Gruber,C., Jesses,J. and Polayes,D.
JOURNAL	Full-length cDNA libraries and normalization
COMMENT	Unpublished Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: segrete@genoscope.cns.fr Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 6304.f

more information about this cluster, see <http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CI0BA005ZH04FP1>. Contact : Peng Liang Email : [filang@lifeech.com](mailto:filang@lifeech.com) URL : <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CI0BA005ZH04FP1.

FEATURES

source

1. 515  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CI0BA005ZH04"  
/cisreg\_type="PLACENTA"  
/clone\_id="Homo sapiens PLACENTA"  
/note="vector: pCMVSPORT 6; 1st strand cDNA was primed with a NOTI-0190 (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

BASE COUNT

44 a 22 c 56 g 173 t 220 others

ORIGIN

Query Match 18.8%; Score 47.4; DB 13; Length 515;  
Best Local Similarity 7.5%; Pred. No. 6.7;  
Matches 15; Conservative 115; Mismatch 70; Indels 0; Gaps 0;

QY 3 GCCCGGAGGCGCGCGGAGTGAGGCTGTATCTCTCTGCGCCTCCACCTCCCGAGCG 62  
Db 315 VVSIVSSSSGGGGGCGSSSSSSSVSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS 374  
QY 63 CAGAAAGCGCGCCACGAGAGACCCCGCAGCGCCGACGTTGCCAGCGTCTGGATCAGAGCA 122  
Db 375 SASASAAAAAASSSSSSSSSSSSSSSSSSSSSSSSAAASSSSSSSSSSSSSSSSSSG 434  
QY 123 GGAGCCAGGAGCGCAGAGACTGCCCGCCCGCCCTCGCTCGCGCCGAGGAGACTCC 182  
Db 435 SSGGAAANANNANNANNNNNGNNSSSSSSSSSSSSSSSSSSSSSSSVMAAASSSSSSS 494  
QY 183 CTCACNAGAGGAGACTCC 202  
Db 495 SSSSSSSSSSSSSSSSSSSSSS 514

RESULT 34

LOCUS AG090948 993 bp DNA linear GSS 03-NOV-2001

DEFINITION Pan troglodytes DNA, clone: PTB-090K14.R, genomic survey sequence.

ACCESSION AG090948

VERSION AG090948.1 GI:16642750

KEYWORDS GSS.

SOURCE Pan troglodytes (chimpanzee)

ORGANISM Pan troglodytes

REFERENCE 1 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,  
2 Tokok, Y., Watanabe, H. and Sakaki, Y.  
BAC end sequences of Library PTB  
Unpublished  
2 (bases 1 to 993)  
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,  
Tokok, Y., Watanabe, H. and Sakaki, Y.

TITLE Direct Submission

JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical  
REFERENCE 1-7-22 Chemical Research (RIKEN), Genomic Sciences Center (GSC), Japan  
AUTHORS 1-7-22 Shuichi-chou, Tsunumi, K., Yokohama, Kengawa 230-0045, Japan  
TITLE (E-mail: [chimpesgsc.riken.go.jp](mailto:chimpesgsc.riken.go.jp), URL: <http://npg.gsc.riken.go.jp/>,  
COMMENT Tel: 81-45-503-9111, Fax: 81-45-503-9170)  
Clones are derived from the chimpanzee BAC library PTB. This BAC end  
was generated during the Red process and may have higher chance of  
clone tracking errors.

PRIMERS

Sequencing: M13Rev

## LIBRARY

Vector : PKS145  
R.Site 1 : SacI  
R.Site 2 : SacI

Location/Qualifiers  
1. .993

/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
/clone="PTB-090K14.R"  
/sex="male"  
/cell\_type="lymphoblast"  
/clone\_lib="PTB Chimpanzee Male BAC library"

BASE COUNT 1 a 544 c 260 g 0 t 188 others  
ORIGIN

Query Match 18.8%; Score 47.4; DB 29; Length 993;  
Best Local Similarity 50.5%; Pred. No. 6.8;  
Matches 99; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 18 GGGAGTGAAGGCTGATCGTCTGGCGGCTCCAGCTCCCGAGGCGGAGAGGCGCCGCG 77  
DB 636 GGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 695  
QY 78 AGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 137  
DB 696 GGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 755  
QY 138 GGAAGTGAAGGCTGATCGTCTGGCGGCTCCAGCTCCCGAGGAGGAGGAGGAGGAGG 197  
DB 756 GGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 815  
QY 198 CTCCCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 213  
DB 816 CGCGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 831

RESULT 35  
BO948741 1144 bp mRNA linear EST 21-AUG-2002  
LOCUS AGENCOURT 8801058 NIH\_MGC\_130 Mus musculus cDNA clone IMAGE:6392591  
DEFINITION 5', mRNA Sequence.  
ACCESSION BO948741  
VERSION BO948741.1 GI:22364219  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclerogamphali; Muridae; Murinae; Mus.  
REFERENCE NIH-MGC http://mgi.nci.nih.gov/.  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished  
JOURNAL  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cga@bbs-r@mail.nih.gov  
Tissue Procurement: Mark Macnouchie, Ph.D. and Nancy L. Freeman, Ph.D.

CDNA Library Preparation: Resgen, Invitrogen Corp  
DNA Sequencing by: The I.M.A.G.E. Consortium (LNLN)  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:  
http://image.llnl.gov  
Plate: LLM123882 row: k column: 24  
High quality sequence stop: 381.  
Location/Qualifiers  
1. .1144  
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/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/clone="IMAGE:6392591"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_130"

## FEATURES

source  
1. .1144  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/clone="IMAGE:6392591"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_130"

BASE COUNT 90 a 425 c 527 g 52 t 50 others  
ORIGIN

Query Match 18.8%; Score 47.4; DB 13; Length 1144;  
Best Local Similarity 48.7%; Pred. No. 6.8;  
Matches 114; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

QY 12 GCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 71  
DB 845 GCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 786  
QY 72 CCCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 131  
DB 785 GCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 726  
QY 132 GAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 191  
DB 725 GAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 666  
QY 192 GGAAGTGAAGGCTGATCGTCTGGCGGCTCCAGCTCCCGAGGAGGAGGAGGAGGAGG 245  
DB 665 CGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 612

RESULT 36  
BM544979 1235 bp mRNA linear EST 20-FEB-2002  
LOCUS AGENCOURT 6497460 NIH\_MGC\_125 Homo sapiens cDNA clone IMAGE:5588765  
DEFINITION 5', mRNA Sequence.  
ACCESSION BM544979  
VERSION BM544979.1 GI:18776686  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE NIH-MGC http://mgi.nci.nih.gov/.  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished  
JOURNAL  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cga@bbs-r@mail.nih.gov  
Tissue Procurement: Invitrogen  
CDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: The I.M.A.G.E. Consortium (LNLN)  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:  
http://image.llnl.gov  
Plate: LLM12360 row: g column: 06  
High quality sequence stop: 710.  
Location/Qualifiers  
1. .1235  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5588765"  
/lab\_host="DH10B"  
/clone\_lib="NIH\_MGC\_125"  
/note="Organ: ovary (pool of 3); Vector: pCMV-Sport6; Site 1: EcoRV (destroyed); Site 2: NotI; RNA source: pool of three ovaries, from females ranging in age from 38 to 49 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 2.1 kb, insert size range 1-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 036."

## FEATURES

source  
1. .1235  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5588765"  
/lab\_host="DH10B"  
/clone\_lib="NIH\_MGC\_125"  
/note="Organ: ovary (pool of 3); Vector: pCMV-Sport6; Site 1: EcoRV (destroyed); Site 2: NotI; RNA source: pool of three ovaries, from females ranging in age from 38 to 49 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 2.1 kb, insert size range 1-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 036."

BASE COUNT 213 a 377 c 395 g 162 t 88 others

Query Match 18.8%; Score 47.4; DB 12; Length 1235;  
Best Local Similarity 47.6%; Pred. No. 6.9;  
Matches 108; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

11 GGGGGGGGGAGTGAAGAGCTGATCGTCTGGCGCTTCCAGCTCCCGAGAGGAGG 70  
940 GGGGAGTCCCGGG 999  
71 GGGGAG 130  
1000 CCCCCCGGG 1059  
131 GGGGAG 190  
1060 GGGGAG 1119  
191 AGGGAAGCTCTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 237  
1120 NGGG 1166

RESULT 37  
BX442207/c 924 bp mRNA linear EST 15-MAY-2003  
LOCUS BX442207 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone  
DEFINITION CS0DF027YD08 5-PRIME, mRNA sequence.

ACCESSION BX442207  
VERSION BX442207  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 924)  
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 Evry cedex - France  
Email: seqref@genoscope.cns.fr. Web: www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen Contact: Feng Liang Email: fliang@life.com URL:  
http://fulllength.invitrogen.com/Invitrogen Corporation 1600  
Paradey Avenue genoscope sequence ID: CS0DF027YD04Qp1.

FEATURES  
source  
1..924  
/organism="Homo sapiens"  
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/db\_xref="taxon:9606"  
/clone="CS0DF027YD08"  
/tissue\_type="FETAL BRAIN"  
/dev\_stage="fetal"  
/clone\_lib="Homo sapiens FETAL BRAIN"  
/note="Organ: brain; Vector: pCMVSPORT\_6; 1st strand cDNA  
was primed with a NotI-oligo (dt) primer. Five prime end  
enriched, double-strand cDNA was digested with Not I and  
cloned into the Not I and EcoRV sites of the pCMVSPORT 6  
vector. Library was not normalized."

BASE COUNT 76 a 322 c 351 g 32 t 143 others

Query Match 18.7%; Score 47.2; DB 13; Length 924;  
Best Local Similarity 38.6%; Pred. No. 7.5;  
Matches 91; Conservative 35; Mismatches 110; Indels 0; Gaps 0;

1 CGCGGGAG 60  
827 CGCGGGAG 768

61 CGCAG 120  
767 CGCGGGAG 708  
121 CAGGAG 180  
707 SSCCGGAG 648  
181 CCTTACAG 236  
647 CCGGAG 592

RESULT 38  
CNS010DY/c 976 bp DNA linear GSS 26-JUL-1999  
LOCUS CNS010DY/c  
DEFINITION Drosophila melanogaster genome survey sequence SP6 end of BAC  
BACN03N21 of DrosBAC library from Drosophila melanogaster (fruit  
fly), genomic survey sequence.

ACCESSION AL098845.1 GI:5610456  
VERSION AL098845  
KEYWORDS GSS.  
SOURCE Drosophila melanogaster (fruit fly)  
ORGANISM Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 976)  
Genoscope.  
Direct Submission  
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage;  
BP 191 91006 Evry cedex - FRANCE (E-mail: seqref@genoscope.cns.fr)

COMMENT - Web: www.genoscope.cns.fr  
A determination of this BAC-end sequence was carried out as part of a  
collaboration with the European Drosophila Genome Project (EDGP) -  
http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC  
library (Bros BAC) was made by Alain Billaud at CEPH (Centre  
d'Etude du Polymorphisme Humain) with funding provided by a MRC  
project grant. The DNA was prepared from embryos by Alain Bucheton  
and Genevieve Payan. It has been constructed in the vector  
pBelobAC11.

FEATURES  
source  
1..976  
/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7227"  
/clone="BACN03N21"  
/clone\_lib="DrosBAC"  
/plasmid="pBelobAC11"  
/note="end: SP6"

BASE COUNT 199 a 151 c 170 g 190 t 266 others

Query Match 18.7%; Score 47.2; DB 29; Length 976;  
Best Local Similarity 33.3%; Pred. No. 7.5;  
Matches 78; Conservative 45; Mismatches 111; Indels 0; Gaps 0;

4 CGCGGAG 63  
546 SCSS 487  
64 AGAAG 123  
486 CGCGGAG 427  
124 GAGCAG 183  
426 AGGCGGAG 367  
184 TCACAG 237  
366 SAVAG 313

```

RESULT 39
BX380510
LOCUS
DEFINITION BX380510 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
clone CS0D1054YE15 5-PRIME, mRNA sequence.
ACCESSION
VERSION BX380510
KEYWORDS BX380510.1 GI:30448885
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 994)
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France Web : www.genoscope.cns.fr
Email: seqref@genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0D1054AC08QPL.

FEATURES
source
1..994
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1054YE15"
/issue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 273 a 200 c 211 g 139 t 171 others
ORIGIN
Query Match 18.7%; Score 47.2; DB 13; Length 994;
Best Local Similarity 37.1%; Pred. No. 7.5;
Matches 85; Conservative 41; Mismatches 103; Indels 0; Gaps 0;

QY 4 CGGGAGGCGCGCGGAGTGAAGCTGATGCTGCTGCGCTGCACTCCCGAGGCG 63
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 380 CCCCVVRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 64 AGAAGCGCGCGCGAGAGATCCCGAGCTGCGAGCTGCGAGCTGCGAGCGAG 123
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 440 CCGCGCGCGCGCGAGAGATCCCGAGCTGCGAGCTGCGAGCTGCGAGCGAG 123
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 124 GAGACGAGAGCGAGAGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGAGCTCC 183
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 500 CCGTAAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 499
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 184 TCACGAGAGAGAGCTCCCTCAACCGCGCGAGCGCTGCGAGGAGGCGCGC 232
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 560 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 608
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 40
BX407619
LOCUS
DEFINITION BX407619 Homo sapiens PLACENTA Homo sapiens CDNA clone CS0DE005Y119
5-PRIME, mRNA sequence.
ACCESSION
VERSION BX407619
KEYWORDS BX407619.1 GI:30762809
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

```

```

REFERENCE
1 (bases 1 to 1000)
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6789.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0A5005ZD02QPL&cluster=6789.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0A5005D02QPL.

FEATURES
source
1..1000
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE005Y119"
/issue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/notes="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo (dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and EcoRV sites of
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

BASE COUNT 226 a 205 c 283 g 57 t 229 others
ORIGIN
Query Match 18.7%; Score 47.2; DB 13; Length 1000;
Best Local Similarity 21.1%; Pred. No. 7.5;
Matches 50; Conservative 95; Mismatches 92; Indels 0; Gaps 0;

QY 2 GCGCGGAGAGCGCGCGAGTGAAGCTGATGCTGCTGCGCTGCACTCCCGAGC 61
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 443 GVCSSGGGGGGGGGGGVMARGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 502
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 62 GCGAAGCGCGCGCGAGAGATCCCGAGCTGCGAGCTGCGAGCTGCGAGCGAGC 121
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 503 SCSSGGGGGGCGCGCGAGAGATCCCGAGCTGCGAGCTGCGAGCTGCGAGCGAG 562
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 122 AGGACGAGAGCGAGAGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGAGCTCC 181
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 563 AVSSSVSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS 622
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 182 CCGTACGAGAGAGAGCTCCCTCAACCGCGCGAGCGCTGCGAGGAGGCGCGC 238
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 623 SSGSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS 679
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Search completed: November 6, 2003, 09:03:35
Job time : 1456.19 secs

```

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 6, 2003, 06:13:41; Search time 1957.81 Seconds

(without alignments)  
6749.284 Million cell updates/sec

Title: US-10-081-817a-19\_COPY\_229\_551

Perfect score: 323

Sequence: 1 gcgcgtggggcagaccgca.....gcgcgcgcgagcccgcc 323

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database:

GenEmbl:  
1: gb\_da:\*  
2: gb\_hcg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_srs:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_da:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_srs:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_hcg\_hum:\*  
31: em\_hcg\_inv:\*  
32: em\_hcg\_other:\*  
33: em\_hcg\_mus:\*  
34: em\_hcg\_pln:\*  
35: em\_hcg\_rnd:\*  
36: em\_hcg\_mam:\*  
37: em\_hcg\_vrt:\*  
38: em\_ey:\*  
39: em\_hgco\_hum:\*  
40: em\_hgco\_mus:\*  
41: em\_hgco\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	312	96.6	127488	2 AC022095	AC022095 Homo sapi
C 2	312	96.6	168347	2 AC025336	AC025336 Homo sapi
C 3	312	96.6	190024	9 AC122714	AC122714 Homo sapi
C 4	304.8	94.4	130129	2 AC108083	AC108083 Homo sapi
5	301	93.2	166777	2 AC106813	AC106813 Homo sapi
6	120	37.2	562	6 BD082141	BD082141 Reagents
7	117	36.2	190	6 BD082137	BD082137 Reagents
8	78	24.1	519	6 BD082142	BD082142 Reagents
9	78	24.1	569	6 AX201348	AX201348 Sequence
10	78	24.1	570	6 AR252648	AR252648 Sequence
11	78	24.1	570	6 AX403520	AX403520 Sequence
12	77	23.8	244	6 BD082138	BD082138 Reagents
13	58	18.0	167624	2 AC143286	AC143286 Macaca mu
C 14	55.4	17.2	187413	2 AC141871	AC141871 Mus muscu
C 15	55.4	17.2	210420	2 BX470203	BX470203 Mus muscu
C 16	54.8	17.0	167077	2 AC081023	AC081023 Papio anu
C 17	54.8	17.0	219952	2 AC084804	AC084804 Mus muscu
18	54.6	16.9	2685	2 HUMHBA3	HUMHBA3
19	54.6	16.9	43058	6 AX332810	AX332810 Sequence
20	54.6	16.9	43058	6 AX333047	AX333047 Sequence
21	54.6	16.9	43058	6 AX411306	AX411306 Sequence
22	54.6	16.9	43058	6 HSGG1	HSGG1
C 23	54.6	16.9	53370	2 AC126375	AC126375 Homo sapi
C 24	54.6	16.9	258002	9 AE006462	AE006462 Homo sapi
C 25	52.6	16.3	1133	9 AF327440	AF327440 Homo sapi
C 26	52.6	16.3	149252	9 AC012615	AC012615 Homo sapi
27	52.4	16.2	135119	2 AC011578	AC011578 Homo sapi
28	52.2	16.2	557	5 XELRGE12	XELRGE12
29	52.2	16.2	3924	5 XELRGE12	XELRGE12
30	52.2	16.2	7634	5 XELRGE12	XELRGE12
31	52.2	16.2	8153	5 XELRGE12	XELRGE12
C 32	52.2	16.2	52390	2 AC100946	AC100946 Mus muscu
C 33	52.2	16.2	123865	2 AC144397	AC144397 Rattus no
C 34	52.2	16.2	209257	2 AC123927	AC123927 Mus muscu
C 35	52	16.1	12562	9 AB053222	AB053222 Homo sapi
C 36	52	16.1	87746	9 AC109826	AC109826 Homo sapi
C 37	51.8	16.0	67246	2 AC105035	AC105035 Homo sapi
C 38	51.8	16.0	71032	2 AC084084	AC084084 Homo sapi
C 39	51.8	16.0	171574	2 AC012300	AC012300 Homo sapi
C 40	51.4	15.9	44508	2 AC136063	AC136063 Rattus no
C 41	51.4	15.9	237915	2 AC140280	AC140280 Mus muscu
C 42	51.2	15.9	48144	2 AC069166	AC069166 Homo sapi
C 43	51.2	15.9	113196	9 HSJ097K14	AL121829 Human DNA
C 44	51	15.8	1007	11 PM3H11G	AL685749 Penicilliu
C 45	51	15.8	79023	2 AC021951	AC021951 Homo sapi

#### ALIGNMENTS

RESULT 1  
AC022095/c 127488 bp DNA linear HTG 20-APR-2001  
LOCUS Homo sapiens chromosome 5 clone CTB-36B8, WORKING DRAFT SEQUENCE,  
DEFINITION 13 unordered pieces.  
ACCESSION AC022095 GI:13699618  
VERSION AC022095.5  
HTG: HTGS PHASE1; HTGS\_DRAFT; HTGS\_ACTIVEFIN.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Bukaryofa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 127488)  
DOE Joint Genome Institute.  
Sequencing of Human Chromosome 5





```

Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information
Center project name: 16686
Center clone name: 451.H.23
----- Summary Statistics
Sequencing vector: M13. M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap version 0.960721
Consensus quality: 150524 bases at least Q40
Consensus quality: 159524 bases at least Q20
Consensus quality: 163013 bases at least Q20
Insert size: 165247; sum-of-contigs
Quality coverage: 3.6 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 32 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1
1389: contig of 1389 bp in length
1390: gap of 100 bp
1490: contig of 1641 bp in length
3131: gap of 100 bp
3230: contig of 1712 bp in length
4942: gap of 100 bp
5042: contig of 1939 bp in length
6981: gap of 100 bp
7081: contig of 1627 bp in length
8708: gap of 100 bp
8808: contig of 1478 bp in length
10287: gap of 100 bp
10386: contig of 1826 bp in length
12212: gap of 100 bp
12312: contig of 2346 bp in length
14658: gap of 100 bp
14758: contig of 3183 bp in length
17941: gap of 100 bp
18041: contig of 3256 bp in length
21297: gap of 100 bp
21397: contig of 3595 bp in length
24992: gap of 100 bp
25092: contig of 2676 bp in length
27668: gap of 100 bp
27869: contig of 3320 bp in length
31189: gap of 100 bp
31288: contig of 2426 bp in length
33714: gap of 100 bp
33814: contig of 3463 bp in length
37277: gap of 100 bp
37378: contig of 4925 bp in length
42302: gap of 100 bp
42402: contig of 5414 bp in length
47816: gap of 100 bp
47917: contig of 4670 bp in length
52586: gap of 100 bp
52887: contig of 3881 bp in length
56857: gap of 100 bp
56868: contig of 4890 bp in length
61657: gap of 100 bp
61658: contig of 5067 bp in length
66724: gap of 100 bp
66824: contig of 4744 bp in length
71568: gap of 100 bp
71668: contig of 4910 bp in length
76578: gap of 100 bp
76678: contig of 6634 bp in length
83312: gap of 100 bp
83413: contig of 6641 bp in length
90053: gap of 100 bp
90154: contig of 9273 bp in length
99426: contig of 9273 bp in length

```

```

FEATURES
Source
* 99427 99526: gap of 100 bp
* 99527 108015: contig of 8488 bp in length
* 108016 108115: gap of 100 bp
* 108116 118144: contig of 10029 bp in length
* 118145 118244: gap of 100 bp
* 118245 130468: contig of 12224 bp in length
* 130469 142339: gap of 100 bp
* 142340 142339: contig of 11671 bp in length
* 142339 142339: gap of 100 bp
* 142335 157135: contig of 14796 bp in length
* 157136 157236: gap of 100 bp
* 157236 168347: contig of 11112 bp in length.
Location/Qualifiers
1. .168347
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="5"
/map="5"
/clone="RP11-451H23"
/clone_1lb="RP11 Human Male BAC"
1. .1389
/note="assembly_fragment"
1490. .3130
/note="assembly_fragment"
3231. .4942
/note="assembly_fragment"
5043. .6981
/note="assembly_fragment"
7082. .8708
/note="assembly_fragment"
8809. .10286
/note="assembly_fragment"
10387. .12212
/note="assembly_fragment"
12313. .14658
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42403. .47816
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52887. .56857
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71669. .76578
/note="assembly_fragment"
76679. .83312
/note="assembly_fragment"
83413. .90053
/note="assembly_fragment"
90154. .99426
/note="assembly_fragment"

```

```
misc_feature 99527. 108015 /note="assembly_fragment"
misc_feature 108116 118144 /note="assembly_fragment"
misc_feature 118245 130468 /note="assembly_fragment"
misc_feature 130569 142239 /note="assembly_fragment"
```

Query Match	96.6%	Score 312;	DB 2;	Length 168347;
Best Local Similarity	99.7%	Pred. No. 4.9e-47;		
Matches 323; Conservative	0;	Mismatches 0;	Indels 1;	Gaps 1

0y 1 GCGCGTGGGGTTCAGACCGCAAGCGAAGGTGGGGCCGGGGGTGGGGCTCGCGAGACAAA 60  
 Db 144892 GCGCGTGGGGTTCAGACCGCAAGCGAAGGTGGGGCCGGGGGTGGGGCTTCGCGAGACAAA 144933

QY	61	36	CGGGGCTGCT-CTCTCAGAGGGGCCCCAGCGGCTGGCAAGGAAATCCCTCGAGGCC	119
Db	144332	GGCCGGGCTGCTGCTCTCTCAGAGGGGCCCCAGCGGCTGGCAAGGAAATCCCTCGAGGCC	144873	

QY	120	179
CGGGCAGGAAAGGGGACAGGGGCTTCCAGGGCCCGCGGCGCAGCAGGAATTGGCCA		
CGGGCAGGAAAGGGGACAGGGCTTCCAGGGCCCGCGGCGCAGCAGGAATTGGCCA	144813	
CGGGCAGGAAAGGGGACAGGGCTTCCAGGGCCCGCGGCGCAGCAGGAATTGGCCA	144813	

QY	180	GGGCA CGGC CGT GAG CGG AG CGG GCA GGG C TTT TCT CAG AG CCG GCG GCG CGC T	239
Db	144812	GGGCA CGCG CCG GAG CGG AG CGG GCA GGG C TTT TCT CAG AG CCG GCG GCG CGC T	144753

QY 240 GSAGGCGCGAGGACCGGGGATTAAGAGCCCTGCTGCGCCCGGGCAGCCGAGGTTC 299

144752 GGAGGGCGCGAGGACCGGGGTTAAGAGCCCTGCTGCGCCCGGGCAGCCGAGGTTC 146933

QY	300	CCGCGCGCCCCCGAGCCCCCGCGCC	323
144692			
144693			
144694			
144695			
144696			
144697			
144698			
144699			
144700			
144701			
144702			
144703			
144704			
144705			
144706			
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144767			
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144772			
144773			
144774			
144775			
144776			
144777			
144778			
144779			
144780			
144781			
144782			
144783			
144784			
144785			
144786			
144787			
144788			
144789			
144790			
144791			
144792			

RESULT 3			
AC122714/c			
LOCUS	190024 bp	DNA	linear
DEFINITION	Homo sapiens chromosome 5 clone RP1-451H23, complete sequence.		

VERSION	AC122714.2	GI:28827858
KEYWORDS		
SOURCE	HTG.	
	Homo sapiens (human)	

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Carnivora; Homnidae; Homo.  
1 (bases 1 to 190024)

TITLE	DATE RECEIVED	DATE FORWARDED	REMARKS	CONCURRENCE
Direct Submission				
Unpublished				
2 (bases 1 to 190024)				

TITLE  
 DIRECT SUBMISSION  
 Submitted (25-MAY-2002) Production Sequencing Facility, DOE Joint  
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

REFERENCES  
 AUTHORS  
 TITLE  
 JOURNAL  
 DOE Joint Genome Institute and Stanford Human Genome Center.  
 Direct Submission  
 Submitted (04-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell

COMMENT  
On Mar 4, 2003 this sequence version replaced g1:21206277.  
Draft Sequence Produced by DOE Joint Genome Institute  
www.jgi.doe.gov

Finishing completed at Stanford Human Genome Center  
www.shgc.stanford.edu  
Quality: Phrap Quality >=40 99.8% of Sequence;  
Estimated Total Number of Errors is 0.9

FEATURES  
NOTE: Shatter Libraries failed to verify the dinucleotide repeat  
region 124370-125308. Unsure number of repeat copies  
124370-125308. Forced join 124996.  
location/Qualifiers

```

source
1..190024
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="5"
/clone="RP11-451H23"
124370..125308
/notes="NOTE: Shatter libraries failed to verify the
dinucleotide repeat region 124370-125308. Unsure number
of repeat copies 124370-125308. Forced join 124996."

misc_feature
BASE COUNT 45607 a 46028 c 46121 g 5268 t
ORIGIN

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Query Match	96.6%	Score 312;	DB 9;	Length 19002;
Best Local Similarity	99.7%	Pred. No. 4.8e-47;		
Matches 323; Conservative	0;	Mismatches 0;	Indels 1;	Gaps 1;

QY 1 GCGCGGTGGGGTCTAGACCCGCAAGCGAAGGTGGGGGCCGGGGTGGGGCTCTCGCGGAGACAA 60  
Db 81261 GCGCGTGGGGTCTAGACCGCAAGCGAAGGTGGGGGCCGGGGTGGGGCTCTCGCGGAGACAA 81207

QY	61	GGCGGGGCTGCTTCTCTCAGAGGGCCCCAGCGCTGCCAAGAGAAATCTTCGAGGCC	119
Db	81201	GGCGGGGCTGCTTCTCTCAGAGGGCCCCAGCGCTGCCAAGAGGAATCTTCGAGGCC	81144

Qy 120 CGGGCAGGGAGAGGGGCGACGGGCTTCCACAGGGCCCGCGGCCGACAGAGAGAGAGTTGGCCA 179

Db 81141 CGGGCAGGGAGAGGGGCGACGGGCTTCCACAGGGCCCGCGGCCGACAGAGAGAGAGTTGGCCA 81083

Qy 180 GGGCACGGCCGTTGAGCCGAGCCGGCGAGGGCTTTTCTCAGAGAGCGCGGGCGAGGGCGCGCT 239

Db 81081 GGGCACGGCCGTTGAGCCGAGCCGGCGAGGGCTTTTCTCAGAGAGCGCGGGCGAGGGCGCGCT 81022AAGGGCGCGCT

Oy 240 GGAGGGCGAGACCCGGATATAAGAGCCTCGTGGCCTTGGCCGGGAGACCCGAGGTTCC 299  
 Db 81021 GGAGGGCGAGACCCGGGATATAGAAGACCTCGTGGCCTTGGCCGGGAGACCCGAGGTTCC 8096

QY	300	CCGCGCGCCCGAGCCCCCGCGCC	323
DB	809361	CCGCGCGCCCCCGAGCCCCCGCGCC	80938

RESULT 4	
AC108083/c	
LOCUS	130129 bp DNA linear HTG 25-JUN-2002
DEFINITION	Homo sapiens chromosome 5 clone CTD-2013L15, WORKING DRAFT

ACCESSION AC108083.1  
VERSION AC108083.1  
KEYWORDS HTG; HTGS PHASE1; HTGS\_DRAFT; HTGS\_ACTIVEPIN.

**ORGANISM**  
Homo sapiens (*Homo sapiens*)  
Eukaryote; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Euteria; Primates; Carnivora; Hominoidea; Homo.

REFERENCE  
DOE JOINT GENOME INSTITUTE.  
Sequencing of Human Chromosome 5  
Unpublished

AUTHORS  
TITLE  
JOURNAL

REFERENCE  
DOE Joint Genome Institute.  
Z (access 1 to 1301429)  
TITLE  
JOURNAL  
Submitted (25-JAN-2002) Production Sequencing Facility, DOE Joint

COMMENT  
-----  
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
-----  
Genome Center  
Center: Joint Genome Institute  
Center Code: JGI

```

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Web site: http://www.j91.doe.gov
-----
Project Information
Center Project Name: 632820

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Center clone name: CITB-H1_2013L15
-----
Summary Statistics
```

Consensus quality: 124488 bases at least Q40  
 Consensus quality: 128031 bases at least Q30  
 Consensus quality: 128842 bases at least Q20  
 Estimated insert size: 135000; agarose-fp estimation  
 Estimated insert size: 129829; sum-of-contigs estimation  
 Quality coverage: 7.66 in Q20 bases; agarose-fp estimation  
 Quality coverage: 7.97 in Q20 bases; sum-of-contigs estimation.  
 NOTE: This is a 'working draft' sequence. It currently  
 consists of 4 contigs. The true order of the pieces  
 is not known and their order in this sequence record is  
 arbitrary. Gaps between the contigs are represented as  
 runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

1 4320: contig of 4320 bp in length  
 \* 4321 4420: gap of unknown length  
 \* 4421 23712: contig of 19292 bp in length  
 \* 23713 23813: gap of unknown length  
 \* 23813 48602: contig of 24790 bp in length  
 \* 48603 48702: gap of unknown length  
 \* 48703 130129: contig of 81427 bp in length.

FEATURES  
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 1.130129  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /chromosome="5"  
 /clone="CTD-2013L15"  
 /clone\_lib="Caltech human BAC library D"  
 /clone\_1ib="3297 c 30949 g 31146 t 300 others

BASE COUNT  
 35337 a 3297 c 30949 g 31146 t 300 others

ORIGIN  
 Query Match 94.4%; Score 304.8; DB 2; Length 130129;  
 Best Local Similarity 99.1%; Pred. No. 1e-45; 2; Indels 1; Gaps 1;  
 Matches 317; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 GCGCGTGGGTCAAGACCGCAAGCAAGGTGCGGGCCGGGAGTGGCTTCGCGAGACAA 60  
 DB 24359 GCGCGTGGGTCAAGACCGCAAGCAAGGTGCGGGCCGGGAGTGGCTTCGCGAGACAA 24300  
 QY 61 GCGCGGCTGCTCTCTCAAGAGGCGCCAGCGCTTCGCAAGAGAAATCTCTCAAGGCC 119  
 DB 24299 GCGCGGCTGCTCTCTCAAGAGGCGCCAGCGCTTCGCAAGAGAAATCTCTCAAGGCC 24240  
 QY 120 CCGGCGAGGAGAGGGGCAAGGGCTTCCAGAGGCCCGCCGCGCGCAGAGAGAAATTGGCCA 179  
 DB 24239 CCGGCGAGGAGAGGGGCAAGGGCTTCCAGAGGCCCGCCGCGCGCAGAGAGAAATTGGCCA 24180  
 QY 180 GGGCAAGCGCTGAGCGAGCGGCGAGGCTTCTCAGAGAGCGCGCGAGGCGCGGCT 239  
 DB 24179 GGGCAAGCGCTGAGCGAGCGGCGAGGCTTCTCAGAGAGCGCGCGAGGCGCGGCT 24120  
 QY 240 GAGAGGGGCGAGGAGCGCGGATATAGAAAGCTCGTGGCTTGGCCGAGCGCAGGTTCC 299  
 DB 24119 GAGAGGGGCGAGGAGCGCGGATATAGAAAGCTCGTGGCTTGGCCGAGCGCAGGTTCC 24060  
 QY 300 CCGCGCGCGCGCGAGCGCGCG 319  
 DB 24059 CCGCGCGCGCGCGAGCGCGCG 24040

RESULT 5  
 AC106813 AC106813 166777 bp DNA 11near HTG 07-MAR-2002  
 LOCUS Homo sapiens chromosome 5 clone RP11-586L9, WORKING DRAFT SEQUENCE,  
 DEFINITION 3 joined pieces.  
 AC106813 3 GI:19224876  
 ACCESSION AC106813  
 VERSION HTG; HTGS\_PHA82; HTGS\_DRAFT; HTGS\_ACTIVEFIN.  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens (human)  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 1 (bases 1 to 166777)  
 DOE Joint Genome Institute.  
 Sequencing of Human Chromosome 5  
 Unpublished  
 2 (bases 1 to 166777)  
 DOE Joint Genome Institute.  
 Direct Submission  
 Submitted (12-JAN-2002) Production Sequencing Facility, DOE Joint  
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
 3 (bases 1 to 166777)  
 DOE Joint Genome Institute.  
 Direct Submission  
 Submitted (07-MAR-2002) Production Sequencing Facility, DOE Joint  
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
 On Mar 7, 2002 this sequence version replaced gi:1836924.  
 -----Genome  
 Center: Joint Genome Institute  
 Center Code: JGI  
 Web site: <http://www.jgi.doe.gov>

Project Information  
 Center Project Name: 1519801  
 Center clone name: RP11-586L9

Summary Statistics  
 Consensus quality: 163497 bases at least Q40  
 Consensus quality: 166071 bases at least Q30  
 Consensus quality: 166432 bases at least Q20  
 Estimated insert size: 166250; agarose-fp estimation  
 Estimated insert size: 165777; sum-of-contigs estimation  
 Quality coverage: 9.4 in Q20 bases; agarose-fp estimation  
 Quality coverage: 10.51 in Q20 bases; sum-of-contigs estimation.  
 NOTE: This is a 'working draft' sequence. It currently  
 consists of 3 contigs. Gaps between the contigs  
 are represented as runs of N. The order of the pieces  
 is believed to be correct as given, however the sizes  
 of the gaps between them are based on estimates that have  
 been provided by the submitter.  
 \* This sequence will be replaced  
 \* by the finished sequence as soon as it is available and  
 \* the accession number will be preserved.

1 62237: contig of 62237 bp in length  
 \* 62238 62337: gap of unknown length  
 \* 62338 75837: contig of 13500 bp in length  
 \* 75838 75937: gap of unknown length  
 \* 75938 166777: contig of 90840 bp in length.

FEATURES  
 source  
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 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /chromosome="5"  
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 /clone\_lib="RP11-586L9"  
 /clone\_1ib="RP11-586L9"  
 /clone\_1ib="39804 c 41258 g 40888 t 200 others

BASE COUNT  
 44627 a 39804 c 41258 g 40888 t 200 others

ORIGIN  
 Query Match 93.2%; Score 301; DB 2; Length 166777;  
 Best Local Similarity 99.4%; Pred. No. 4.5e-45; 2; Indels 2; Gaps 2;  
 Matches 323; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1 GCGCGTGGGTCAAGACCGCAAGCAAGGTGCGGGCCGGGAGTGGCTTCGCGAGACAA 60  
 DB 119314 GCGCGTGGGTCAAGACCGCAAGCAAGGTGCGGGCCGGGAGTGGCTTCGCGAGACAA 119373  
 QY 61 GCGCGGCTGCTCTCTCAAGAGGCGCCAGCGCTTCGCAAGAGAAATCTCTCAAGGCC 119  
 DB 119374 GCGCGGCTGCTCTCTCAAGAGGCGCCAGCGCTTCGCAAGAGAAATCTCTCAAGGCC 119433  
 QY 120 CCGGCGAGGAGAGGGGCAAGGGCTTCCAGAGGCCCGCCGCGCGCAGAGAGAAATTGGCCA 179  
 DB 119434 CCGGCGAGGAGAGGGGCAAGGGCTTCCAGAGGCCCGCCGCGCGCAGAGAGAAATTGGCCA 119493

RESULT 6  
LOCUS BD082141 562 bp DNA linear PAT 27-AUG-2002  
DEFINITION Reagents and methods useful for detecting diseases of the lung.  
ACCESSION BD082141.1 GI:22627751  
VERSION BD082141.1  
KEYWORDS JP 2001522225-A/5.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoidae; Andropogoneae; Zea.  
1 (bases 1 to 562)  
Medel,P.A.B., Cohen,M., Colpites,T.L., Friedman,P.N., Gordon,J.,  
Granados,E.N., Hodges,S.C., Klaas,M.R., Kratochvil,J.D., Rapp,L.R.,  
Russell,J.C. and Stroupe,S.D.  
Reagents and methods useful for detecting diseases of the lung  
Patent: JP 2001522225-A 5 13-NOV-2001;  
ABBOTT LABORATORIES  
PN JP 2001522225-A/5  
PD 13-NOV-2001  
PF 30-JAN-1998 JP 1998533078  
PR 31-JAN-1997 US 08/791710  
PI PATRICIA A BILLING MEDEL,MAURICE COHEN,TRACEY L COLPITTS,PAULA  
N FRIEDMAN,  
JULIAN GORDON,EDWARD N GRANADOS,STEVEN C HODGES,MICHAEL R PI  
KLAAS,  
JUN D KRATOCHVIL,LISA ROBERTS RAPP,JOHN C RUSSELL,STEPHEN D  
PI STROUPE  
PC C12N15/63,C12N5/10,C12Q1/68,C07K14/47//C07K16/30,G01N33/574 CC  
Strandness: Single;  
CC Topology: Linear;  
FH Key Location/Qualifiers.  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:4577"  
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Best Local Similarity 99.2%; Pred.No.4,4e-12;  
Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 203 GCAGGCTTTCTCAGAGGCGGCGAGGCGCGCTGTGAGGGGCGAGGACCGGGTATTA 262  
DB 1 GCAGGCTTTCTCAGGNGCGCGGCGAGGCGCGCTGTGAGGGGCGAGGACCGGGTATTA 60  
QY 263 GAAGCTCTGTGGCTTGGCCCGGCGAGCCGCGAGGTTCCCGCGCGCCCGAGGCTCCCGCGC 322  
DB 61 GAAGCTCTGTGGCTTGGCCCGGCGAGCCGCGAGGTTCCCGCGCGCCCGAGGCTCCCGCGC 120  
QY 323 C 323  
DB 121 C 121

RESULT 7  
LOCUS BD082137 190 bp DNA linear PAT 27-AUG-2002  
DEFINITION Reagents and methods useful for detecting diseases of the lung.  
ACCESSION BD082137.1 GI:22627747  
VERSION BD082137.1  
KEYWORDS JP 2001522225-A/1.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoidae; Andropogoneae; Zea.  
1 (bases 1 to 190)  
Medel,P.A.B., Cohen,M., Colpites,T.L., Friedman,P.N., Gordon,J.,  
Granados,E.N., Hodges,S.C., Klaas,M.R., Kratochvil,J.D., Rapp,L.R.,  
Russell,J.C. and Stroupe,S.D.  
Reagents and methods useful for detecting diseases of the lung  
Patent: JP 2001522225-A 1 13-NOV-2001;  
ABBOTT LABORATORIES  
PN JP 2001522225-A/1  
PD 13-NOV-2001  
PF 30-JAN-1998 JP 1998533078  
PR 31-JAN-1997 US 08/791710  
PI PATRICIA A BILLING MEDEL,MAURICE COHEN,TRACEY L COLPITTS,PAULA  
N FRIEDMAN,  
JULIAN GORDON,EDWARD N GRANADOS,STEVEN C HODGES,MICHAEL R PI  
KLAAS,  
JUN D KRATOCHVIL,LISA ROBERTS RAPP,JOHN C RUSSELL,STEPHEN D  
PI STROUPE  
PC C12N15/63,C12N5/10,C12Q1/68,C07K14/47//C07K16/30,G01N33/574 CC  
Strandness: Single;  
CC Topology: Linear;  
FH Key Location/Qualifiers.  
FEATURES  
source 1..190  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:4577"  
BASE COUNT 18 a 69 c 67 g 32 t 4 others  
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Query Match 36.2%; Score 117; DB 6; Length 190;  
Best Local Similarity 96.7%; Pred.No.2e-11; 4; Indels 0; Gaps 0;  
Matches 117; Conservative 0; Mismatches 4;  
QY 203 GCAGGCTTTCTCAGAGGCGGCGGAGGCGCGCTGTGAGGGGCGAGGACCGGGTATTA 262  
DB 1 GCAGGCTTTCTCAGGNGCGCGGCGAGGCGCGCTGTGAGGGGCGAGGACCGGGTATTA 60  
QY 263 GAAGCTCTGTGGCTTGGCCCGGCGAGCCGCGAGGTTCCCGCGCGCCCGAGGCTCCCGCGC 322  
DB 61 GAAGCTCTGTGGCTTGGCCCGGCGAGCCGCGAGGTTCCCGCGCGCCCGAGGCTCCCGCGC 120  
QY 323 C 323  
DB 121 C 121  
RESULT 8  
LOCUS BD082142 519 bp DNA linear PAT 27-AUG-2002  
DEFINITION Reagents and methods useful for detecting diseases of the lung.  
ACCESSION BD082142.1 GI:22627752  
VERSION BD082142.1  
KEYWORDS JP 2001522225-A/6.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoidae; Andropogoneae; Zea.  
1 (bases 1 to 519)  
Medel,P.A.B., Cohen,M., Colpites,T.L., Friedman,P.N., Gordon,J.,

Granados, E.N., Hodges, S.C., Klass, M.R., Kratochvil, J.D., Rapp, L.R., Russell, J.C., and Stroupe, S.D.  
Reagents and methods useful for detecting diseases of the lung  
Patent: JP 2001522225-A 6 13-NOV-2001;  
ABBOTT LABORATORIES  
PN JP 2001522225-A/6  
PD 13-NOV-2001  
PF 30-JAN-1998 JP 198533078  
PR 31-JAN-1997 US 08/791710  
PI PATRICIA A BILLING MEDEL, MAURICE COHEN, TRACEY L COLPITTS, PAULA  
PI N FRIDMAN,  
PI JULIAN GORDON, EDWARD N GRANADOS, STEVEN C HODGES, MICHAEL R PI  
PI KLAS,  
PI JON D KRATOCHVIL, LISA ROBERTS RAPP, JOHN C RUSSELL, STEPHEN D  
PI STROUPE  
PI C12N15/63, C12N5/10, C12Q1/68, C07K14/47//C07K16/30, G01N33/574 CC  
PC C12N15/63, C12N5/10, C12Q1/68, C07K14/47//C07K16/30, G01N33/574 CC  
CC Strandedness: Single;  
FH Key  
FEATURES  
Location/Qualifiers  
1.519  
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/mol\_type="genomic DNA"  
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BASE COUNT 78 a 190 c 170 g 81 t  
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Query Match 24.1%; Score 78; DB 6; Length 519;  
Best Local Similarity 100.0%; Pred. No. 0.00015;  
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 246 GCGAGGACCGGGATATAGAAGCCTCGTGGCTTGGCCCGGAGCGGAGGTTCCCGGCGC 305  
DB 1 GCGAGGACCGGGATATAGAAGCCTCGTGGCTTGGCCCGGAGCGGAGGTTCCCGGCGC 60  
QY 306 GCCCGAGCGCCCGCGCGC 323  
DB 61 GCCCGAGCGCCCGCGCGC 78  
RESULT 9  
AX201348 569 bp DNA linear PAT 30-AUG-2001  
LOCUS AX201348  
DEFINITION Sequence 27 from Patent WO0153486.  
ACCESSION AX201348  
VERSION AX201348.1 GI:15391167  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 Ashkenazi, A.J., Goddard, A., Godowski, P.J., Gurney, A.L.,  
Hillan, R.J., Marsters, S.A., Pan, J., Piltl, R.M., Roy, M.A., Smith, V.,  
Stone, D.M., Watanabe, C.K., and Wood, W.I.  
Compositions and methods for the treatment of tumour  
Patent: WO 0153486-A 27 26-JUL-2001;  
Genentech, Inc. (US)  
TITLE Location/Qualifiers  
JOURNAL  
FEATURES  
1.569  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
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BASE COUNT 128 a 190 c 170 g 81 t  
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Best Local Similarity 100.0%; Pred. No. 0.00015;  
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 246 GCGAGGACCGGGATATAGAAGCCTCGTGGCTTGGCCCGGAGCGGAGGTTCCCGGCGC 305  
DB 1 GCGAGGACCGGGATATAGAAGCCTCGTGGCTTGGCCCGGAGCGGAGGTTCCCGGCGC 60

DB 1 GCGAGGACCGGGATATAGAAGCCTCGTGGCTTGGCCCGGAGCGGAGGTTCCCGGCGC 60  
QY 306 GCCCGAGCGCCCGCGCGC 323  
DB 61 GCCCGAGCGCCCGCGCGC 78  
RESULT 10  
AR252648 570 bp DNA linear PAT 20-DEC-2002  
LOCUS AR252648  
DEFINITION Sequence 407 from patent US 6478825.  
ACCESSION AR252648  
VERSION AR252648.1 GI:27300556  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
1 (bases 1 to 570)  
Wintebottom, J.M., Shimp, L., Boyce, T.M., and Kaes, D.  
Implant, method of making same and use of the implant for the  
treatment of bone defects  
Patent: US 6478825-A 407 12-NOV-2002;  
TITLE Location/Qualifiers  
JOURNAL  
FEATURES  
1.570  
/organism="unknown"  
BASE COUNT 129 a 190 c 170 g 81 t  
ORIGIN  
Query Match 24.1%; Score 78; DB 6; Length 570;  
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Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 246 GCGAGGACCGGGATATAGAAGCCTCGTGGCTTGGCCCGGAGCGGAGGTTCCCGGCGC 305  
DB 1 GCGAGGACCGGGATATAGAAGCCTCGTGGCTTGGCCCGGAGCGGAGGTTCCCGGCGC 60  
QY 306 GCCCGAGCGCCCGCGCGC 323  
DB 61 GCCCGAGCGCCCGCGCGC 78  
RESULT 11  
AX403520 570 bp DNA linear PAT 14-JUN-2002  
LOCUS AX403520  
DEFINITION Sequence 407 from Patent WO0073454.  
ACCESSION AX403520  
VERSION AX403520.1 GI:21437002  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 Ashkenazi, A.J., Baker, K.P., Botstein, D., Desnoyers, L., Batou, D.,  
Ferrara, N., Gerber, H., Gerltzen, M., Goddard, A., Godowski, P.,  
Grimaldi, C.J., Gurney, A.L., Klavin, I., Napier, M.A., Pan, J.,  
Pooni, N.F., Roy, M., Stewart, T.A., Tumas, D., Watanabe, C.K.,  
Williams, P., Wood, W.I., and Zhang, Z.  
Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
Patent: WO 0073454-A 407 07-DEC-2000;  
Genentech Inc. (US)  
TITLE Location/Qualifiers  
JOURNAL  
FEATURES  
1.570  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
BASE COUNT 129 a 190 c 170 g 81 t  
ORIGIN  
Query Match 24.1%; Score 78; DB 6; Length 570;  
Best Local Similarity 100.0%; Pred. No. 0.00015;  
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 GCGAGAGACCGGGTATAGAGAGCTCGTGACCTTGCCCGGAGAGCCGAGGTTCCCGCGC 305  
DB 1 GCGAGAGACCGGGTATAGAGAGCTCGTGACCTTGCCCGGAGAGCCGAGGTTCCCGCGC 60  
QY 306 GCCCGAGAGCCCGCGCGC 323  
DB 61 GCCCGAGAGCCCGCGCGC 78

RESULT 12  
LOCUS BD082138 244 bp DNA linear PAT 27-AUG-2002  
DEFINITION Reagents and methods useful for detecting diseases of the lung.  
ACCESSION BD082138  
VERSION BD082138.1 GI:25627748  
KEYWORDS JP 2001522225-A/2.  
SOURCE Zee mays  
ORGANISM Zee mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zee.  
1 (bases 1 to 244)  
Medel, P.A.B., Cohen, M., Colpitts, T.L., Friedman, P.N., Gordon, J., Grandos, E.N., Hodges, S.C., Klass, M.R., Kratochvil, J.D., Rapp, L.R., Russell, J.C. and Stroppe, S.D.  
Reagents and methods useful for detecting diseases of the lung  
Patent: JP 2001522225-A 2 13-NOV-2001;  
ABBOTT LABORATORIES  
PN JP 2001522225-A/2  
PD 13-NOV-2001  
PF 30-JAN-1998 JP 1998533078  
PR 31-JAN-1997 US 08/791770  
PI PATRICIA A BILLING MEDEL, MAURICE COHEN, TRACEY L COLPITTS, PAULA N FRIEDMAN,  
PI JULIAN GORDON, EDWARD N GRANADOS, STEVEN C HODGES, MICHAEL R PI  
KLASS, JON D KRATOCHVIL, LISA ROBERTS RAPP, JOHN C RUSSELL, STEPHEN D  
PI STROUPE  
PC C12N15/63, C12N5/10, C12Q1/68, C07K14/47//C07K16/30, G01N33/574 CC  
Strandedness: Single;  
CC Topology: linear;  
FH Key Location/Qualifiers.  
FEATURES  
source 1..244  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:4577"  
BASE COUNT 25 a 97 c 82 g 39 t 1 others  
ORIGIN

Query Match 23.8%; Score 77; DB 6; Length 244;  
Best Local Similarity 98.7%; Pred. No. 0.00027;  
Matches 77; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 246 GCGAGAGACCGGGTATAGAGAGCTCGTGACCTTGCCCGGAGAGCCGAGGTTCCCGCGC 305  
DB 1 GCGAGAGACCGGGTATAGAGAGCTCGTGACCTTGCCCGGAGAGCCGAGGTTCCCGCGC 60  
QY 306 GCCCGAGAGCCCGCGCGC 323  
DB 61 GCCCGAGAGCCCGCGCGC 78

RESULT 13  
LOCUS AC143286 167624 bp DNA linear HTG 09-APR-2003  
DEFINITION Macaca mulatta clone CH250-270J2, \*\*\* SEQUENCING IN PROGRESS \*\*\*.  
ACCESSION AC143286.1 GI:29567825  
VERSION AC143286.1  
KEYWORDS HTG; HTGS\_PHASE2; HTGS\_PGI.  
SOURCE Macaca mulatta (rhesus monkey)

ORGANISM Macaca mulatta  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecoidea; Macaca.  
1 (bases 1 to 167624)  
Cauro, M. and Miosavljevic, A.  
Pooled genomic indexing (PGI): mathematical analysis and experiment design  
(in) Guigo, R. and Gusfield, D. (Eds.):  
ALGORITHMS IN BIOINFORMATICS, SECOND INTERNATIONAL WORKSHOP, WABI  
2002, ROWE, ITALY, SEPTEMBER 17-21, 2002, PROCEEDINGS: 10-28;  
Springer (2002)  
2 (bases 1 to 167624)

REFERENCE  
AUTHORS

Miosavljevic, A., Sodergren, E., Cauro, M., Li, B., Jackson, A.R., Adams, C., Ado-Oduola, B., Ali-Osman, F.R., Allen, C., Albrooks, S.L., Amaratunga, H.C., Are, J.R., Ayala, M., Banks, T., Barbard, J., Benton, J., Bimaga, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brileva, M., Brown, E., Brown, M., Bryant, N.P., Buhey, C., Butcher, P., Burkett, C., Burrell, K.L., Byrd, N.C., Cartron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, Z., Chiu, D., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy, Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Egan, A., Earhart, C., Edwards, C.C., Elhaj, C., Emerling, S., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Han, J., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hodges, M., Hollway, C., Hollins, B., Honsi, F., Howard, S., Huber, J., Hult, S., Hume, J., Ioshikhes, I., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korah, J., Kovar, C., Kratochvil, J., Kureh, A., Landry, N., Leal, B., Lee, E., Lewis, L., Lewis, L., Li, J., Li, Z., Licharge, O., Liu, C., Liu, W., Lonsaged, H., Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapa, P., Macandell, I., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhinney, E., McLeod, M.P., Meador, M., Mei, G., Merscher, S., Metzger, M., Miller, A., Miner, G., Morris, Z., Mitchell, T., Mohabadi, K., Montgomery, K.I., Morgan, N., Morris, S., Moser, M., Neal, D., Nelson, D., Newson, U., Newson, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokemko, S., Ogutu, M., Okunolu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojurokan, I., Rolle, M., Shostart, N., Sleson, I., Sodergren, E., Sonalke, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Swalek, A., Taylor, P., Tamerisa, A., Tamerisa, K., Thomas, J., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalón, D., Vanson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williams, A., Wlezyk, R., Woodman, S., Worley, K., Wu, C., Wu, Y., Wu, Y., Zhou, J., Zorilla, S., Kuchelapati, R., Weinstock, G. and Gibbs, R.  
Unpublished  
3 (bases 1 to 167624)  
Worley, K.C.  
Direct Submission  
Submitted (05-APR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
4 (bases 1 to 167624)  
Worley, K.C.  
Direct Submission  
Submitted (09-APR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
\*\*\*\*\* Genome Center \*\*\*\*\*  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>



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ORIGIN

Query Match 17.2% Score 55.4; DB 2; Length 187413;  
Best Local Similarity 47.1%; Pred.No.0.43;  
Matches 152; Conservative 0; Mismatches 171; Indels 0; Gaps 0;

1 GCGCGTGGGCTGAGACCGGAAAGCGAGGTGGGCGCGGCTTCCGCGAGACAA 60  
Db 99885 GGGGGGGGGCGCGGGCGCGCGCGCGCGCGCGGGGGGGGGGGCGCGC 99826  
Qy 61 GCGCGGGCTGCT 120  
Db 99825 CG 99766  
Qy 121 GGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180  
Db 99765 GGGGGGGGGCGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 99706  
Qy 181 GCGACGCGCGCTGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 240  
Db 99705 CG 99646  
Qy 241 GAGGGCGCGAGACCGGCTTATAGAGCGCTTCTCTCTCTCTCTCTCTCTCT 300  
Db 99645 GCG 99586  
Qy 301 CG 323  
Db 99585 CGCT 99563

RESULT 15  
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LOCUS Mus musculus chromosome X clone RP23-290J11, \*\*\* SEQUENCING IN  
DEFINITION PROCRESS \*\*\* 32 unordered pieces.  
ACCESSION BX470203 GI:30524787  
VERSION HTG; HTGS PHASE1; HTGS DRAFT; HTGS FULLTOP.  
KEYWORDS Mus musculus (house mouse)  
SOURCE Mus musculus  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 210420)  
McLaren, S  
Direct Submission  
Submitted (28-MAY-2003) Wellcome Trust Sanger Institute, Hinxton,  
Cambridgeshire, CB10 1SA, UK. E-mail enquiries: clonerequest@sanger.ac.uk  
humquerry@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk  
On May 10, 2003 this sequence version replaced gi:3042443.  
Sequence from the Mouse Genome Sequencing Consortium whole genome  
shotgun may have been used to confirm this sequence. Sequence data  
from the whole genome shotgun alone has only been used where it has  
a phred quality of at least 30.

COMMENT  
----- Genome Center  
Center: Wellcome Trust Sanger Institute  
Center code: SC  
Web site: http://www.sanger.ac.uk  
Contact: humquerry@sanger.ac.uk  
----- Project Information  
Center project name: BM290J11  
----- Summary Statistics  
Assembly program: XGAP4; version 4.5  
Chemistry: Dye-terminator; 100% of reads  
Consensus quality: 202018 bases at least Q40

Consensus quality: 203190 bases at least Q30  
Consensus quality: 204024 bases at least Q20  
Insert size: 207320; sum-of-contigs  
Insert size: 224229; 3.3% error; agarose-fp  
Quality coverage: 5.59x in Q20 bases; sum-of-contigs Quality  
coverage: 5.42x in Q20 bases; agarose-fp

NOTE: This is a 'working draft' sequence. It currently  
consists of 32 contigs. The true order of the pieces  
is not known and their order in this sequence record is  
arbitrary. Gaps between the contigs are represented as  
runs of N, but the exact sizes of the gaps are unknown.  
This record will be updated with the finished sequence  
as soon as it is available and the accession number will  
be preserved.

1 3800: contig of 3800 bp in length  
3801 3900: gap of 100 bp  
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14368 14467: gap of 100 bp  
14468 23787: contig of 9320 bp in length  
23788 23888: gap of 100 bp  
23888 33457: contig of 9570 bp in length  
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52028 52127: gap of 100 bp  
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57573 57673: gap of 100 bp  
57673 60264: contig of 2592 bp in length  
60265 60365: gap of 100 bp  
60365 67527: contig of 7163 bp in length  
67528 67627: gap of 100 bp  
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81609 81708: gap of 100 bp  
81709 87644: contig of 5936 bp in length  
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103110 111904: contig of 8795 bp in length  
111905 112004: gap of 100 bp  
112005 118667: contig of 6663 bp in length  
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121126 121225: gap of 100 bp  
121226 124217: contig of 2992 bp in length  
124218 124317: gap of 100 bp  
124318 130093: contig of 5776 bp in length  
130094 130193: gap of 100 bp  
130194 143295: contig of 13102 bp in length  
143296 143395: gap of 100 bp  
143396 157267: contig of 13871 bp in length  
157268 157366: gap of 100 bp  
157367 160923: contig of 3557 bp in length  
160924 161023: gap of 100 bp  
161024 165472: contig of 4449 bp in length  
165473 165572: gap of 100 bp  
165573 168489: contig of 2917 bp in length  
168490 168589: gap of 100 bp  
168590 172389: contig of 3800 bp in length  
172390 172489: gap of 100 bp  
172490 175893: contig of 3404 bp in length  
175894 175993: gap of 100 bp  
175994 180720: contig of 4727 bp in length  
180721 180820: gap of 100 bp  
180821 184771: contig of 3951 bp in length  
184772 184871: gap of 100 bp  
184872 190258: contig of 5387 bp in length  
190259 190358: gap of 100 bp  
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[illegible]

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Db	58055 GGGGNGGNGNNGNNNGNNGNNGNNGNNGNNGNNGNNGNNGNNGNNGNNGNNGN 57996	
Db	61 GGCGGGGGCTGCTCTCTCATAGAGGGGCCAGGGCTTCGCAAGAAGTCTTAGAGCC 120	
Db	57995 NCGGGGGCCCCG 57936	
Db	121 GGGCAGGAAAGGGGGGCACGGGCTTCCAGAGCCCGCGCGCGCGCGCGCGAGATTGGCAG 180	
Db	57935 GGGGGGGCCCCGGGGGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 57876	
Db	181 GGCACGGCCGTGAGCGGAGCGGGGCACAGGCGTTTCTCATAGAGCCCGCGCGCGCGCGCTG 240	
Db	57875 GGG 57816	
Db	241 GAGGGGCGAGGACCGGG 257	
Db	57815 GGG 57799	
RESULT 16		
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LOCUS		
DEFINITION	Papio anubis clone RP41-323P4, WORKING DRAFT SEQUENCE, 5 unordered pieces.	
ACCESSION	AC091093	
VERSION	AC091093.1 GI:13487950	
KEYWORDS	HTG; HTRS PHASRL; HTRS DPAFL	
SOURCE	Papio anubis (olive baboon)	
ORGANISM	Papio anubis	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cereopithecinae; Papio.	
REFERENCE	1 (bases 1 to 167077)	
AUTHORS	Meyer, K., Beckwith-Green, S.M., Benjamin, B., Blakesley, R.W., Grant, S., Guan, X., Gupta, J., Ho, S.-U., Idol, U.R., Karlins, E., Lee-Yan, S.-O., Legaspi, R., Lim, M., Maduro, Q.L., Maduro, V.B., Masilko, C., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Prasad, P., Shevchenko, Y.Y., Snyder, B., Stancinich, S., Thomas, J.W., Thomas, A.J., Touchman, J.W., Turgison, C., Vogt, D.L., Walker, M.A., Wetherby, K.D., Zhang, L.H. and Green, E.D.	
TITLE	NISC Comparative Sequencing Initiative	
JOURNAL	Unpublished	
REFERENCE	2 (bases 1 to 167077)	

Fri Nov 7 08:10:01 2003

us-10-081-817a-19\_copy\_229\_551.rge

Page 12

AUTHORS Green, E.D.  
TITLE Direct Submission  
JOURNAL Submitted (25-MAR-2001) NIH Intramural Sequencing Center, 8717  
Govermont Circle, Gaithersburg, MD 20877, USA

-----Genome Center  
Center: NIH Intramural Sequencing Center  
Center code: NISC  
Web site: <http://www.nisc.nih.gov>  
Contact: [nisc\\_mouse@nigl.nih.gov](mailto:nisc_mouse@nigl.nih.gov)  
-----Project Information  
Center project name: amz  
Center clone name: 323P04

-----Summary Statistics  
Sequencing vector: plasmid; n/a; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.990319  
Consensus quality: 164327 bases at least Q40  
Consensus quality: 164859 bases at least Q30  
Consensus quality: 165145 bases at least Q20  
Insert size: 135000; agarose-fp  
Insert size: 144000; pulse-field-gel  
Insert size: 16677; sum-of-coverage  
Quality coverage: 9.16x in Q20 bases; agarose-fp  
Quality coverage: 8.59x in Q20 bases; pulse-field-gel  
Quality coverage: 7.42x in Q20 bases; sum-of-coverage

-----NOTE: This is a 'working draft' sequence. It currently  
\* consists of 5 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 2680: contig of 2680 bp in length  
\* 2681 2780: gap of unknown length  
\* 2781 12589: contig of 9809 bp in length  
\* 12590 12689: gap of unknown length  
\* 12690 65711: contig of 53022 bp in length  
\* 65712 65811: gap of unknown length  
\* 65812 104335: contig of 38524 bp in length  
\* 104336 104435: gap of unknown length  
\* 104436 167077: contig of 62642 bp in length.

-----Location/Qualifiers  
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/clone\_id="RP41-323P4"  
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Best Local Similarity 48.3%; Pired. No. 0.56;  
Matches 152; Conservative 0; Mismatches 163; Indels 0; Gaps 0;

2 CGCGTGGGTCAACCGCAAGCGAGGTGCGCGCGGTGGCTCCGCGAGCAAG 61  
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Qy 62 GCGCGGCGCTGCTCTCTCAGAGGAGCGCGGCGCTGCGCAAGAGAGTCTCGAGGCGCG 121  
Db 166861 GCGCGGCGCGCGCGCGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 166802  
Qy 122 GCGAGGAGGAGGAGCGCGCGCTTCCAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCG 181  
Db 166801 CGCGCGGCGCGCGCGGAGCGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 166742  
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Qy 242 AGCGCGAGAGCGCGGCTTAAAGAGCGCTGAGCGCTTCCCGGCGCGCGCGCGCGCGCG 301  
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Qy 302 GCGCGCGCGCGAGCGCG 316  
Db 166621 GCGGCGCGAGAGCGCG 166607

RESULT 17  
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LOCUS AC084804.1  
DEFINITION Mus musculus clone RP23-314K21 strain C57BL6/J, WORKING DRAFT  
ACCESSION AC084804  
VERSION AC084804.10 GI:17488575  
KEYWORDS HTG, HTGS PHASE1, HTGS DRAFT.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 219952)  
Grills, G., Han, J., Montgomery, K.T., Chin, D., Decker, J., Fusina, M.,  
Goltz, J., Haider, A., Hall, L., Ioshikhes, I.P., Lee, E., Long, J.,  
Perera, A., Shm, C., Thomas, E. and Kuchertapatti, R.  
High Throughput Mouse Sequencing  
Unpublished  
2 (bases 1 to 219952)  
Grills, G., Han, J., Montgomery, K.T., Chin, D., Decker, J., Fusina, M.,  
Goltz, J., Haider, A., Hall, L., Ioshikhes, I.P., Lee, E., Long, J.,  
Perera, A., Shm, C., Thomas, E. and Kuchertapatti, R.  
Direct Submission  
Submitted (18-NOV-2000) Department of Molecular Genetics, Albert  
Einstein College of Medicine Genome Center, 1300 Morris Park Ave.,  
Bronx, NY 10461, USA  
On Dec 11, 2001 this sequence version replaced gi:13560369.

-----Genome Center  
Center: Harvard Partners Genome Center  
Center Code: HPGC  
Web site: <http://www.hpcg.org/Sequence/mouse.html>  
Contact: [hpgc@mdel.mgh.harvard.edu](mailto:hpgc@mdel.mgh.harvard.edu)  
-----Summary Statistics  
Center project name: AEZ  
Sequencing vector: pUC18; L08752  
Chemistry: Dye-terminator Big Dye; 100%  
\*Consensus quality: 207914 at least Q20  
\*Consensus quality: 205077 at least Q30  
\*Consensus quality: 200559 at least Q40  
\*Consensus quality: 200559 at least Q40  
\*Estimated insert size: agarose-fp - N/A  
\*Estimated insert size: 219052 - sum-of-coverage  
Quality coverage: 10.7 x in Q20 bases; sum-of-coverage estimation

COMMENT

-----NOTE: This is a 'working draft' sequence. It currently  
\* consists of 46 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence

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* as soon as it is available and the accession number will
* be preserved.
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132932: contig of 11076 bp in length
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168000: gap of unknown length
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173255: gap of unknown length
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184387: gap of unknown length
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193014: contig of 4251 bp in length
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197265: contig of 4251 bp in length
197266: gap of unknown length
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199581: contig of 1405 bp in length
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201026: gap of unknown length
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208141: gap of unknown length
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209852: contig of 697 bp in length
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FEATURES
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REFERENCE 1 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
AUTHORS Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,  
Horrihan, S., Soppet, D.R., and Weaver, Z.  
TITLE Cancer gene determination and therapeutic screening using signature  
gene sets  
JOURNAL Patent: WO 0194629-A 3319 13-DEC-2001;  
Avalon Pharmaceuticals (US)  
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VERSION AX333047.1 GI:18123681  
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Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,  
Horrihan, S., Soppet, D.R., and Weaver, Z.  
TITLE Cancer gene determination and therapeutic screening using signature  
gene sets  
JOURNAL Patent: WO 0194629-A 3556 13-DEC-2001;  
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Best Local Similarity 50.2%; Pred. No. 0.83;  
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Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 Alvarez, C., Horne, D., Perez-da-Silva, S., and Vockley, J.G.  
AUTHORS Gene expression profiles in liver cancer  
TITLE Patent: WO 0229103-A 3953 11-APR-2002;  
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ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 53370) Birren B., Nusbaum C. and Lander E. Homo sapiens chromosome 18, clone CTD-2333M9 Unpublished		
TITLE	2 (bases 1 to 53370)		
JOURNAL	Birren, N., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barne, N., Bestert, V., Bloom, T., Boguski, J., Boulikas, B., Camara, P., Chang, J., Chazaro, B., Chepel, Y., Collymore, A., Cook, A., Cooke, P., DeArrelano, K., Dewar, K., Diaz, J. S., Dodge, S., Fero, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horion, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatsis, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., MacDonald, P., Major, J., Matthews, C., McCarthy, M., Meldrum, J., Menais, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schnupack, R., Seaman, S., Severy, J., Smith, C., Spencer, B., Stange-Rothmann, N., Stojanovic, N., Talamas, J., Teafaye, S., Theodore, J., Topham, K., Travers, M., Vasilev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, W.		
COMMENT	Direct Submission Submitted (05-JUL-2002) Whitehead Institute/MIT Center for Genome Research, 330 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.P.A. & Green, P. (1996-1997) <a href="http://ftp.genome.washington.edu/RN/RepeatMasker.html">http://ftp.genome.washington.edu/RN/RepeatMasker.html</a> ----- Genome Center Center: Whitehead Institute / MIT Center for Genome Research Center code: MIBR Web site: <a href="http://www-seq.wi.mit.edu">http://www-seq.wi.mit.edu</a> Contact: <a href="mailto:sequence_submission@genome.wi.mit.edu">sequence_submission@genome.wi.mit.edu</a> ----- Project Information Center Project name: L27663 Center Clone name: 2333_M_9 -----		

\* NOTE: This record contains 66 individual sequencing reads that have not been assembled into

\* NOTE: This record contains 66 individual  
\* sequencing reads that have not been assembled into

\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

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#### FEATURES

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AUTHORS      Flint,J., Thomas,K., Micklem,G., Raynham,H., Clark,K.,
Doggett,N.A., King,A. and Higgs,D.R.
TITLE        The relationship between chromosome structure and function at a
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JOURNAL      Nat. Genet. 15 (3), 252-257 (1997)
MEDLINE      97207543
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Higgs,D.R.
TITLE        Sequence, structure and pathology of the fully annotated terminal 2
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JOURNAL      Hum. Mol. Genet. 10 (4), 339-352 (2001)
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Higgs,D.R.
TITLE        Direct Submission
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Oxon OX3 9DS, UK
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misc_feature 10639..27638
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repeat_region complement(11258..11842)
/note="L1MC/D; RepeatMasker predicted
23/10/2000"
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23/10/2000"
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/rpt_family="SINE/Alu"
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gene 412932..>16397
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16377..>16397)
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/note="GENSCAN prediction; no supporting evidence known at
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complement(13389..13696)
/note="AluSc; RepeatMasker predicted
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23/10/2000"
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23/10/2000"
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/note="AluSc; RepeatMasker predicted
23/10/2000"
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/note="MER65a; RepeatMasker predicted
23/10/2000"
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gene complement(17109..29489)

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Best Local Similarity 50.2%; Pred. No. 0.55; Indels 1; Gaps 1;
Matches 161; Conservative 0; Mismatches 159;

QY 1 GCGGTGGGGTCAACCCGAAAGAGTCCGGGCGGCGTGGCTTCCGAGACAA 60
Db 154697 GCGGTGGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCG 154756
QY 61 GCGCGGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
Db 154757 GCGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCG 154816
QY 121 GCGCAGGAAAGGGGCGAGCGGCTTCCAGAGCCCGCGCGCGCAGCAGAAATTGCGCAG 180
Db 154817 GCGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCG 154876
QY 181 GGCACGGCCGTGAGCGGAGCGGCGAGCGGCTTCTCTGAGAGCGC-GGGCAGAGCCGCGCT 239
Db 154877 GCGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCG 154936
QY 240 GGAGGGCGGAGGAGCGGGGTATGAGAGCTCGGGCTTCCGCGGAGCGAGAGTTCC 299
Db 154937 CGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCG 154996
QY 300 CCGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCG 320
Db 154997 GCGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCG 155017

RESULT 25
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LOCUS AF327440
DEFINITION Homo sapiens BTE-binding protein 4 (BTEB4) mRNA, complete cds.
ACCESSION AF327440
VERSION AF327440.1 GI:13195440
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE 1 (bases 1 to 1133)
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS Conley,A.A. and Urrutia,R.
TITLE Isolation of a novel zinc finger transcription factor from the
this organ (Abstract 1153)
Pancreas 21, 437 (2000)
2 (bases 1 to 1133)
Conley,A.A. and Urrutia,R.
REFERENCE Submitted (08-DEC-2000) GI Research Unit, Mayo Clinic, 200 1st SW,
Rochester, MN 55905, USA
FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="19"
/cell_line="CFPac-1"
/tissue_type="exocrine pancreas"

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CDS

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WQCDKKFARSDLARHRTHTGKRFPSCPLCKRPTSDHLAKARHPGFHDLRL  
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BASE COUNT 144 a 480 c 344 g 165 t  
ORIGIN

Query Match 16.3%; Score 52.6; DB 9; Length 1133;  
Best Local Similarity 49.8%; Pred. No. 4.4;  
Matches 160; Conservative 0; Mismatches 159; Indels 2; Gaps 1;

OY 3 GCGTGGGTGACAGCCGCAAGAGAGTGGCGGGGCTCGCGAGACAAAG 62  
DB 410 GCTTGGCGCAGTCCGGAAGGAGACAGCGGTGCTTTGGCGGAGGCGCGCG 351  
OY 63 CCGGGCTGCTCTCTCAGAGGCGCCAGCGCTCGAGAGAGTCTCGAGCGCG 122  
DB 350 CCGGGGCGCGCGCCAGAGCGGAGCGAGCGCTGAGAGAGAGGCGGAGCG 291  
OY 123 GCAGGAGAGGAGGAGCGGCTTCCAGGCGCGCGCGCGAGCAAGTTGGCAGG 182  
DB 290 CCGCGGAGCGGCTCGGAGTCCGCGAGTCCGCG--CAGAGTCTGCGGCGAGCA 233  
OY 183 CAGCGCGTGAAGCGGAGCGGCGAGGCTTTCTCAGAGCGCGGCGAGCGCTGA 242  
DB 232 GGTGGGCGCGCGCGGCGCGCGCGCGCGCGAGAGCGGCGGCGGCGGTG 173  
OY 243 GGGGCGAGAGCGGAGTATTAAGAGCTCTGCGCTTGGCGGAGCGCGAGTTCCCG 302  
DB 172 GCCCGGGGCTCCCGGAGTGAAGCGGCTCGCGCGCGCGCGCAGTCAGCGCGG 113  
OY 303 CGCGCGCGAGCGCGCGCGCGCG 323  
DB 112 CGGGGCGCGCGCGCGCTCGGGGC 92

RESULT 26  
AC012615 149252 bp DNA linear PRI 03-AUG-2002  
LOCUS Homo sapiens chromosome 19 clone CTB-31020, complete sequence.  
DEFINITION  
AC012615  
VERSION  
AC012615.4 GI:22094313  
KEYWORDS  
HTG, HUGS-PHASE0.  
SOURCE  
ORGANISM  
Homo sapiens (human)  
REFERENCE  
AUTHORS  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 149252)  
TITLE  
DOE Joint Genome Institute and Stanford Human Genome Center.  
REFERENCE  
AUTHORS  
Unpublished  
2 (bases 1 to 149252)  
TITLE  
DOE Joint Genome Institute.  
REFERENCE  
AUTHORS  
Direct Submissions  
Submitted (31-OCT-1999) Production Sequencing Facility, DOE Joint  
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
3 (bases 1 to 149252)  
TITLE  
DOE Joint Genome Institute and Stanford Human Genome Center.  
REFERENCE  
AUTHORS  
Direct Submissions  
Submitted (03-AUG-2002) DOE Joint Genome Institute, 2800 Mitchell  
Drive, Walnut Creek, CA 94598, USA  
COMMENT  
On Aug 3, 2002 this sequence version replaced gi:7711554.

Draft Sequence Produced by DOE Joint Genome Institute  
www.jgi.doe.gov  
Finishing Completed at Stanford Human Genome Center  
www.sbgc.stanford.edu  
Quality: Phrap Quality >=40.99.8% of Sequence;  
Retained Total Number of Errors is 0.5  
NOTE: BACTERIAL TRANSPOSON excised at 118353.

FEATURES  
Source  
Location/Qualifiers

1..149252  
/organism="Homo sapiens"  
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Best Local Similarity 49.8%; Pred. No. 1.4;  
Matches 160; Conservative 0; Mismatches 159; Indels 2; Gaps 1;

OY 3 GCGTGGGTGACAGCCGCAAGAGAGTGGCGGGGCTCGCGAGACAAAG 62  
DB 55535 GCTTGGCGCAGTCCGGAAGGAGACAGCGGTGCTTTGGCGGAGGCGCGCG 55594  
OY 63 CCGGGCTGCTCTCTCAGAGGCGCCAGCGCTCGAGAGAGTCTCGAGCGCG 122  
DB 55595 CCGGGGCGCGCGCCAGAGCGGAGCGAGCGCTGAGAGAGAGGCGGAGCG 55654  
OY 123 GCAGGAGAGGAGGAGCGGCTTCCAGGCGCGCGCGCGAGCAAGTTGGCAGG 182  
DB 55655 CCGCGGAGCGGCTCGGAGTCCGCGAGTCCGCG--CAGAGTCTGCGGCGAGCA 55712  
OY 183 CAGCGCGTGAAGCGGAGCGGCGAGGCTTTCTCAGAGCGCGGCGAGCGCTGA 242  
DB 55713 GGTGGGCGCGCGCGCGCGCGCGCGCGCGCGAGAGCGGCGGCGGCGGTG 55772  
OY 243 GGGGCGAGAGCGGAGTATTAAGAGCTCTGCGCTTGGCGGAGCGCGAGTTCCCG 302  
DB 55773 GCCCGGGGCTCCCGGAGTGAAGCGGCTCGCGCGCGCGCGCAGTCAGCGCGG 55832  
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DB 55833 CGGGGCGCGCGCGCGCTCGGGGC 55853

RESULT 27  
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LOCUS Homo sapiens clone RP11-12P9, LOW-PASS SEQUENCE SAMPLING.  
DEFINITION  
AC011578  
VERSION  
AC011578.4 GI:9123847  
KEYWORDS  
HTG, HUGS-PHASE0.  
SOURCE  
ORGANISM  
Homo sapiens (human)  
REFERENCE  
AUTHORS  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 135119)  
TITLE  
Homo sapiens, clone RP11-12P9  
REFERENCE  
AUTHORS  
Unpublished  
2 (bases 1 to 135119)  
TITLE  
Britten, B., Linton, L., Nussbaum, C., Lander, E., Allen, N., Anderson, M.,  
Baldwin, J., Barne, N., Beckerly, R., Boguslavsky, L., Bouhgalter, B.,  
Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,  
Cooke, P., Dearliano, K., Dewar, K., Domingo, M., Donelan, L., Doyle, M.,  
Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D.,  
Gallagan, J., Gardina, S., Grant, G., Hages, B., Heath, R., Horton, L.,  
Howland, J., Johnson, R., Jones, C., Kann, L., Karas, A., Klein, D.,  
Lehoczky, J., Lieu, C., Locke, K., MacDonald, P., Margulis, N.,  
McEwan, P., McGurk, A., McKernan, K., McDonald, P., Melarini, J.,  
Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,  
Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,

TITLE  
JOURNAL  
COMMENT

Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,  
Testafaye, S., Tittel, A., Vassilev, H., Vo, A., Wheeler, J., Wu, X.,  
Wymann, D., Ye, W. J., Zimmer, A. and Zody, M.  
Direct Submission  
Submitted (07-Oct-1999) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Jul 13, 2000 this sequence version replaced gi:7107923.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: MIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence\_submission@genome.wi.mit.edu

Project Information  
Center project name: L3313

Center clone name: 12\_F\_9

NOTE: This record contains 16 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

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3446 3445: gap of 100 bp  
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4288 4288: gap of 100 bp  
4489 4490: contig of 762 bp in length  
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5151 5150: gap of 100 bp  
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43759 43758: gap of 100 bp  
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* 53140 53903: contig of 764 bp in length
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* 54004 54783: contig of 760 bp in length
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* 54884 55629: contig of 766 bp in length
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* 58272 59016: contig of 745 bp in length
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Matches 143; Conservative 0;

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Qy 83 GGGCCCCAGCGCTTGCAGAGAGAACTCTCGAGCGCGCGAGGAGGAGCGGCGC 142
Db 13343 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 13402
Qy 143 TTCCAGAGCGCGCGCGCGCGCGAGAGATTGGCCAGGCGACGCGCTGTAGCGGCG 202
Db 13403 GCGAGGGGGCGCGAGGGGGCGGGGGGGGGCGGGGGGGGGGGGGGGGG 13462
Qy 203 GCGAGGCTTCTCAGAGAGCGCGGCGAGCGCGCTGTAGAGGGCGAGGACCGGGTATTA 262
Db 13463 CGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 13522
Qy 263 GAAGCTCTGTGGCTTGGCGGCGAGCGCGAGATTCCCGCGCGCGCGCGAGCGC 316
Db 13523 GGGGGCGAGCGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 13576

RESULT 28
XELRGE12 557 bp DNA linear VRT 28-APR-1993
LOCUS XELRGE12 oocyte rRNA, complete internal transcribed spacer 1 (ITS
DEFINITION 1), clone pX1101.
ACCESSION K01371 GI:214706
VERSION K01371.1
KEYWORDS Internal transcribed spacer; ribosomal RNA.
SEGMENT 2 of 3
SOURCE Xenopus laevis (African clawed frog)
ORGANISM Xenopus laevis
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Xenopus.
REFERENCE 1 (bases 1 to 557)
AUTHORS Stewart, M.A., Hall, L.M. and Maden, B.E.
TITLE Multiple heterogeneities in the transcribed spacers of ribosomal
DNA from Xenopus laevis

JOURNAL Nucleic Acids Res. 11 (3), 629-646 (1983)
MEDLINE 83168891
PUBMED 6300760
COMMENT Original source text: Xenopus laevis DNA, clone pX1101.
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Best Local Similarity 50.5%; Pred. No. 6.2; Mismatches 148; Indels 1; Gaps 1;
Matches 152; Conservative 0;

Qy 23 GCGAAGTGGGAGCGCGGCTTGGCGAGACAAAGCGCGCTCTCTCTCA 82
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Qy 83 GGGCCCCAGCGCGCTTGCAGAGAGAACTCTCGAGCGCGCGAGGAGGAGCGGCGC 142
Db 218 GGGCGCGCGCGGGGTACTAGCGG-GGGCGGGGGCGGGGGGGCTGGCGCGGAGCGGGCG 276
Qy 143 TTCCAGAGCGCGCGCGCGCGAGAGATTGGCCAGGCGACGCGCTGTAGCGGCGCG 202
Db 277 GCGCCAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 336
Qy 203 GCGAGGCTTCTCAGAGAGCGCGGCGAGCGCGCGCGCTGTAGAGGGCGAGACCGGGTATTA 262
Db 337 AGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 396
Qy 263 GAAGCTCTGTGGCTTGGCGGCGAGCGCGAGATTCCCGCGCGCGCGCGCGCGCGCG 322
Db 397 GCGGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 456
Qy 323 C 323
Db 457 C 457

RESULT 29
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LOCUS XELRGE12 x.laevis external transcribed spacer (ets) & 18S, 5.8S, 28S (5',
DEFINITION end) rRNA genes, clone pX1101.
ACCESSION J00999 GI:214711
VERSION J00999.1
KEYWORDS 18S ribosomal RNA; 28S ribosomal RNA; 5.8S ribosomal RNA; external
transcribed spacer; ribosomal RNA.
SEGMENT 2 of 2
SOURCE Xenopus laevis (African clawed frog)
ORGANISM Xenopus laevis
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Xenopus.
REFERENCE 1 (bases 977 to 1275)
AUTHORS Salim, M. and Maden, B.E.
TITLE Nucleotide sequence encoding the 5' end of Xenopus laevis 18S rRNA
Nucleic Acids Res. 8 (13), 2871-2884 (1980)
MEDLINE 81053719
PUBMED 6253895
REFERENCE 2 (bases 2599 to 3924)
AUTHORS Hall, L.M. and Maden, B.E.
TITLE Nucleotide sequence through the 18S-28S intergene region of a
vertebrate ribosomal transcription unit
Nucleic Acids Res. 8 (24), 5993-6005 (1980)
MEDLINE 81124313
PUBMED 6258158
REFERENCE 3 (bases 1001 to 2825)
AUTHORS Salim, M. and Maden, B.E.
TITLE Nucleotide sequence of Xenopus laevis 18S ribosomal RNA inferred
from gene sequence

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JOURNAL Nature 291 (5812), 205-208 (1981)  
MEDLINE 81197642  
PubMed 7015146  
REFERENCE 4 (bases 1 to 1060)  
AUTHORS Maden, B.E., Moss, M., and Salim, M.  
TITLE Nucleotide sequence of an external transcribed spacer in xenopus laevis rDNA: sequences flanking the 5' and 3' ends of 18S rRNA are non-complementary  
JOURNAL Nucleic Acids Res. 10 (7), 2387-2398 (1982)  
MEDLINE 82221416  
PubMed 6283480  
COMMENT Original source text: xenopus laevis dna; clone px1r101 [Nucleic Acids Res. 8, 2871-2884 (1980)], [2], [3], [4].  
[3] comparison with s.cerevisiae 18S rDNA revealed extensive regions of high homology interspersed with tracts having little or no homology. Major regions of high homology contain almost all the rna methyl groups. Major regions of low homology are considerably richer in 'c' and 'g' in xenopus than in the yeast [3]. [4] found that there are not initiation (atg) codons in the ets region and that, as in other x.laevis rDNA clones, the sequence preceding the ets is duplicated, with a few changes, in the 'bam island' sequence of the non-transcribed spacer.  
Location/Qualifiers

## FEATURES

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115..117  
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289..3924  
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577..582  
/note="[4] uncertain about 'g' string length"  
1001..2825  
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3383..3544  
/product="5.8S ribosomal RNA"  
3807..3924  
/product="28S ribosomal RNA"  
BASE COUNT 685 a 1363 c 1297 g 579 t  
ORIGIN 163 bp upstream of hinfI site.

Query Match 16.2%; Score 52.2; DB 5; Length 3924;  
Best Local Similarity 50.5%; Pred. No. 3.9;  
Matches 152; Conservative 0; Mismatches 148; Indels 1; Gaps 1;

QY 23 GCGAAGTGTGCGGCGCGGCTCTCGGAGACAAAGCGCGCTGCTCTCTCA 82  
DB 2983 GCGAAGGCGCGGCGCGGCTCTCGGAGACAAAGCGCGCGCTCTCTCTCA 3042  
QY 83 GGGCCCCAGCGCTGCGAAGAGTCTCGAGCGCGGCGAGGAGGAGGCGA 142  
DB 3043 GGGCCCCAGCGCTGCGAAGAGTCTCGAGCGCGGCGAGGAGGAGGCG 3101  
QY 143 TTCGAGGCGCGCGCGCGCGCGAGAGTTCGCGAGCGCGCGCTGAGCGAG 202  
DB 3102 GCGGAGGCGCGCGCGCGCGCGAGAGTTCGCGAGCGCGCGCTGAGCG 3161  
QY 203 GCGAGGCTTTCTAGAGAGCGCGCGCGAGCGCGCTGAGCGAGGAGGAG 262  
DB 3162 AGACCGCGCGCGCGCGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAG 3221  
QY 263 GAAGCTGTGCGCTTTCGCGGAGCGCGAGGAGGAGGAGGAGGAGGAGG 322  
DB 3222 GCGGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGAGGAGGAGGAGG 3281  
QY 323 C 323  
DB 3282 C 3282

RESULT 30  
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LOCUS XL28SR 7634 bp DNA linear VRT 06-JUN-2003  
DEFINITION X.laevis 28S ribosomal RNA gene for 28S rRNA.  
ACCESSION X59734  
VERSION X59734.1 GI:64487  
KEYWORDS 18S ribosomal RNA; 28S ribosomal DNA; 40S ribosomal subunit; 5.8S ribosomal DNA; ribosomal RNA transcription unit.  
SOURCE Xenopus laevis (African clawed frog)  
ORGANISM Xenopus laevis  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae; Xenopodinae; Xenopus.  
1 (bases 1 to 7634)  
Xenopus borealis and Xenopus laevis 28S ribosomal DNA and the complete 40S ribosomal precursor RNA coding units of both species  
Proc. R. Soc. Lond., B, Biol. Sci. 245 (1312), 65-71 (1991)  
92052296  
Location/Qualifiers

## FEATURES

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1..262  
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Query Match 16.2%; Score 52.2; DB 5; Length 7634;  
Best Local Similarity 50.5%; Pred. No. 3.4;  
Matches 152; Conservative 0; Mismatches 148; Indels 1; Gaps 1;

QY 23 GCGAAGTGTGCGGCGCGGCTCTCGGAGACAAAGCGCGCTGCTCTCTCA 82  
DB 2696 GCGAAGGCGCGGCGCGGCTCTCGGAGACAAAGCGCGCGCTCTCTCTCA 2755  
QY 83 GGGCCCCAGCGCTGCGAAGAGTCTCGAGCGCGGCGAGGAGGAGGCGA 142  
DB 2756 GGGCCCCAGCGCTGCGAAGAGTCTCGAGCGCGGCGAGGAGGAGGCG 2814  
QY 143 TTCGAGGCGCGCGCGCGCGAGAGTTCGCGAGCGCGCGCTGAGCGAG 202  
DB 2815 GCGGAGGCGCGCGCGCGCGAGAGTTCGCGAGCGCGCGCTGAGCGAG 2874  
QY 203 GCGAGGCTTTCTAGAGAGCGCGCGCGAGCGCGCTGAGCGAGGAGGAG 262  
DB 2875 AGACCGCGCGCGCGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAG 2934  
QY 263 GAAGCTGTGCGCTTTCGCGGAGCGCGAGGAGGAGGAGGAGGAGGAGG 322  
DB 2935 GCGGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGAGGAGGAGGAG 2994  
QY 323 C 323  
DB 2995 C 2995

RESULT 31  
 LOCUS XLRN01 8153 bp DNA linear VRT 01-OCT-1996  
 DEFINITION Xenopus laevis genes for 18S, 5.8S and 28S ribosomal RNAs.  
 ACCESSION X02995 J00999 J01001 J01002 J01006 J01007 K01369 K01370  
 K01371 K01372 K01376 K01535 V01444 V01445 V01446 V01447  
 V01448 V01449 V01450 V01451 V01452 V01453 V01454 V01456 X00136  
 X01071  
 VERSION X02995.1 GI:65056  
 KEYWORDS 18S ribosomal RNA; 28S ribosomal RNA; 5.8S ribosomal RNA;  
 repetitive sequence; ribosomal RNA.  
 SOURCE Xenopus laevis (African clawed frog)  
 ORGANISM Xenopus laevis  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;  
 Xenopodinae; Xenopus.  
 REFERENCE 1 (bases 1 to 24)  
 Boseley, P., Moss, T., Machler, M., Portmann, R. and Birnstiel, M.  
 Sequence organization of the spacer DNA in a ribosomal gene unit of  
 Xenopus laevis  
 CELL 17 (1), 19-31 (1979)  
 JOURNAL 79211270  
 MEDLINE 455459  
 PUBMED 2 (bases 25 to 1029)  
 REFERENCE Mader, B.E., Moss, M. and Salim, M.  
 Nucleotide sequence of an external transcribed spacer in Xenopus  
 laevis rDNA: sequences flanking the 5' and 3' ends of 18S rRNA are  
 non-complementary  
 Nucleic Acids Res. 10 (7), 2387-2398 (1982)  
 JOURNAL 82221416  
 MEDLINE 6283480  
 PUBMED 3 (bases 1030 to 2854)  
 REFERENCE Salim, M. and Mader, B.E.  
 Nucleotide sequence of Xenopus laevis 18S ribosomal RNA inferred  
 from gene sequence  
 Nature 291 (5812), 205-208 (1981)  
 JOURNAL 81197642  
 MEDLINE 7015146  
 PUBMED 4 (bases 2855 to 3953)  
 REFERENCE Hall, L.M. and Mader, B.E.  
 Nucleotide sequence through the 18S-28S intergene region of a  
 vertebrate ribosomal transcription unit  
 Nucleic Acids Res. 8 (24), 5993-6005 (1980)  
 JOURNAL 81124313  
 MEDLINE 6258158  
 PUBMED 5 (bases 3954 to 7917)  
 REFERENCE Ware, V.C., Tague, B.W., Clark, C.G., Gourse, R.L., Brand, R.C. and  
 Gerbi, S.A.  
 Sequence analysis of 28S ribosomal DNA from the amphibian Xenopus  
 laevis  
 Nucleic Acids Res. 11 (22), 7795-7817 (1983)  
 JOURNAL 84069805  
 MEDLINE 6359063  
 PUBMED 6 (bases 7918 to 8153)  
 REFERENCE Solinger-Webb, B. and Reeder, R.H.  
 The nucleotide sequence of the initiation and termination sites for  
 ribosomal RNA transcription in X. laevis  
 Cell 18 (2), 485-499 (1979)  
 JOURNAL 80045030  
 MEDLINE 498280  
 PUBMED 7 (bases 1 to 8153)  
 REFERENCE Moss, T., Boseley, P.G. and Birnstiel, M.L.  
 More ribosomal spacer sequences from Xenopus laevis  
 Nucleic Acids Res. 8 (3), 467-485 (1980)  
 JOURNAL 81076644  
 MEDLINE 7003549  
 PUBMED 8 (bases 1 to 8153)  
 REFERENCE Salim, M. and Mader, B.E.  
 Nucleotide sequence encoding the 5' end of Xenopus laevis 18S rRNA  
 Nucleic Acids Res. 8 (13), 2871-2884 (1980)  
 JOURNAL 81053719

PUBMED 6253895  
 REFERENCE 9 (bases 1 to 8153)  
 AUTHORS Stewart, M.A., Hall, L.M. and Mader, B.E.  
 TITLE Multiple heterogeneities in the transcribed spacers of ribosomal  
 DNA from Xenopus laevis  
 JOURNAL 83168891  
 MEDLINE 6300760  
 PUBMED 10 (bases 1 to 8153)  
 REFERENCE Mader, B.E., Forbes, J.M., Stewart, M.A. and Eason, R.  
 18S coding sequences in amplified ribosomal DNA from Xenopus laevis  
 occur as highly homogeneous, unmethylated, and lack major open  
 reading frames  
 EMBO J. 1 (5), 597-601 (1982)  
 JOURNAL 84236020  
 MEDLINE 6329693  
 PUBMED 11 (bases 1 to 8153)  
 REFERENCE Boseley, P.G., Tuyns, A. and Birnstiel, M.L.  
 Mapping of the Xenopus laevis 5.8S rDNA by restriction and DNA  
 sequencing  
 Nucleic Acids Res. 5 (4), 1121-1137 (1978)  
 JOURNAL 78178358  
 MEDLINE 652517  
 PUBMED 12 (bases 1 to 8153)  
 REFERENCE Ford, P.J. and Mathieson, T.  
 The nucleotide sequences of 5.8-S ribosomal RNA from Xenopus laevis  
 and Xenopus borealis  
 Eur. J. Biochem. 87 (1), 199-214 (1978)  
 JOURNAL 78214616  
 MEDLINE 666689  
 PUBMED  
 COMMENT This sequence was assembled from refs. 1-6 above. The rRNA gene is  
 present as multiple tandem repeats. The non-transcribed region is  
 approximately 5Kb long, and includes entries XLRN3 and XLRN6.  
 There is considerable variation between gene copies in all the  
 non-coding regions, as described in 1-7 and references therein.  
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 /product="18S ribosomal RNA"  
 intron 2855..3411  
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 rRNA 3412..3573  
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 intron 3574..3835  
 /note="internal transcribed spacer 2"  
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 ORIGIN  
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 Best Local Similarity 50.5%; Pred. No. 3.3; Indels 1; Gaps 1;  
 Matches 152; Conservative 0; Mismatches 148;  
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 Db 3012 GCGAGGG 3071  
 Cy 83 GGGGCCGAGCGCTGCGCAAGAGAGTCTTCAGAGCGCGGAGAGGAGGCGACGGGC 142  
 Db 3072 GGGCGCGCGCGGGTACTGACCG-GGGCGGGGCGCGGGGGCTGGCGCGGAGCGGGCG 3130  
 Cy 143 TTCCCGAGGGCGCGCGGCGGACAGAGAGTTCGCGAGGCGACGGCGTGAAGCGAGCGG 202

Db 3131 GCCCAGAGGCGCTCCGCGCTCCCGGCTCCGCGAGACCCGCGCGGCGTTGCA 3190  
Qy 203 GCAGAGCTTCTGAGAGCGCGGCGAGCGCGCTGAGAGGCGAGACCGGATATA 262  
Db 3191 AGACCCCGCGCGCGCGGCGGAGGCGCGGAGAGCGCGGAGAGGAGGAGGAG 3250  
Qy 263 GAAGCCCTGCTGCGCTTCCCGCGGCGAGCGCGGCTCCCGCGCGCGCGCGCGC 322  
Db 3251 CGCGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGAGACCCGCTCCCGCGCGCGC 3310  
Qy 323 C 323  
Db 3311 C 3311

RESULT 32  
LOCUS ACT100946/c 52390 bp DNA linear HTG 23-NOV-2001  
DEFINITION Mus musculus clone RP23-73E24, LOW-PASS SEQUENCE SAMPLING.  
ACCESSION ACT100946.1 GI:17059720  
VERSION ACT100946.1  
KEYWORDS HTG; HTGS PHASEO.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 52390)  
Britten, B., Linton, L., Nusbaum, C. and Lander, E.  
Unpublished  
2 (bases 1 to 52390)  
Britten, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,  
Anderson, S., Barina, N., Baetjen, V., Boguslavsky, L., Bouckigalter, B.,  
Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,  
Cokepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A.,  
Cooke, P., DeAngelis, K., Dewar, K., Diaz, J. S., Dodge, S., Fato, S.,  
Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, N.,  
Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,  
Hagos, B., Heaford, A., Horton, L., Hulme, W., Hume, I., Johnson, R.,  
Jones, C., Kamat, A., Karatas, A., Kells, C., Lacroque, K.,  
Lamaze, R., Landers, T., Lehoczy, J., Levine, R., Liu, G.,  
Maclean, C., MacDonald, P., Major, J., Margulis, N., Matthews, C.,  
McCarthy, M., McGowan, P., McKernan, K., McPheters, R., Meldrum, J.,  
Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,  
Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D.,  
Oliver, J., Peterson, K., Phunhahang, P., Pierre, N., Pollara, V.,  
Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,  
Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupbach, R.,  
Seaman, S., Severy, P., Spencer, B., Strange-Thomann, N., Stojanovic, N.,  
Struse, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,  
Topham, K., Travers, M., Travis, N., Triggillo, J., Vassiliev, H.,  
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,  
Zaitoun, J., Zembek, L., Zimmer, A. and Zody, W.

TITLE  
JOURNAL  
COMMENT  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence\_submissions@genome.wi.mit.edu  
Project Information  
Center project name: L14623  
Center clone name: 73\_E\_24

\* NOTE: This record contains 66 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for

\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.  
1 699: contig of 699 bp in length  
700 799: gap of 100 bp  
800 1483: contig of 684 bp in length  
1484 1583: gap of 100 bp  
1584 2389: contig of 706 bp in length  
2390 3395: gap of 100 bp  
3396 3998: contig of 706 bp in length  
3999 4698: contig of 703 bp in length  
4699 4997: gap of 100 bp  
4998 4997: contig of 699 bp in length  
4999 4997: gap of 100 bp  
5000 4997: contig of 698 bp in length  
5001 5595: gap of 100 bp  
5596 6290: contig of 694 bp in length  
6291 6389: gap of 100 bp  
6390 7069: contig of 680 bp in length  
7070 7170: gap of 100 bp  
7171 7669: contig of 700 bp in length  
7670 7970: gap of 100 bp  
7971 8666: contig of 697 bp in length  
8667 9471: contig of 705 bp in length  
9472 9571: gap of 100 bp  
9572 10273: contig of 702 bp in length  
10274 10373: gap of 100 bp  
10374 11220: contig of 747 bp in length  
11221 11899: contig of 679 bp in length  
11900 11999: gap of 100 bp  
12000 12700: contig of 701 bp in length  
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13597 14392: contig of 696 bp in length  
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16378 16945: gap of 100 bp  
16946 16945: gap of 682 bp in length  
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18979 19078: gap of 100 bp  
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21357 21456: gap of 100 bp  
21457 22158: contig of 702 bp in length  
22159 22258: gap of 100 bp  
22260 22962: contig of 704 bp in length  
22963 23062: gap of 100 bp  
23063 23770: contig of 708 bp in length  
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24541 24640: gap of 100 bp  
24641 25329: contig of 689 bp in length  
25330 25429: gap of 100 bp  
25430 26119: contig of 690 bp in length  
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[illegible]

RESULT 35	AB053222	12562 bp	DNA	linear	PR1_08-JAN-2003
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DEFINITION	AB053222				
	Homo sapiens gene for N-acetylglucosaminyltransferase IVa, partial				
ACCESSION	AB053222				
VERSION	AB053222.1	GI:27544617			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORANISM	Homo sapiens				

1  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES

1  
Minowa, M. T. and Takeuchi, M.  
Alternative splicing in human N-acetylglucosaminyltransferase IVa  
Gene  
Unpublished  
2 (bases 1 to 1262)  
Minowa, M. T. and Yoshida, A.  
Direct Submission  
Submitted (05-JAN-2001) Aruto Yoshida, Central labs. for Key  
Technology, Kirin Brewery Co. Ltd., Kanazawa-ku, Fuku-ura, 1-13-5  
Yokohama, Kanagawa 236-0004, Japan (E-mail: ayoshida@kirin.co.jp,  
Tel: 81-45-788-7761, Fax: 81-45-788-4042)  
Location/Qualifiers

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	/note="alternative splicing exon1' or exon2"
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ACCESSION	AC109826		PRI 27-JAN-2003
VERSION	AC109826.4		complete sequence.
KEYWORDS	GT:27905024		
COMMENT	HTG.		
	Homo sapiens (human)		

ORGANISM	REFERENCE
<i>Homo sapiens</i>	1 (bases 1 to 8746)
Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
Sulston, J.E. and Waterston, R.	Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)	
99063792	

RECEIVED  
 3/8/07  
 JOURNAL  
 TITLE  
 The sequence of Homo sapiens BAC clone RPL1-764D5  
 Unpublished (2001)  
 3 (bases 1 to 87746)  
 WATERSTON, R.H.  
 DIRECT SUBMISSION  
 Submitted (07-FEB-2002) Genome Sequencing Center, Washington University, St. Louis, MO, USA

UNIVERSITY SCHOOL OF MEDICINE, 4444 FOREST PARK PARKWAY, ST. LOUIS MO 63108, USA (Dr 87746)

WATKINSON, R. H.  
DIRECT SUBMISSION  
Submitted (11-MAR-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis MO 63108, USA  
5 (bases 1 to 87746)

REFERENCE TITLE	AUTHORS	JOURNAL
Waterston, R. Direct Submission Submitted (27-NOV-2002)	Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA	
6 (bases 1 to 87746)		
Waterston, R. Direct Submission Submitted (27-JAN-2003)	Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA	
On Jan 27, 2003 this sequence version replaced g1:257779545.		

----- Genome Center  
Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: <http://genome.wustl.edu/gsc>  
Contact: saplens@atson.wustl.edu  
----- Summary Statistics  
Center project name: H NH0764D05  
Drafting Center: WIBR

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence



QY 74 TCTCTAGAGGGGCCCCAGCGCCCTGCCAGAGAGTCTCTGAGAGCCCGGCGAGAGAGG 133  
Db 24102 AGCGGGGGGGGGCGAGCGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 24043  
QY 134 GGCAGCGGCTTCCAGAGGGCCCGCGCGCGAGAGAGAGTGGCCAGGGGACCGCCCTGA 193  
Db 24042 GGGCGGGGCTTACAGCAGCTCCCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 23983  
QY 194 GCGGAGCGGCGAGGGCTTTCTCAGAGAGCGGGCGAGAGCGCGCTGAGAGGGCGAGAC 253  
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QY 254 CGGGTATPAGAGCTCTGCGCTTGGCCCGCGAGCGCGAGTTCCTCCCGCGCGCGAG 313  
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RESULT 37  
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LOCUS Homo sapiens chromosome 8 clone CTD-230711 map 8, LOW-PASS SEQUENCE  
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AC105035.1 GI:17977414  
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KEYWORDS Homo sapiens (human)  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.  
TITLE 1 (bases 1 to 67246)  
JOURNAL Homo sapiens chromosome 8, clone CTD-230711  
AUTHORS Unpublished  
2 (bases 1 to 67246)  
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,  
Anderson, S., Barina, N., Baatien, V., Boguslavsky, L., Bouknight, B.,  
Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,  
Choe, P., Colangelo, M., Collins, S., Collymore, A., Cook, A.,  
Cooke, P., DeArrelano, K., Dewar, K., Diaz, J. S., Dodge, S., Fato, S.,  
Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, N.,  
Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,  
Hagos, R., Heaford, A., Horton, L., Hulme, W., Hulse, I., Johnson, R.,  
Jones, C., Kamat, A., Karas, A., Kelle, C., Lacroque, K.,  
Lamas, R., Landers, T., Lehotzky, J., Levine, R., Liu, G.,  
Maclean, C., MacDonald, P., Major, J., Margulis, N., Matthews, C.,  
McCarthy, M., McEwan, P., McKernan, K., McPherson, R., Melidiri, J.,  
Mensut, L., Milova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,  
Nobu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D.,  
O'Neil, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,  
Raymond, C., Rietz, M., Rieback, M., Riley, R., Riese, C., Rogov, P.,  
Roman, S., Sevel, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,  
Strass, N., Subramanian, A., Talamas, J., Tefayeh, S., Theodore, J.,  
Topman, K., Travers, M., Travis, N., Triggillo, J., Vassiliev, H.,  
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, M. J., Young, G.,  
Zahoun, J., Zember, J., Zimmer, A. and Zody, M.

TITLE  
JOURNAL  
COMMENT  
Direct Submission  
Submitted (22-DEC-2001) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
All repeats were identified using RepeatMasker:  
Smith, A. P. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence\_submissions@genome.wi.mit.edu

Project Information

Center project name: L23018

Center clone name: 2307\_I\_1

\* NOTE: This record contains 82 individual

\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying relationships among clones that may be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.  
\* 742: contig of 742 bp in length  
\* 1 743 842: gap of 100 bp  
\* 843 1510: contig of 668 bp in length  
\* 1511 1610: gap of 100 bp  
\* 1611 2313: contig of 703 bp in length  
\* 2314 2413: gap of 100 bp  
\* 2414 3143: contig of 730 bp in length  
\* 3144 3243: gap of 100 bp  
\* 3244 3667: contig of 724 bp in length  
\* 3668 4067: gap of 100 bp  
\* 4068 4789: contig of 722 bp in length  
\* 4790 4889: gap of 100 bp  
\* 4890 5612: contig of 723 bp in length  
\* 5613 6439: contig of 727 bp in length  
\* 6440 6539: gap of 100 bp  
\* 6540 7265: contig of 726 bp in length  
\* 7266 7365: gap of 100 bp  
\* 7366 8052: contig of 687 bp in length  
\* 8053 8152: gap of 100 bp  
\* 8153 8875: contig of 723 bp in length  
\* 8876 8975: gap of 100 bp  
\* 8976 9690: contig of 715 bp in length  
\* 9691 9790: gap of 100 bp  
\* 9791 10533: contig of 743 bp in length  
\* 10534 10633: gap of 100 bp  
\* 10634 11332: contig of 659 bp in length  
\* 11333 11432: gap of 100 bp  
\* 11433 12142: contig of 710 bp in length  
\* 12143 12242: gap of 100 bp  
\* 12243 12952: contig of 710 bp in length  
\* 12953 13052: gap of 100 bp  
\* 13053 13751: contig of 699 bp in length  
\* 13752 13851: gap of 100 bp  
\* 13852 14586: contig of 735 bp in length  
\* 14587 14686: gap of 100 bp  
\* 14687 15417: contig of 731 bp in length  
\* 15418 15517: gap of 100 bp  
\* 15518 16346: gap of 729 bp in length  
\* 16347 17064: contig of 718 bp in length  
\* 17065 17164: gap of 100 bp  
\* 17165 17906: contig of 742 bp in length  
\* 17907 18006: gap of 100 bp  
\* 18007 18723: contig of 717 bp in length  
\* 18724 18823: gap of 100 bp  
\* 18824 19552: contig of 729 bp in length  
\* 19553 19652: gap of 100 bp  
\* 19653 20338: contig of 686 bp in length  
\* 20339 20438: gap of 100 bp  
\* 20439 21123: contig of 685 bp in length  
\* 21124 21223: gap of 100 bp  
\* 21223 21952: contig of 729 bp in length  
\* 21953 22052: gap of 100 bp  
\* 22053 22778: contig of 726 bp in length  
\* 22779 22878: gap of 100 bp  
\* 22879 23598: contig of 720 bp in length  
\* 23599 23698: gap of 100 bp  
\* 23699 24428: contig of 730 bp in length  
\* 24429 24528: gap of 100 bp  
\* 24529 25263: contig of 735 bp in length  
\* 25264 25364: gap of 100 bp  
\* 25365 26090: contig of 727 bp in length

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*      *      *      *      *      *      *      *      *      *      *      *      *      *      *      *
26091 26190: gap of 100 bp
26191 26191: contig of 729 bp in length
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27020 27045: contig of 726 bp in length
27746 27845: gap of 100 bp
27846 28559: contig of 714 bp in length
28560 28659: gap of 100 bp
28660 29371: contig of 712 bp in length
29372 29471: gap of 100 bp
29472 30176: contig of 705 bp in length
30177 30276: gap of 100 bp
30277 31012: contig of 736 bp in length
31013 31112: gap of 100 bp
31113 31837: contig of 725 bp in length
31838 31937: gap of 100 bp
31938 32600: contig of 663 bp in length
32601 32700: gap of 100 bp
32701 33430: contig of 730 bp in length
33431 33530: gap of 100 bp
33531 34355: contig of 725 bp in length
34356 35092: contig of 737 bp in length
35093 35192: gap of 100 bp
35193 35900: contig of 708 bp in length
35901 36715: contig of 715 bp in length
36716 37526: gap of 100 bp
37527 37626: contig of 711 bp in length
37627 38344: gap of 100 bp
38345 38444: gap of 100 bp
38445 39182: contig of 738 bp in length
39183 39282: gap of 100 bp
39283 40016: contig of 734 bp in length
40017 40850: gap of 100 bp
40851 40950: contig of 734 bp in length
40951 41640: contig of 690 bp in length
41641 41740: gap of 100 bp
41741 42472: contig of 732 bp in length
42473 42572: gap of 100 bp
42573 43300: contig of 728 bp in length
43301 43400: gap of 100 bp
43401 44126: contig of 726 bp in length
44127 44226: gap of 100 bp
44227 44913: contig of 687 bp in length
44914 45013: gap of 100 bp
45014 45719: contig of 706 bp in length
45720 46534: gap of 100 bp
46535 47352: contig of 715 bp in length
47353 47452: gap of 100 bp
47453 48187: contig of 718 bp in length
48188 48287: gap of 100 bp
48289 49016: contig of 729 bp in length
49017 49116: gap of 100 bp
49117 49850: contig of 734 bp in length
49851 50683: gap of 100 bp
50684 50769: contig of 715 bp in length
50770 51511: gap of 100 bp
51512 51611: contig of 742 bp in length
51613 52338: gap of 100 bp
52339 52438: contig of 727 bp in length
52439 53172: gap of 100 bp
53173 53272: contig of 734 bp in length
53273 54007: gap of 100 bp
54008 54107: contig of 735 bp in length
54109 54809: gap of 100 bp
54810 54909: contig of 702 bp in length
54911 55614: gap of 100 bp
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Query Match      16.0%; Score 51.8; DB 2; Length 67246;
Best Local Similarity 50.4%; Pred. No. 2.4;
Matches 125; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

1  GCGGCTGGGCTGACAGCCGCAAGCGAAGTCCGCGCGCGGCTTCTGAGAGCA 60
11329 GGGGGGGGGGAGAGGGGAGAGAGGGCGGGGGGGGGGGGGGGGGGGGGGGGG
61  GCGGCGGCGCTTCTCTCTCAAGAGGGGCCCGCCCTCCCAAGAGAGTCTTCAAGAGCC 120
11259 GCGGGCGGGGGGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
121  GCGGCGGAGAGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 180
11209 GCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1150
181  GCGGCGGCGCTGAGAGCGGAGCGGGCGGCTTCTCAAGAGCGGGGGAGAGGGCGCTG 240
11149 GCGCGGAGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 11090
241  GAGGGGCG 248
11089 GGGGGGGG 11082

RESULT 38
AC084084
LOCUS
DEFINITION
AC084084 Homo sapiens chromosome 8 clone RP11-314C19 map 8, LOW-PASS
SEQUENCE SAMPLING.
AC084084.2 GI:13446278
AC084084.2 HTG: HTGS PHASE0.
VERSION
HTG: HTGS PHASE0.
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 71032)
REFERENCE
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 8, clone RP11-314C19
Unpublished
2 (bases 1 to 71032)
REFERENCE
Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Beda, F., Boguslavsky, L.,
Boukhalil, B., Brown, A., Burkett, G., Campopiano, A., Casale, A.,
Chapel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
D'Amico, K., Deng, K., Diaz, J.S., Dodge, S., Ferreira, P.,
Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M.,
Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L.,
Iliev, I., Johnson, R., Jones, C., Kann, L., Karas, A., Larocque, K.,
Lima, R., Lander, E., Lander, T., McCarthy, M., McEwan, P., McKernan, K.,
McDonald, P., Margulis, N., Menais, L., Mihova, T., Mlenga, V.,
McPherson, R., Mridha, U., Naylor, J., Norman, C.H., O'Connor, T.,
O'Donnell, P., O'Neill, D., Olivares, T.M., Oliveira, J., Peterson, K.,
Pier, N., Pisan, C., Pollara, V., Raymond, C., Rieback, M., Riley, R.,
Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P.,
Sougnuez, C., Spencer, B., Stange, Thoman, N., Stojanovic, N.,
Straus, N., Subramanian, A., Talamas, U., Testa, S., Theodore, J.,
Tirrell, A., Travers, M., Triggillo, U., Vassiliev, H., Viel, R., Vo, A.,
Wilson, B., Wu, X., Wyman, D., Ye, W.D., Young, G., Zaitoun, J.,
Zimmer, A. and Zody, M.
Direct Submission
Submitted (12-OCT-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 25, 2001 this sequence version replaced gi:10799449.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research

```

TITLE  
JOURNAL

Center code: WDR  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence\_submissions@genome.wi.mit.edu  
Project Information  
Center project name: L11327  
Center clone name: 314\_C\_19

NOTE: This record contains 85 individual  
sequencing reads that have not been assembled into  
contigs. Runs of N are used to separate the reads  
and the order in which they appear is completely  
arbitrary. Low-pass sequence sampling is useful for  
identifying clones that may be gene-rich and allows  
overlap relationships among clones to be deduced.  
However, it should not be assumed that this clone  
will be sequenced to completion. In the event that  
the record is updated, the accession number will  
be preserved.

1 720: contig of 720 bp in length  
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3399 4153: contig of 754 bp in length  
4153 4253: gap of 100 bp  
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4978 5078: gap of 100 bp  
5078 5815: contig of 737 bp in length  
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5915 6648: contig of 733 bp in length  
6648 6748: gap of 100 bp  
6748 7520: contig of 772 bp in length  
7520 7620: gap of 100 bp  
7620 8347: contig of 727 bp in length  
8347 8447: gap of 100 bp  
8447 9227: contig of 780 bp in length  
9227 9327: gap of 100 bp  
9327 10052: contig of 725 bp in length  
10052 10152: gap of 100 bp  
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10969 11718: contig of 745 bp in length  
11718 11818: gap of 100 bp  
11818 12657: contig of 733 bp in length  
12657 13412: gap of 100 bp  
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14355 14586: gap of 100 bp  
14586 15086: contig of 731 bp in length  
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15186 15901: contig of 715 bp in length  
15901 16001: gap of 100 bp  
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16711 16811: gap of 100 bp  
16811 17539: contig of 728 bp in length  
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17639 18351: contig of 712 bp in length  
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19162 19262: gap of 100 bp  
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27575 28437: gap of 100 bp  
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28538 29258: contig of 721 bp in length  
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32639 32759: gap of 100 bp  
32759 33501: contig of 743 bp in length  
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33602 34347: contig of 746 bp in length  
34348 35165: contig of 718 bp in length  
35166 35265: gap of 100 bp  
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36099 36803: contig of 704 bp in length  
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39276 39376: contig of 721 bp in length  
39377 40113: gap of 100 bp  
40114 40948: contig of 735 bp in length  
40949 41799: gap of 100 bp  
41799 41893: contig of 744 bp in length  
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42631 42730: contig of 738 bp in length  
42731 43459: gap of 100 bp  
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46043 46775: contig of 722 bp in length  
46776 46875: gap of 100 bp  
46877 47609: contig of 733 bp in length  
47610 47709: gap of 100 bp  
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48547 49285: contig of 737 bp in length  
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50179 50278: gap of 100 bp  
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51847 51946: contig of 738 bp in length  
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52673 52773: contig of 726 bp in length  
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Query Match 16.0% Score 51.8; DB 2; Length 71032;  
 Best Local Similarity 43.9%; Pred. No. 2.4; Indels 0; Gaps 0;  
 Matches 134; Conservative 0; Mismatches 171; Indels 0; Gaps 0;

53606 54330: contig of 725 bp in length  
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 \* 55167 55266: gap of 100 bp  
 \* 55267 55979: contig of 713 bp in length  
 \* 55980 56079: gap of 100 bp  
 \* 56080 56923: contig of 744 bp in length  
 \* 56924 57626: gap of 100 bp  
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12 CAGACCGGAAAGCGAGGTCGGGGGCTGCGGCGGAGCAAGAGCGGCGCTG 71  
 28055 CCGCCCGCTGAGGGTCACTCAGCGCGGATCAGAGCGAGCGGCGCGGAGG 28114  
 72 CCTCTCAGAGGGGCCCAAGGCGCTGCGAAGAGTCTTCAGAGCGGCGGAGG 131  
 28115 CCGCAGAGGGGGGAGGCGCGGCGAGGCGAGGCGAGGCGAGGCGGCGGCG 28174  
 132 GGGGCAAGGCGCTTCCAGGGCGCGCGCGCGAGGAGGAGTGGCCAGGGCGA 191  
 28175 GCGGAGGCGACNNACCGAACCGCGCGCGGCGGCGGCGGCGGCGGCGGCG 28234  
 192 GAGCGAGCGCGGCGAGGCGCTTCTCAGAGCGGCGGCGAGGCGGCGGCGGCG 251  
 28235 GGGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 28294  
 252 ACCGGGTATAGAGACCTGTCGCTGCGCGGCGGCGGCGGCGGCGGCGGCGG 311  
 28295 CCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 28354  
 312 AGCCG 316  
 28355 CCGCC 28359

RESULT 39  
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 LOCUS Homo sapiens chromosome 17 clone RP11-248L3 map 17, \*\*\* SEQUENCING  
 DEFINITION IN PROGRESS \*\*\*; 48 unordered pieces.  
 AC012300 2: GT:7230237  
 AC012300 HTG PHASE1  
 KEYWORDS Homo sapiens (human)  
 SOURCE  
 ORGANISM Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 Birkner, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,  
 Baldwin, J., Barina, N., Beckerly, R., Boguslavsky, L., Boukhalter, B.,  
 Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,  
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 Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,  
 Stange, S., Stojanovic, N., Subramanian, A., Talamas, J.,  
 Testa, S., Tirrell, A., Vasilev, H., Vo, A., Wheeler, J., Wu, X.,  
 Wymann, D., Ye, W. J., Zimmer, A. and Zody, M.  
 TITLE  
 JOURNAL Direct Submission  
 Submitted (22-OCT-1999) Whitehead Institute/MIT Center for Genome

## COMMENT

Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Mar 12, 2000 this sequence version replaced g1:6094565.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center  
 Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WIBR  
 Web site: http://www-seq.wi.mit.edu  
 Contact: sequence\_submissions@genome.wi.mit.edu

----- Project Information  
 Center project name: L670  
 Center clone name: 248\_L3

NOTE: This is a 'working draft' sequence. It currently  
 consists of 48 contigs. The true order of the pieces  
 is not known and their order in this sequence record is  
 arbitrary. Gaps between the contigs are represented as  
 runs of N, but the exact sizes of the gaps are unknown.  
 This record will be updated with the finished sequence  
 as soon as it is available and the accession number will  
 be preserved.

1 1038: contig of 1038 bp in length  
 \* 1039 1138: gap of 100 bp  
 \* 1139 1233: contig of 1233 bp in length  
 \* 1234 2473: gap of 100 bp  
 \* 2474 3537: contig of 1064 bp in length  
 \* 3538 3637: gap of 100 bp  
 \* 3638 4776: contig of 1139 bp in length  
 \* 4777 4876: gap of 100 bp  
 \* 4876 6026: contig of 1150 bp in length  
 \* 6027 6126: gap of 100 bp  
 \* 6127 7205: contig of 1079 bp in length  
 \* 7206 7305: gap of 100 bp  
 \* 7306 8345: contig of 1039 bp in length  
 \* 8345 8444: gap of 100 bp  
 \* 8444 9543: contig of 1099 bp in length  
 \* 9544 9643: gap of 100 bp  
 \* 9643 10869: contig of 1226 bp in length  
 \* 10870 10969: gap of 100 bp  
 \* 10970 12118: contig of 1149 bp in length  
 \* 12119 12218: gap of 100 bp  
 \* 12219 13641: contig of 1423 bp in length  
 \* 13642 13741: gap of 100 bp  
 \* 13741 15584: contig of 1843 bp in length  
 \* 15585 15684: gap of 100 bp  
 \* 15684 17014: contig of 1330 bp in length  
 \* 17015 17114: gap of 100 bp  
 \* 17115 18904: contig of 1750 bp in length  
 \* 18905 19004: gap of 100 bp  
 \* 19004 20212: contig of 1206 bp in length  
 \* 20213 20313: gap of 100 bp  
 \* 20313 21330: contig of 1018 bp in length  
 \* 21331 21430: gap of 100 bp  
 \* 21430 22568: contig of 1138 bp in length  
 \* 22569 22668: gap of 100 bp  
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 \* 28658 28757: gap of 100 bp  
 \* 28758 30771: contig of 2013 bp in length  
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 \* 32849 32948: gap of 100 bp  
 \* 32949 35389: contig of 2441 bp in length  
 \* 35390 35490: gap of 100 bp  
 \* 35490 37527: contig of 2038 bp in length  
 \* 37528 37627: gap of 100 bp  
 \* 37627 40579: contig of 2955 bp in length  
 \* 40580 40679: gap of 100 bp  
 \* 40680 43521: contig of 2842 bp in length



Delgado, O., Benson, S., Dermato, C., Ding, Y., Ditt, H., Divya, K.,  
 Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duvál, B., Eaves, K.,  
 Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falla, T., Fan, G.,  
 Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,  
 Fraser, C.M., Gebisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,  
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 Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,  
 Lorenshewali, L., Louisedge, H., Lozada, R., Long, X., Ma, J.,  
 Maheshwari, M., Mahindratne, M., Mahmoud, M., Mallory, K., Mangum, A.,  
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 Mawhney, S., McLeod, M., McNeill, T., Meenen, E., Milosavljevic, A.,  
 Miner, G., Minda, E., Montemayor, J., Moore, S., Morgan, M., Morris, K.,  
 Morris, S., Mundasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D.,  
 Newton, N., Nguyen, N., Norris, S., Nwoketeme, O., Okunolu, G.,  
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 Popovic, D., Prims, E., Pu, L.-L., Puzos, M., Quiroz, J., Rachlin, E.,  
 Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y.,  
 Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A.,  
 Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Severy, G., Scherer, S.,  
 Scott, G., Shateman, S., Shen, H., Shetty, J., Shvartsberg, A.,  
 Sisson, I., Sitter, C.D., Smajd, D., Steed, A., Stedegren, E.,  
 Song, X.-Z., Sorelle, R., Soosa, J., Steimle, M., Strong, R., Sutton, A.,  
 Swack, A., Tabore, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S.,  
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 Waldron, L., Welker, B., Wang, J., Wang, Q., Wang, S., Warren, J.,  
 Warren, R., Wei, X., White, P., Williams, G., Willis, R., Wlezyk, R.,  
 Woodson, H., Woley, K., Wright, D., Wright, R., Wu, J., Yakub, S.,  
 Yan, J., Yoon, L., Yoon, V., Yu, P., Zhang, J., Zhou, J., Zhou, X.,  
 Zhao, S., Dunn, D., von Niederhagen, A., Weise, R., Smith, D.R.,  
 Holt, R.A., Smith, H.O., Weinstock, G., and Gibbs, R.A.

Direct Submissions  
 2 (bases 1 to 44508)  
 Rat Genome Sequencing Consortium.  
 Direct Submissions  
 Submitted (29-Oct-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA

COMMENT  
 Genome Center  
 Center: Baylor College of Medicine  
 Center code: BCM  
 Web site: <http://www.hgsc.bcm.tmc.edu/>  
 Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)  
 Project Information  
 Center project name: KDBL  
 Center clone name: CH230-426019  
 Summary Statistics  
 Sequencing vector: Plasmid  
 Chemistry: Dye-terminator Big Dye 100% of reads  
 Assembly program: Phrap; version 0.990329  
 Consensus quality: 24050 bases at least Q40  
 Consensus quality: 27314 bases at least Q30  
 Consensus quality: 29291 bases at least Q20

\* NOTE: Estimated insert size may differ from sequence length  
 (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_drafi\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_drafi_data.html))  
 \* NOTE: This is a "working draft" sequence. It currently  
 consists of 26 contigs. The true order of the pieces  
 is not known and their order in this sequence record is  
 arbitrary. Gaps between the contigs are represented as  
 runs of N, but the exact sizes of the gaps are unknown.  
 This record will be updated with the finished sequence  
 as soon as it is available and the accession number will  
 be preserved.

1 1009: contig of 1009 bp in length

Query Match	Best Local Similarity	Score	DB 2	Length	44508
Matches 148; Conservative	47.9%	Pred. No. 3.1	Mismatches 161; Indels 0; Gaps 0		
7	GGGGTCAGACCGCAAGAGTGGCGGGCGGGGCTGGCGCTCGAGACCAAGCCCGG	66			
Db	GGGGCGCGCGCGCGCGCGCGCGGAGAGAGAGAGAGCGGCTCGCGGGAGAGAGCGCCCG	897			
QY	GGCTGCTCTCTCAAGAGGCGCCAGCGCTTCCCAAGAGAAATCTTCAAGCGCCCGGGCAG	126			
Db	CCCGCGCGCGCGCGCGCGCGCGCGCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	837			
QY	GGAAAGGGGACAGGGGCTTCCAGAGGCGCGCGCGCGCGAGCAGAGAAATTTGGCCAGGCGACG	186			

Accession	Sequence	Position
Db	AGGGGGGAAACGGGGGGGGCCCGGAGCGGGGACCGGGGCGCGGGGGGTCAAGAGGAGGG	777
QY	187 GCCGTGAGCGAGACGCGGACAGGGCTTTCTCAGAGACGCGGGGAGAGCCGGGGCTGAGAGGG	246
Db	776 CCGGGGGGGGCGCGGAGCGACGAAAAGAGGGGGGCGGGGCGCGGGCGCGGG	717
QY	247 CGAGGACCGGGGTATAGAGAGCTCGTGCGCTTGGCCGGGGCAGCGGAGTTCCCGCGGG	306
Db	716 CGCGGGGCGCGGGGGGGCGCGCGGGCGGGCGGGCGGGGCGCGGGGGCGCGGGGCG	657
QY	307 CCCCGAGGC	315
Db	656 GCCGGCGGC	648

Search completed: November 6, 2003, 08:07:12  
Job time : 1962.81 secs

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XX Diagnosing and/or determining a predisposition to a cellular  
 PI proliferative disorder of breast tissue, in particular breast cancer,  
 PT by determining the state of methylation of one or more nucleic acids  
 PT isolated from the subject  
 XX  
 XX Disclosure, Fig 9a, 115p, English.  
 XX  
 CC The present invention relates to a method of diagnosing a cellular  
 CC proliferative disorder of breast tissue, which involves determining the  
 CC state of methylation of one or more nucleic acids isolated from the  
 CC subject, where the state of methylation of the nucleic acids as compared  
 CC with a state of methylation from a subject not having the cellular  
 CC proliferative disorder of breast tissue is indicative of a cellular  
 CC proliferative disorder of breast tissue in the subject. The nucleic acids  
 CC may be TWIST, HMOX5, NES-1, retinoic acid receptor beta (RARbeta),  
 CC oestrogen receptor, cyclin D2, Wilms' tumour gene (WT-1), 14.3.3 sigma,  
 CC HIN-1 or RASBP1A. The method is useful for diagnosing and/or determining  
 CC a predisposition to a cellular proliferative disorder, in particular  
 CC breast cancer including ductal carcinoma in situ, lobular carcinoma,  
 CC colloid carcinoma, tubular carcinoma, medullary carcinoma, metaplastic  
 CC carcinoma, intraductal carcinoma in situ, lobular carcinoma in situ and  
 CC papillary carcinoma in situ. The present sequence is a gene fragment used  
 CC in the exemplification of the invention.  
 CC  
 XX Sequence 1794 BP, 240 A, 646 C, 522 G, 318 T, 68 other;  
 SO  
 Query Match 91.9%; Score 296.8; DB 24; Length 1794;  
 Best Local Similarity 93.7%; Pred. No. 8,5e-53;  
 Matches 238; Conservative 0; Mismatches 20; Indels 0; Gaps 0;  
 QY 6 TGGGCTCAGACCCGCAAGCGAAGTCCGCGGCTGGGCTTCGCGAGACAAAGCCG 65  
 DB 854 TGGGGTCAGACCGCAAGCGAAGTCCGCGGCTGGGCTTCGCGAGACAAAGCCG 913  
 QY 66 GGCCTCCCTCTCTCAGAGGGCCCGCAGCGCTTGCAGAGAAAGTCTCGAGCCCGCGGCA 125  
 DB 914 GGCCTCCCTCTCTCAGAGGGCCCGCAGCGCTTGCAGAGAAAGTCTCGAGCCCGCGGCA 973  
 QY 126 GGGAGAGGGGCAAGGGGCTTCCAGAGGGCCCGCGCGCGAGAGAAAGTGGCCAGAGGCA 185  
 DB 974 GGGAGAGGGGCAAGGGGCTTCCAGAGGGCCCGCGCGCGAGAGAAAGTGGCCAGAGGCA 1033  
 QY 186 GGGCGTGAAGCGAGCGAGGGGCTTCTCAGAGAGCGGGGAGAGGCGCGCTGAGAGG 245  
 DB 1034 GGGCGTGAAGCGAGCGAGGGGCTTCTCAGAGAGCGGGGAGAGGCGCGCTGAGAGG 1093  
 QY 246 GCGAGAGACCGGGTATAGAGCTCGTGGCTTGGCCCGGAGCGCGAGTCCCGCGGC 305  
 DB 1094 GNN 1153  
 QY 306 GCGCCGAGCGCCCGCGCCG 323  
 DB 1154 GCGCCGAGCGCCCGCGCCG 1171  
 RESULT 2  
 ID AAV54620 standard; cDNA, 562 BP.  
 XX AAV54620;  
 AC  
 XX 25-MAR-2003 (updated)  
 DT 30-OCT-1998 (first entry)  
 XX  
 DE LU105 specific consensus polynucleotide sequence.  
 XX  
 KM LU105; lung disease marker; immunosassay; lung disease; cancer;  
 KM blood; plasma; serum; ss.  
 XX Homo sapiens.  
 OS  
 XX  
 FH Key Location/Qualifiers

FT CDS 122..436  
 FT /tag= a  
 FT /transl\_except= (pos:176..178, aa:Val)  
 FT /product= "LU105 polypeptide"  
 XX  
 XX W09833926-A1.  
 XX  
 XX 06-AUG-1998.  
 XX  
 XX 30-JAN-1998; 98WO-US01766.  
 XX  
 XX 31-JAN-1997; 97US-0791710.  
 XX  
 XX (ABBO ) ABBOTT LAB.  
 XX  
 XX Billing-medet PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;  
 PI Granados EN, Hodges SC, Klags MR, Kratochvil JD, Robertstrapp L;  
 PI Russell JC, Stroupe SD;  
 XX WPI: 1998-437479/37.  
 DR P-PSDB; AAW5868.  
 XX  
 XX New nucleic acid for the lung disease marker LU105 - polypeptides,  
 PT antibodies and genes, used for diagnosis, prevention, treatment of  
 PT lung disease, specifically cancer  
 XX  
 XX Claim 11, Fig 1, 123p; English.  
 XX  
 CC Sequences shown in AAV54616 to AAV54621 represent LU105 specific  
 CC polynucleotide sequences. These are used in the method of the invention  
 CC for detecting target LU105 nucleic acid. The method comprises treating a  
 CC sample with at least one LU105 specific nucleic acid, or its complement  
 CC which is at least 50 percent identical with the LU105 specific nucleic  
 CC acid sequences (AAV54616 to AAV54621). LU105 is a lung disease marker.  
 CC Cells transfected with a recombinant expression system that contains  
 CC LU105 polypeptides which are used to raise antibodies. The antibodies are  
 CC used to detect the LU105 antigen, and correspondingly this antigen is  
 CC used to detect specific antibodies, in usual immunoassays. The LU105  
 CC polypeptides and nucleic acid sequences are used for diagnosis, staging,  
 CC monitoring, prognosis, prevention, treatment and determination of  
 CC susceptibility to, lung disease, specifically cancer. The LU105  
 CC polypeptides are also used to screen for specific binding agents, useful  
 CC therapeutically. LU105 is a marker for lung disease (present at high  
 CC concentration in altered form or in an unusual body compartment). LU105  
 CC can be detected in blood, plasma or serum in an inexpensive, non-invasive  
 CC test.  
 CC (updated on 25-MAR-2003 to correct PI field.)  
 CC  
 XX  
 XX Sequence 562 BP; 82 A; 200 C; 192 G; 86 T; 2 other;  
 SO  
 Query Match 37.2%; Score 120; DB 19; Length 562;  
 Best Local Similarity 39.2%; Pred. No. 3,2e-16;  
 Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 203 GCAAGGCTTCTCAGAGCGCGGCGAGGCGCGCTGAGAGGGCGAGAGACCGGGTATTA 262  
 DB 1 GCAAGGCTTCTCAGAGCGCGGCGAGGCGCGGCTGAGAGGGCGAGAGACCGGGTATTA 60  
 QY 263 GAAAGCTGTGGCTTCCCGGAGCGAGCGAGGTTCCCGCGCGCGCGCGCGCGCGCG 322  
 DB 61 GAAAGCTGTGGCTTCCCGGAGCGAGCGAGGTTCCCGCGCGCGCGCGCGCGCGCG 120  
 QY 323 C 323  
 DB 121 C 121  
 RESULT 3  
 ID AAV54616 standard; cDNA, 190 BP.  
 XX AAV54616;  
 AC AAV54616;

XX 25-MAR-2003 (updated)  
 DT 30-OCT-1998 (first entry)  
 DE LUI05 specific polynucleotide sequence from clone 3353867.  
 XX LUI05; lung disease marker; immunoassay; lung disease; cancer;  
 KM blood; plasma; serum; ss.  
 OS Homo sapiens.  
 PN WO983926-A1.  
 XX 06-AUG-1998.  
 PF 30-JAN-1998; 98WO-US01766.  
 PR 31-JAN-1997; 97US-0791710.  
 XX (ABBO) ABBOTT LAB.  
 PA Billing-medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;  
 PI Grandos EN, Hodges SC, Klass MR, Kratochvil JD, Robertstrapp L;  
 PI Russell JC, Stroepe SD;  
 XX WPI; 1998-437479/37.  
 DR New nucleic acid for the lung disease marker LUI05 - polypeptides,  
 PI antibodies and genes, used for diagnosis, prevention, treatment of  
 PT lung disease, specifically cancer  
 XX Claim 11; Fig 1; 123pp; English.  
 PS Sequences shown in AAV54616 to AAV54621 represent LUI05 specific  
 CC polynucleotide sequences. These are used in the method of the invention  
 CC for detecting target LUI05 nucleic acid. The method comprises treating a  
 CC sample with at least one LUI05 specific nucleic acid, or its complement  
 CC which is at least 50 percent identical with the LUI05 specific nucleic  
 CC acid sequences (AAV54616 to AAV54621). LUI05 is a lung disease marker.  
 CC Cells transformed with a recombinant expression system that contains  
 CC LUI05 specific nucleic acid fragments, are used to express recombinant  
 CC LUI05 polypeptides which are used to raise antibodies. The antibodies are  
 CC used to detect the LUI05 antigen, and correspondingly this antigen is  
 CC polypeptides and nucleic acid sequences are used for diagnosis, staging,  
 CC monitoring, prognosis, prevention, treatment and determination of  
 CC susceptibility to, lung disease, specifically cancer. The LUI05  
 CC therapeutics are also used to screen for specific binding agents, useful  
 CC concentration, in altered form or in an unusual body compartment). LUI05  
 CC can be detected in blood, plasma or serum in an inexpensive, non-invasive  
 CC test.  
 CC (updated on 25-MAR-2003 to correct PI field.)  
 CC  
 SO Sequence 190 BP; 18 A; 69 C; 67 G; 32 T; 4 other;  
 Query Match 36.2%; Score 117; DB 19; Length 190;  
 Best Local Similarity 96.7%; Pred. No. 1,4e-15;  
 Matches 117; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 203 GCAGGCTTCTAGAGAGCGCGGCGAGCGCGCTGAGGGGCGAGACCGGCTATTA 262  
 DB 1 GCAGGCTTCTAGAGAGCGCGGCGAGCGCGCTGAGGGGCGAGACCGGCTATTA 60  
 QY 263 GAAGCTCTGCTGCTGCGCGGCGAGCGCGAGCTTCCCGCGCGCCCGAGCGCCCGCGGC 322  
 DB 61 GAAGCTCTGCTGCTGCGCGGCGAGCGCGAGTTCCTCCGCGCGCCCGAGCGCCCGCGGC 120  
 QY 323 C 323  
 DB 121 C 121

RESULT 4  
 ID AA298173 standard; cDNA; 543 BP.  
 XX AA298173;  
 AC AA298173;  
 DT 11-MAY-2000 (first entry)  
 DE Human signal peptide containing protein HSP-65 cDNA SEQ ID NO:199.  
 XX Human signal peptide containing protein; HSP; diagnosis; cancer;  
 KM inflammation; cardiovascular disease; anticancer; anti-inflammatory;  
 KM antimicrobial; nocotropic; neuroprotective; cardiovascular; hepatocytic;  
 KM antiaesthetic; gene therapy; cell proliferation; neurological disorder;  
 KM reproductive disorder; developmental disorder; arteriosclerosis;  
 KM cirrhosis; psoriasis; acquired immune deficiency syndrome; anemia;  
 KM asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;  
 KM Parkinson's disease; Huntington's disease; ovulatory defect;  
 KM muscular dystrophy; ss.  
 XX Homo sapiens.  
 OS  
 XX WO200000610-A2.  
 PN 06-JAN-2000.  
 BD 25-JUN-1999; 99WO-US14484.  
 XX 26-JUN-1998; 98US-0090762.  
 PR 31-JUN-1998; 98US-0094983.  
 PR 01-OCT-1998; 98US-0102686.  
 PR 11-DEC-1998; 98US-0112129.  
 XX (INCY-) INCYTE PHARM INC.  
 PA Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn ME;  
 PI Akperblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;  
 PI Bandman O;  
 XX WPI; 2000-160673/14.  
 DR P-PSDB; AAY87288.  
 PT New human signal peptide-containing proteins useful in treatment,  
 PT prevention and diagnosis of e.g. cancer, inflammation and  
 CC cardiovascular disease  
 PS Claim 9; Page 289; 327pp; English.  
 CC AA298109 to AA298242 encode AAY87224 to AAY87357 which represent the  
 CC human signal peptide-containing proteins HSP-1 to HSP-134. HSPs have  
 CC anticancer, anti-inflammatory, antimicrobial, nocotropic, hepatocytic,  
 CC neuroprotective, cardiovascular and antiaesthetic activities, and can  
 CC be used in gene therapy. HSPs can be used to treat or prevent disorders  
 CC associated with decreased activity or function of HSP. Antagonists of  
 CC HSP are used to treat or prevent disorders associated with increased  
 CC activity or function of HSP. Such diseases include cell proliferation  
 CC (including cancer), inflammation, cardiovascular, neurological,  
 CC reproductive or developmental disorders, (e.g. arteriosclerosis,  
 CC cirrhosis), psoriasis, acquired immune deficiency syndrome, anemia, or  
 CC asthma, Crohn's disease, microbial or other infections, congestive or  
 CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's  
 CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSP  
 CC nucleic acids can be used for the recombinant production of HSP, for  
 CC detecting HSP in standard hybridisation and amplification assays (for  
 CC diagnosis and monitoring), in gene therapy, as antisense, or  
 CC triplex-forming or ribozyme therapeutics, for detecting related sequences  
 CC or genetic variations, and for chromosomal mapping. HSP are also used to  
 CC raise specific antibodies (Ab) and to screen for agonists and  
 CC antagonists (potential therapeutic agents). Ab are used to diagnose, or  
 CC monitor, HSP-related diseases (in usual immunoassays), as therapeutic  
 CC antagonists, in competitive drug screens, and for purification of HSP  
 CC from natural sources.

SQ Sequence 543 BP; 89 A; 194 C; 178 G; 82 T; 0 other;

Query Match 28.5%; Score 92; DB 21; Length 543;  
Best Local Similarity 100.0%; Pred. No. 2e-10;  
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 232 CCGGCGCTGAGAGGGGCGAGACCGGGTATTAAGAGCCTCTGCGCTTGCCTGGCGAGCCG 291  
DB 1 CCGGCGCTGAGAGGGGCGAGACCGGGTATTAAGAGCCTCTGCGCTTGCCTGGCGAGCCG 60

QY 292 CAGGTTCCCGCGCGCGCGCGAGCCCGCGCGCC 323  
DB 61 CAGGTTCCCGCGCGCGCGCGAGCCCGCGCGCC 92

RESULT 5

AA229723 standard; DNA; 543 BP.

AA229723;

27-MAR-2000 (first entry)

Human lung specific gene lng107.

Lung Specific Gene; LSG; lng107; human; diagnostic marker;

prognosticate; lung cancer; diagnosis; ds.

Homo sapiens.

Location/Qualifiers

Key 93.407  
CDS /tag= a  
/product= "LSG lng107 protein"

W0960160-A1.

25-NOV-1999.

12-MAY-1999; 99WO-US10344.

21-MAY-1998; 98US-0086212.

(DIAD-) DIADEXUS LLC.

Yang F, Macina RA, Sun Y;

WPI; 2000-116320/10.

P-PSDB; AAY44458.

A new method for diagnosing, monitoring and staging lung cancer -

Claim 6; Page 36; 40pp; English.

The present sequence is a lung specific gene (LSG) lng107 from human

clone ID 566271. The LSG has high level of tissue specificity for lungs

and is overexpressed in cancerous tissues. The sequence serves as a

diagnostic marker for detecting, monitoring staging and prognosticating

lung cancer. The diagnosis involves comparing levels of LSG in samples

obtained from patient and normal control.

Sequence 543 BP; 89 A; 194 C; 178 G; 82 T; 0 other;

Query Match 28.5%; Score 92; DB 21; Length 543;  
Best Local Similarity 100.0%; Pred. No. 2e-10;  
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 232 CCGGCGCTGAGAGGGGCGAGACCGGGTATTAAGAGCCTCTGCGCTTGCCTGGCGAGCCG 291  
DB 1 CCGGCGCTGAGAGGGGCGAGACCGGGTATTAAGAGCCTCTGCGCTTGCCTGGCGAGCCG 60

QY 292 CAGGTTCCCGCGCGCGCGCGAGCCCGCGCGCC 323

DB 61 CAGGTTCCCGCGCGCGCGCGAGCCCGCGCGCC 92

RESULT 6  
AAV54621 standard; cDNA; 519 BP.

AAV54621;

25-MAR-2003 (updated)  
30-OCT-1998 (first entry)  
LNU05 polypeptide encoding cDNA clone 1327836IH.

LNU05; lung disease marker; immunoassay; lung disease; cancer;

blood; plasma; serum; ss.

Homo sapiens.

Location/Qualifiers

Key 79.393  
CDS /tag= a  
/transl\_except= (pos:136..138, aa:Val)  
/product= "LNU05 polypeptide"

W09833926-A1.

06-AUG-1998.

30-JAN-1998; 98WO-US01766.

31-JAN-1997; 97US-0791710.

(ABBO) ABBOTT LAB.

Billing-medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;

Granados EN, Hodges SC, Klass MR, Kratochvil JD, Robertstrapp L;

Russell JC, Strome SD;

WPI; 1998-437479/37.

P-PSDB; AAW75868.

New nucleic acid for the lung disease marker LNU05 - polypeptides,

antibodies and genes, used for diagnosis, prevention, treatment of

lung disease, specifically cancer

Claim 11; Fig 1; 123pp; English.

Sequences shown in AAV54616 to AAV54621 represent LNU05 specific

polynucleotide sequences. These are used in the method of the invention

for detecting target LNU05 nucleic acid. The method comprises treating a

sample with at least one LNU05 specific nucleic acid, or its complement

which is at least 50 percent identical with the LNU05 specific nucleic

acid sequences (AAV54616 to AAV54621). LNU05 is a lung disease marker.

Cells transformed with a recombinant expression system that contains

LNU05 specific nucleic acid fragments, are used to express recombinant

LNU05 polypeptides which are used to raise antibodies. The antibodies are

used to detect the LNU05 antigen, and correspondingly this antigen is

used to detect specific antibodies, in usual immunoassays. The LNU05

polypeptides and nucleic acid sequences are used for diagnosis, staging,

monitoring, prognosis, prevention, treatment and determination of

susceptibility to, lung disease, specifically cancer. The LNU05

polypeptides are also used to screen for specific binding agents, useful

therapeutically. LNU05 is a marker for lung disease (present at high

concentration, in altered form or in an unusual body compartment). LNU05

can be detected in blood, plasma or serum in an inexpensive, non-invasive

test.

(Updated on 25-MAR-2003 to correct PI field.)

Sequence 519 BP; 78 A; 190 C; 170 G; 81 T; 0 other;

Query Match 24.1%; Score 78; DB 19; Length 519;  
Best Local Similarity 100.0%; Pred. No. 1.5e-07;





PR 12-JUN-1998; 98US-0083090.  
 PR 12-JUN-1998; 98US-0083105.  
 PR 16-JUN-1998; 98US-0083410.  
 PR 16-JUN-1998; 98US-0083412.  
 PR 16-JUN-1998; 98US-0083514.  
 PR 17-JUN-1998; 98US-0083512.  
 PR 17-JUN-1998; 98US-0083518.  
 PR 17-JUN-1998; 98US-0083598.  
 PR 17-JUN-1998; 98US-0083600.  
 PR 17-JUN-1998; 98US-0083602.  
 PR 18-JUN-1998; 98US-0083607.  
 PR 18-JUN-1998; 98US-0083608.  
 PR 19-JUN-1998; 98US-0083947.  
 PR 19-JUN-1998; 98US-0083948.  
 PR 22-JUN-1998; 98US-0090246.  
 PR 22-JUN-1998; 98US-0090252.  
 PR 22-JUN-1998; 98US-0090254.  
 PR 23-JUN-1998; 98US-0090349.  
 PR 23-JUN-1998; 98US-0090355.  
 PR 24-JUN-1998; 98US-0090429.  
 PR 24-JUN-1998; 98US-0090431.  
 PR 24-JUN-1998; 98US-0090435.  
 PR 24-JUN-1998; 98US-0090444.  
 PR 24-JUN-1998; 98US-0090445.  
 PR 24-JUN-1998; 98US-0090461.  
 PR 24-JUN-1998; 98US-0090472.  
 PR 24-JUN-1998; 98US-0090538.  
 PR 24-JUN-1998; 98US-0090540.  
 PR 24-JUN-1998; 98US-0090557.  
 PR 25-JUN-1998; 98US-0090676.  
 PR 25-JUN-1998; 98US-0090678.  
 PR 25-JUN-1998; 98US-0090688.  
 PR 25-JUN-1998; 98US-0090690.  
 PR 25-JUN-1998; 98US-0090691.  
 PR 25-JUN-1998; 98US-0090694.  
 PR 25-JUN-1998; 98US-0090695.  
 PR 26-JUN-1998; 98US-0090862.  
 PR 26-JUN-1998; 98US-0090863.  
 PR 01-JUL-1998; 98US-0091358.  
 PR 01-JUL-1998; 98US-0091360.  
 PR 01-JUL-1998; 98US-0091544.  
 PR 02-JUL-1998; 98US-0091478.  
 PR 02-JUL-1998; 98US-0091519.  
 PR 02-JUL-1998; 98US-0091626.  
 PR 02-JUL-1998; 98US-0091628.  
 PR 02-JUL-1998; 98US-0091633.  
 PR 02-JUL-1998; 98US-0091646.  
 PR 07-JUL-1998; 98US-0091973.  
 PR 07-JUL-1998; 98US-0091978.  
 PR 09-JUL-1998; 98US-0092182.  
 PR 10-JUL-1998; 98US-0092472.  
 PR 20-JUL-1998; 98US-0093339.  
 PR 30-JUL-1998; 98US-0094651.  
 PR 04-AUG-1998; 98US-0095285.  
 PR 04-AUG-1998; 98US-0095301.  
 PR 04-AUG-1998; 98US-0095302.  
 PR 04-AUG-1998; 98US-0095318.  
 PR 04-AUG-1998; 98US-0095321.  
 PR 10-AUG-1998; 98US-0095325.  
 PR 10-AUG-1998; 98US-0095329.  
 PR 10-AUG-1998; 98US-0096012.  
 PR 11-AUG-1998; 98US-0096143.  
 PR 11-AUG-1998; 98US-0096146.  
 PR 12-AUG-1998; 98US-0096329.

PR 17-AUG-1998; 98US-0096757.  
 PR 17-AUG-1998; 98US-0096766.  
 PR 17-AUG-1998; 98US-0096768.  
 PR 17-AUG-1998; 98US-0096773.  
 PR 17-AUG-1998; 98US-0096791.  
 PR 17-AUG-1998; 98US-0096867.  
 PR 17-AUG-1998; 98US-0096891.  
 PR 17-AUG-1998; 98US-0096894.  
 PR 17-AUG-1998; 98US-0096895.  
 PR 17-AUG-1998; 98US-0096897.  
 PR 18-AUG-1998; 98US-0096949.  
 PR 18-AUG-1998; 98US-0096950.  
 PR 18-AUG-1998; 98US-0096959.  
 PR 18-AUG-1998; 98US-0096960.  
 PR 18-AUG-1998; 98US-0097022.  
 PR 19-AUG-1998; 98US-0097141.  
 PR 20-AUG-1998; 98US-0097218.  
 PR 24-AUG-1998; 98US-0097251.  
 PR 26-AUG-1998; 98US-0097321.  
 PR 26-AUG-1998; 98US-0097352.  
 PR 26-AUG-1998; 98US-0097354.  
 PR 26-AUG-1998; 98US-0097355.  
 PR 26-AUG-1998; 98US-0097371.  
 PR 26-AUG-1998; 98US-0097374.  
 PR 26-AUG-1998; 98US-0097379.  
 PR 26-AUG-1998; 98US-0097386.  
 PR 26-AUG-1998; 98US-0098014.  
 PR 31-AUG-1998; 98US-0098525.  
 PR 16-SEP-1998; 98US-0100634.  
 PR 12-JAN-1999; 99US-0115565.  
 XX (GERTH ) GENENTECH INC.  
 XX PA Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;  
 XX PI Wood WI, Yuan J;  
 XX PI WPI: 2000-072883/06.  
 XX DR P-PSDB; MAY6757.  
 XX PT Membrane-bound proteins and related nucleotide sequences -  
 XX PS Claim 2, Fig 289; 822PP; English.  
 CC The invention provides membrane-bound PRO polypeptides and  
 CC polynucleotides encoding them. The PRO sequences of the invention were  
 CC identified based on extracellular domain homology screening. The PRO  
 CC sequences have homology with proteins including LDL receptors, TIE  
 CC ligands and various enzymes. The membrane-bound proteins and receptor  
 CC molecules are useful as pharmaceutical and diagnostic agents. Receptor  
 CC immunoadhesins, for instance, can be used as therapeutic agents to block  
 CC receptor-ligand interactions. The membrane-bound proteins can also be  
 CC employed for screening of potential peptide or small molecule inhibitors  
 CC of the relevant receptor/ligand interaction. The PRO encoding sequences  
 CC are useful as hybridization probes, in chromosome and gene mapping and in  
 CC the generation of antisense RNA and DNA. PRO nucleic acid sequences  
 CC by recombinant techniques.  
 XX Sequence 570 BP; 129 A; 190 C; 170 G; 81 T; 0 other;  
 SQ Query Match 24.1%; Score 78; DB 21; Length 570;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-07; Indels 0; Gaps 0;  
 Matches 78; Conservative 0; Mismatches 0;  
 QY 246 GCGAGACCGGGTATAGAGGCTTGGCTTGGCCCGGACACCCAGGTTCCCGGGC 305  
 DB 1 GCGAGACCGGGTATAGAGGCTTGGCTTGGCCCGGACACCCAGGTTCCCGGGC 60  
 QY 306 GCGCGGAGCCCGCCGCC 323  
 DB 61 GCGCGGAGCCCGCCGCC 78

RESULT 9  
AAFA4249  
ID AAFA4249 standard; cDNA; 570 BP.  
XX  
AC AAFA4249;  
XX  
DT 02-APR-2001 (first entry)  
XX  
DE Human PRO1245 (UNQ629) nucleotide sequence SEQ ID NO:407.  
XX  
KW Human; secreted and transmembrane protein; PRO; cytosolic;  
KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;  
KW diagnostic assay; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200073454-A1.  
XX  
PD 07-DEC-2000.  
XX  
PF 30-MAR-2000; 2000MO-US08439.  
XX  
PR 02-JUN-1999; 99WO-US12252.  
PR 23-JUN-1999; 99US-0141037.  
PR 07-JUL-1999; 99US-0143048.  
PR 20-JUL-1999; 99US-0144758.  
PR 26-JUL-1999; 99US-0145698.  
PR 28-JUL-1999; 99US-0146222.  
PR 17-AUG-1999; 99US-0149396.  
PR 15-SEP-1999; 99WO-US21090.  
PR 08-OCT-1999; 99US-0158663.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 05-JAN-2000; 2000MO-US00219.  
PR 06-JAN-2000; 2000MO-US00376.  
PR 11-FEB-2000; 2000MO-US03565.  
PR 18-FEB-2000; 2000MO-US04341.  
PR 22-FEB-2000; 2000MO-US04414.  
PR 24-FEB-2000; 2000MO-US04914.  
PR 24-FEB-2000; 2000MO-US05004.  
PR 02-MAR-2000; 2000MO-US05841.  
PR 15-MAR-2000; 2000MO-US06884.  
PR 20-MAR-2000; 2000MO-US07377.  
XX  
PA (GENTH) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,  
PI Ferreira N, Fong S, Gerber H, Gerlitsen ME, Goddard A, Godowski PJ,  
PI Grimaldi CJ, Gurney AL, Kijavlin IJ, Napier MA, Pan J, Paoni NF,  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,  
PI Zhang Z;  
XX  
DR MPI; 2001-032160/04.  
DR P-PSDB; AAB65280.  
XX  
PT PRO polynucleotides used to produce polypeptides used to target  
PT bioactive molecules such as toxins, radiolabels or antibodies, to  
PT specific cells, to cause targeted cell death -  
XX  
PS Claim 2; Fig 289; 935gp; English.  
XX  
CC The present invention describes human secreted and transmembrane PRO  
CC proteins. The PRO proteins have cytosolic activity. The PRO proteins  
CC can be used for targeted delivery of bioactive molecules, such as  
CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide  
CC sequences, and their fragments, can be used as hybridisation probes, in  
CC chromosomal and gene mapping, and in the generation of anti-sense RNA  
CC and DNA. They may also be used to produce transgenic animals which are  
CC used to develop and screen therapeutically useful reagents. The PRO

CC nucleotide and protein sequence can be used for tissue typing and in  
CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.  
CC AAFA4270 to AAFA4470 represent PCR primers and hybridisation probes used  
CC in the isolation of human PRO sequences. AAFA4087 to AAFA4269 and  
CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein  
CC sequences given in the exemplification of the present invention.  
XX  
SQ Sequence 570 BP; 129 A; 190 C; 170 G; 81 T; 0 other;  
XX  
Query Match 24.1%; Score 78; DB 22; Length 570;  
Best Local Similarity 100.0%; Pred. No. 1.5e-07;  
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
CY 246 GCGAGGACGGGGATTAAGAGCGTGGGCTTGGCGGAGCGGAGGTTCCCGCGGC 305  
DB 1 GCGAGGACGGGGATTAAGAGCGTGGGCTTGGCGGAGCGGAGGTTCCCGCGGC 60  
CY 306 GCGCGGAGCGCGCGCGCGC 323  
DB 61 GCGCGGAGCGCGCGCGC 78  
XX  
RESULT 10  
ABX80386  
ID ABX80386 standard; DNA; 570 BP.  
XX  
AC ABX80386;  
XX  
DT 28-APR-2003 (first entry)  
XX  
DE Novel human secreted or transmembrane protein PRO1358 DNA.  
XX  
KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
KW cardiac insufficiency disorder; cancer; tumour; immune response;  
KW adrenal cortical capillary endothelial growth; c-fos induction;  
KW vascular endothelial growth factor inhibition; VEGF inhibition;  
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
KW retinal neurons cell survival; rod photoreceptor cell survival;  
KW renal disorder; retinitis pigmentosa; kidney disorder;  
KW mammalian kidney mesangial cell proliferation; Berger disease;  
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
KW chondrocyte redifferentiation; sports injury; arthritis; gene; de.  
XX  
OS Homo sapiens.  
XX  
PN US2002132252-A1.  
XX  
PD 19-SEP-2002.  
XX  
PF 14-NOV-2001; 2001US-0990442.  
XX  
PR 05-NOV-1997; 97WO-US20069.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
PR 07-OCT-1998; 98WO-US21141.  
PR 01-DEC-1998; 98WO-US25108.  
PR 05-JAN-1999; 99WO-US00106.  
PR 08-MAR-1999; 99WO-US05028.  
PR 02-JUN-1999; 99WO-US12252.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 16-DEC-1999; 99WO-US28634.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 06-JAN-2000; 2000MO-US00219.  
PR 11-FEB-2000; 2000MO-US03565.  
PR 18-FEB-2000; 2000MO-US04341.  
PR 22-FEB-2000; 2000MO-US04414.  
PR 24-FEB-2000; 2000MO-US04914.  
PR 24-FEB-2000; 2000MO-US05004.

PR	10-MAR-2000	2000MO-US06541
PR	10-MAR-2000	2000MO-US06319
PR	15-MAR-2000	2000MO-US06684
PR	20-MAR-2000	2000MO-US07377
PR	30-MAR-2000	2000MO-US08439
PR	15-MAY-2000	2000MO-US13358
PR	17-MAY-2000	2000MO-US13705
PR	22-MAY-2000	2000MO-US14042
PR	30-MAY-2000	2000MO-US14941
PR	02-JUN-2000	2000MO-US15264
PR	28-JUN-2000	2000MO-US20710
PR	11-AUG-2000	2000MO-US23031
PR	23-AUG-2000	2000MO-US23352
PR	28-AUG-2000	2000MO-US23338
PR	08-NOV-2000	2000MO-US30952
PR	01-DEC-2000	2000MO-US32678
PR	28-FEB-2001	2001MO-US06520
PR	01-JUN-2001	2001MO-US17500
PR	29-JUN-2001	2001MO-US19692
PR	09-JUL-2001	2001MO-US21066
PR	16-JUN-1997	97US-04787P
PR	17-OCT-1997	97US-06242P
PR	12-NOV-1997	97US-06531P
PR	12-NOV-1997	97US-066770P
PR	25-FEB-1998	98US-075945P
PR	28-MAR-1998	98US-078910P
PR	28-MAR-1998	98US-083322P
PR	07-MAY-1998	98US-084600P
PR	28-MAY-1998	98US-087106P
PR	02-JUN-1998	98US-087607P
PR	02-JUN-1998	98US-087609P
PR	03-JUN-1998	98US-087759P
PR	04-JUN-1998	98US-087827P
PR	04-JUN-1998	98US-088021P
PR	04-JUN-1998	98US-088025P
PR	04-JUN-1998	98US-088026P
PR	04-JUN-1998	98US-088028P
PR	04-JUN-1998	98US-088029P
PR	04-JUN-1998	98US-088030P
PR	04-JUN-1998	98US-088033P
PR	04-JUN-1998	98US-088032P
PR	05-JUN-1998	98US-088167P
PR	05-JUN-1998	98US-088212P
PR	05-JUN-1998	98US-088217P
PR	09-JUN-1998	98US-088455P
PR	09-JUN-1998	98US-088456P
PR	10-JUN-1998	98US-088735P
PR	10-JUN-1998	98US-088742P
PR	10-JUN-1998	98US-088810P
PR	10-JUN-1998	98US-088826P
PR	10-JUN-1998	98US-088826P
PR	11-JUN-1998	98US-088861P
PR	11-JUN-1998	98US-088861P
PR	12-JUN-1998	98US-088861P
PR	12-JUN-1998	98US-089105P
PR	16-JUN-1998	98US-089440P
PR	16-JUN-1998	98US-089512P
PR	17-JUN-1998	98US-089532P
PR	17-JUN-1998	98US-089538P
PR	17-JUN-1998	98US-089559P
PR	17-JUN-1998	98US-089600P
PR	17-JUN-1998	98US-089653P
PR	18-JUN-1998	98US-089801P
PR	18-JUN-1998	98US-089907P
PR	18-JUN-1998	98US-089908P
PR	28-AUG-2001	2001US-094199Z
PR	XX	
PR	XX	
PR	(GETH )	GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Botstein D, Denovoyers L, Eaton DJ;  
XX Bertram EH, Bonner H, Gerfensen ME, Goddard A, Gadowski P  
PI Betancur JG, Bonney AL, Klifavin IJ, Napier MA, Pan J, Peart NF,  
PI Brown MD, Clancy AL, Curney AL, Davidson R, Edwards PM,  
PI Zhang Z; Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,  
XX Zhang Z;  
DR WPJ; 2003-247063/24.  
DR P-PSDB; AB059174.

Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1344 and PRO1375, which stimulate proliferation of stimulated T-lymphocytes and PRO1375, which stimulate proliferation of stimulated T-lymphocytes are therapeutically useful for enhancing immune response and in cancer treatments -

Claim 2; Fig 291; 648pp; English.

The invention describes an isolated human PRO polypeptide. The PRO<sup>1</sup> polypeptides are useful in detecting PRO polypeptides in a sample, in linking a bioactive molecule to a cell expressing a PRO polypeptide, and in modulating at least one biological activity of a cell expressing a PRO polypeptide. PRO131 stimulates hypertrophy of neonatal heart and is thus useful for treating cardiac insufficiency disorders. PRO154 and PRO186 stimulate adrenal cortical capillary endothelial growth and PRO336<sup>1</sup> stimulate adrenal cortical capillary endothelial growth and are thus useful for treating conditions or disorders where angiogenesis would be beneficial, e.g. wound healing and amputation sites of this polypeptide are useful for treating conditions or disorders where angiogenesis would be beneficial. PRO1360 and PRO1387 induce c-fos in endothelial cells and are thus useful for treating conditions or disorders where angiogenesis would be beneficial. PRO184, PRO1346 and PRO1357 stimulate proliferation of endothelial growth factor (bFGF) stimulated proliferation of endothelial cells and is thus useful for inhibiting endothelial cell growth in mammals and is thus useful for inhibiting tumour proliferation of mammals and is thus useful for stimulating proliferation of stimulated T-lymphocytes and are therapeutically useful for enhancing of immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival/proliferation of retinal neurons cells (PRO1132 is also enhances survival/proliferation of retinal photoreceptor cells) and therefore are useful for treating retinal disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO813 and PRO1066 induce proliferation of mammalian kidney mesangial cells, and therefore are useful for treating kidney disorders associated with decreased mesangial cell function such as Berger's disease or Crohn's nephropathies associated with dermatitis, herpesiforms or Crohn's disease. PRO1010, PRO844, PRO1312 and PRO1387 induce the proliferation and/or redifferentiation of chondrocytes in culture and are thus useful for treating sports injuries, and arthritis. This sequence represents a novel human PRO protein polynucleotide.

Sequence 570 BP; 129 A; 190 C; 170 G; 81 T; 0 other;

Query Match 24.1%; Score 78; DB 25; Length 570;

QY 306 GCCCGAGCCCCCGGCC 323  
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Db 61 GCCCGAGCCCCCGGCC 78

RESULT	11
ABX80890	
ID	ABX80890 standard; cDNA; 570 BP

XX ABX80890  
AC

XX	
DT	22-APR-2003 (first entry

XX Human secreted/transmembrane protein CDNA, #163.  
DE

XX Human; gene; ss; PRO; secreted; transmembrane; pharmaceutical;  
KW

KW diagnostic; biosensor; bioeffector; tumour; therapeutic;  
KW gene therapy; tumour-associated antigenic target; TAT; ADEPT;  
KW antibody-dependent enzyme mediated prodrug therapy; cytostatic.  
OS Homo sapiens.  
XX US2003027162-A1.  
XX 06-FEB-2003.  
PD  
XX  
PF 15-NOV-2001; 2001US-0997428.  
XX  
XX 05-NOV-1997; 97WO-US20069.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19337.  
PR 07-OCT-1998; 98WO-US21141.  
PR 01-DEC-1998; 98WO-US25108.  
PR 05-JAN-1999; 99WO-US00106.  
PR 08-MAR-1999; 99WO-US05028.  
PR 02-JUN-1999; 99WO-US12252.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 10-MAR-2000; 2000WO-US05841.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 15-MAY-2000; 2000WO-US13358.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US14941.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 11-AUG-2000; 2000WO-US22031.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23528.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 29-JUN-2001; 2001WO-US19692.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
PR 16-JUN-1997; 97US-049787P.  
PR 17-OCT-1997; 97US-062250P.  
PR 12-NOV-1997; 97US-065186P.  
PR 13-NOV-1997; 97US-065311P.  
PR 24-NOV-1997; 97US-066770P.  
PR 25-FEB-1998; 98US-075945P.  
PR 20-MAR-1998; 98US-078910P.  
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PR 03-JUN-1998; 98US-087837P.  
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PR 04-JUN-1998; 98US-088326P.  
PR 05-JUN-1998; 98US-088167P.  
PR 05-JUN-1998; 98US-088202P.  
PR 05-JUN-1998; 98US-088212P.  
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PR 09-JUN-1998; 98US-088655P.  
PR 10-JUN-1998; 98US-088734P.  
PR 10-JUN-1998; 98US-088738P.  
PR 10-JUN-1998; 98US-088742P.  
PR 10-JUN-1998; 98US-088810P.  
PR 10-JUN-1998; 98US-088824P.  
PR 10-JUN-1998; 98US-088828P.  
PR 11-JUN-1998; 98US-088858P.  
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PR 19-JUN-1998; 98US-089947P.  
PR 19-JUN-1998; 98US-089948P.  
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PR 24-JUN-1998; 98US-090428P.  
PR 24-JUN-1998; 98US-090431P.  
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PR 24-JUN-1998; 98US-090444P.  
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PR 24-JUN-1998; 98US-090472P.  
PR 24-JUN-1998; 98US-090535P.  
PR 24-JUN-1998; 98US-090540P.  
PR 24-JUN-1998; 98US-090542P.  
PR 25-JUN-1998; 98US-090557P.  
PR 25-JUN-1998; 98US-090676P.  
PR 25-JUN-1998; 98US-090678P.  
PR 25-JUN-1998; 98US-090690P.  
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PR 25-JUN-1998; 98US-090694P.  
PR 25-JUN-1998; 98US-090696P.  
PR 25-JUN-1998; 98US-090696P.  
PR 26-JUN-1998; 98US-090862P.  
PR 26-JUN-1998; 98US-090863P.  
PR 01-JUL-1998; 98US-091360P.  
PR 01-JUL-1998; 98US-091544P.  
PR 02-JUL-1998; 98US-091478P.  
PR 02-JUL-1998; 98US-091519P.  
PR 02-JUL-1998; 98US-091626P.  
PR 02-JUL-1998; 98US-091633P.  
PR 02-JUL-1998; 98US-091638P.  
PR 02-JUL-1998; 98US-091646P.  
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PR 07-JUL-1998; 98US-091978P.  
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PR 09-JUL-1998; 98US-092182P.  
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PR 04-AUG-1998; 98US-095282P.

PR 04-AUG-1998; 98US-095285P.  
PR 04-AUG-1998; 98US-095301P.  
PR 04-AUG-1998; 98US-095302P.  
PR 04-AUG-1998; 98US-095318P.  
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PR 04-AUG-1998; 98US-095325P.  
PR 10-AUG-1998; 98US-095916P.  
PR 10-AUG-1998; 98US-095929P.  
PR 10-AUG-1998; 98US-096012P.  
PR 11-AUG-1998; 98US-096143P.  
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PR 12-AUG-1998; 98US-096757P.  
PR 17-AUG-1998; 98US-096766P.  
PR 17-AUG-1998; 98US-096768P.  
PR 17-AUG-1998; 98US-096773P.  
PR 17-AUG-1998; 98US-096791P.  
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PR 17-AUG-1998; 98US-096897P.  
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PR 18-AUG-1998; 98US-096953P.  
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PR 24-AUG-1998; 98US-097952P.  
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PR 26-AUG-1998; 98US-097971P.  
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PR 26-AUG-1998; 98US-097978P.  
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PR 26-AUG-1998; 98US-098014P.  
PR 26-AUG-1998; 98US-098225P.  
PR 31-AUG-1998; 98US-100634P.  
PR 16-SEP-1998; 98US-100858P.  
PR 17-SEP-1998; 98US-113296P.  
PR 22-DEC-1998; 98US-123957P.  
PR 12-MAR-1999; 99US-141037P.  
PR 23-JUN-1999; 99US-141037P.

Query Match 24.1%; Score 78; DB 25; Length 570;  
Best Local Similarity 100.0%; Pred. No. 1.5e-07;  
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 GCGAGAGCCGGGTATAGAGCCTGATGAGCTTGCCCGGAGCCGAGATTCCCGCGC 305  
DB 1 GCGAGAGCCGGGTATAGAGCCTGATGAGCTTGCCCGGAGCCGAGATTCCCGCGC 60  
QY 306 GCGCCGAGCCCGCCGCC 323  
DB 61 GCGCCGAGCCCGCCGCC 78

RESULT 12  
ABX81273  
ID ABX81273 standard; DNA; 570 BP.

AC ABX81273;  
XX  
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XX

DT 22-APR-2003 (first entry)  
XX  
XX

DE Novel human secreted or transmembrane protein PRO1358 DNA.  
XX

KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
KW cardiac insufficiency disorder; cancer; tumour; immune response;  
KW adrenal cortical capillary endothelial growth; c-fos induction;  
KW vascular endothelial growth factor inhibition; VEGF inhibition;

KW

KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
KW retinal neurons cell survival; rod photoreceptor cell survival;  
KW retinal disorder; retinitis pigmentosa; kidney disorder;  
KW mammalian kidney mesangial cell proliferation; Berger disease;  
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
KW chondrocyte redifferentiation; sports injury; arthritis; gene; ds.  
OS Homo sapiens.  
PN US2003027985-A1.  
XX  
XX  
XX  
PD 06-FEB-2003.  
XX  
XX  
PF 14-NOV-2001; 2001US-0990562.  
XX  
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PR 05-NOV-1997; 97WO-US20069.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
PR 07-OCT-1998; 98WO-US21141.  
PR 01-DEC-1998; 98WO-US25108.  
PR 05-JAN-1999; 98WO-US05028.  
PR 08-MAR-1999; 98WO-US12252.  
PR 02-JUN-1999; 98WO-US12092.  
PR 15-SEP-1999; 98WO-US21547.  
PR 15-SEP-1999; 98WO-US21547.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28303.  
PR 01-DEC-1999; 99WO-US28303.  
PR 16-DEC-1999; 99WO-US28303.  
PR 20-DEC-1999; 99WO-US30911.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04341.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 15-MAY-2000; 2000WO-US13358.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US14941.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 28-JUN-2000; 2000WO-US20710.  
PR 11-AUG-2000; 2000WO-US22031.  
PR 23-AUG-2000; 2000WO-US23128.  
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PR 28-FEB-2001; 2001WO-US06520.  
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PR 20-JUN-2001; 2001WO-US19692.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
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PR 17-OCT-1997; 97US-062250P.  
PR 12-NOV-1997; 97US-065318P.  
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PR 07-JUL-1998; 98US-091978P.  
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PR 09-JUL-1998; 98US-092182P.  
PR 10-JUL-1998; 98US-092472P.

PR 20-JUL-1998; 98US-093339P.  
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PR 04-AUG-1998; 98US-095282P.  
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PR 17-AUG-1998; 98US-096894P.  
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PR 18-AUG-1998; 98US-096949P.  
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PR 20-AUG-1998; 98US-097218P.  
PR 24-AUG-1998; 98US-097661P.  
PR 24-AUG-1998; 98US-097662P.  
PR 26-AUG-1998; 98US-097952P.  
PR 26-AUG-1998; 98US-097954P.  
PR 26-AUG-1998; 98US-097955P.  
PR 26-AUG-1998; 98US-097971P.  
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Query Match 24.1%; Score 78; DB 25; Length 570;  
Best Local Similarity 100.0%; Pred. No. 1.5e-07;  
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 GCAGGACCGCGTATTAAGAGCTCTGCGCTTGGCCCGGACAGCCGACGTTCCCGGCC 305  
DB 1 GCAGGACCGCGTATTAAGAGAGCTCTGCGCTTGGCCCGGACAGCCGACGTTCCCGGCC 60  
QY 306 GCCCGAGCCCGCCGCC 323  
DB 61 GCCCGAGCCCGCCGCC 78

RESULT 13  
ABX90363  
ID ABX90363 standard, cDNA, 570 BP.  
XX  
AC ABX90363;  
DT 01-MAY-2003 (first entry)  
XX  
XX Human secreted/transmembrane protein cDNA, #163.  
DB Human secreted/transmembrane protein cDNA, #163.  
XX  
XX Human, gene; ss, PRO, secreted, transmembrane, signal peptide,  
KW pharmaceutical, diagnostic, therapeutic; gene therapy.  
XX  
OS Homo sapiens.  
XX  
XX US2002160384-A1.  
XX

PD 31-OCT-2002.  
 XX 14-NOV-2001; 2001US-0992598.  
 XX 05-NOV-1997; 97WO-US20069.  
 PR 16-SEP-1998; 98WO-US19330.  
 PR 17-SEP-1998; 98WO-US19437.  
 PR 07-OCT-1998; 98WO-US21141.  
 PR 01-DEC-1998; 98WO-US25108.  
 PR 05-JAN-1999; 99WO-US05028.  
 PR 08-MAR-1999; 99WO-US12252.  
 PR 02-JUN-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 01-DEC-1999; 99WO-US28634.  
 PR 16-DEC-1999; 99WO-US30095.  
 PR 20-DEC-1999; 99WO-US30911.  
 PR 05-JAN-2000; 2000WO-US00313.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 22-FEB-2000; 2000WO-US04914.  
 PR 24-FEB-2000; 2000WO-US05004.  
 PR 02-MAR-2000; 2000WO-US05841.  
 PR 10-MAR-2000; 2000WO-US06319.  
 PR 15-MAR-2000; 2000WO-US07377.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 15-MAY-2000; 2000WO-US13358.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.  
 PR 30-MAY-2000; 2000WO-US14941.  
 PR 02-JUN-2000; 2000WO-US15264.  
 PR 28-JUL-2000; 2000WO-US20710.  
 PR 11-AUG-2000; 2000WO-US22031.  
 PR 23-AUG-2000; 2000WO-US23522.  
 PR 24-AUG-2000; 2000WO-US23328.  
 PR 08-NOV-2000; 2000WO-US30952.  
 PR 01-DEC-2000; 2000WO-US32676.  
 PR 28-FEB-2001; 2001WO-US05520.  
 PR 01-JUN-2001; 2001WO-US11800.  
 PR 20-JUN-2001; 2001WO-US11800.  
 PR 29-JUN-2001; 2001WO-US21066.  
 PR 09-JUL-2001; 2001WO-US21735.  
 PR 16-JUL-1997; 97US-0497875.  
 PR 17-OCT-1997; 97US-062250P.  
 PR 12-NOV-1997; 97US-065186P.  
 PR 13-NOV-1997; 97US-065311P.  
 PR 24-NOV-1997; 97US-066770P.  
 PR 25-FEB-1998; 98US-075945P.  
 PR 20-MAR-1998; 98US-078910P.  
 PR 28-APR-1998; 98US-083322P.  
 PR 07-MAY-1998; 98US-084600P.  
 PR 28-MAY-1998; 98US-087106P.  
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 PR 03-JUN-1998; 98US-087827P.  
 PR 04-JUN-1998; 98US-088021P.  
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 PR 04-JUN-1998; 98US-088326P.  
 PR 05-JUN-1998; 98US-088167P.  
 PR 05-JUN-1998; 98US-088202P.  
 PR 05-JUN-1998; 98US-088212P.  
 PR 05-JUN-1998; 98US-088217P.

PR 09-JUN-1998; 98US-088655P.  
 PR 10-JUN-1998; 98US-088734P.  
 PR 10-JUN-1998; 98US-088738P.  
 PR 10-JUN-1998; 98US-088742P.  
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 PR 12-JUN-1998; 98US-089105P.  
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 PR 17-JUN-1998; 98US-089653P.  
 PR 18-JUN-1998; 98US-089801P.  
 PR 18-JUN-1998; 98US-089807P.  
 PR 18-JUN-1998; 98US-089908P.  
 PR 28-AUG-2001; 2001US-0941992.  
 XX (GERTH ) GENENTECH INC.  
 XX Ashkenazi AJ, Baker KP, Bolstein D, Desnoyers LJ, Eaton DR;  
 PI Ferrera N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
 PI Zhang Z;  
 XX WPI; 2003-288106/28.  
 DR P-PSDB; ABU60604.  
 XX New transmembrane polypeptides and nucleic acids encoding the  
 PT polypeptides, useful in gene therapy, in chromosome identification, as  
 PT chromosome markers, or in generating probes -  
 XX  
 PS Claim 2, Fig 289; 650pp; English.  
 XX The invention discloses isolated PRO secreted/transmembrane polypeptides  
 CC comprising a sequence without signal peptide and the nucleic acid  
 CC encoding them. The polypeptides can be used to raise antibodies that  
 CC specifically bind to the PRO polypeptide, for linking a bioactive  
 CC molecule to a cell expressing a PRO protein and for modulating at least  
 CC one biological activity of a cell. The PRO polypeptides or  
 CC polynucleotides are also useful in gene therapy, in chromosome  
 CC identification, as chromosome markers, or in generating probes. The PRO  
 CC polypeptides are useful as molecular markers for protein  
 CC electrophoresis, and the isolated nucleic acids may be used for  
 CC recombinantly expressing those markers. The PRO polypeptides and nucleic  
 CC acids may also be used in tissue typing. Anti-PRO antibodies are useful  
 CC in diagnostic assays for PRO, and in affinity purification of PRO from  
 CC recombinant cell culture or natural sources. The sequences presented in  
 CC ABX90083-ABX90468 are the genes encoding, the primers amplifying and the  
 CC probes detecting the PRO polynucleotides of the invention.  
 CC Note: The sequence data at segdata.uspto.gov/sequence.html.  
 CC format from USPTO at segdata.uspto.gov/sequence.html.  
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 SQ Sequence 570 BP; 129 A; 190 C; 170 G; 81 T; 0 other;  
 Query Match 24.1%; Score 78; DB 25; Length 570;  
 Best Local Similarity 100.0%; Fred No. 1.5e-07;  
 Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 246 GCGAGACCGGGTATTAAGAGCTCTGCGCTTGGCCGAGCGGAGGTTCCCGGCGC 305  
 Db 1 GCGAGACCGGGTATTAAGAGCTCTGCGCTTGGCCGAGCGGAGGTTCCCGGCGC 60  
 QY 306 GCGCGAGCGCGCGCGCGC 323  
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DB 61 GCCCGAGCCCCGGGCC 78

RESULT 14

ABX77974

ID ABX77974 standard; cDNA; 570 BP.

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AC ABX77974;

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DT 14-APR-2003 (first entry)

XX

DE Human PRO polynucleotide #127.

XX

XX Human; PRO; gene; ss; cytosolic; tumour; cancer; breast; lung; stomach;

XX liver; horse; cow; dog; cat; sheep; pig; goat; rabbit; ADPPI;

XX antibody-dependent enzyme mediated prodng therapy.

XX

OS Homo sapiens.

XX

PN US2003027163-A1.

XX

PD 06-FEB-2003.

XX

PF 15-NOV-2001; 2001US-0997666.

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PR 05-NOV-1997; 97WO-US20069.

PR 16-SEP-1998; 98WO-US19330.

PR 17-SEP-1998; 98WO-US19437.

PR 07-OCT-1998; 98WO-US21141.

PR 01-DEC-1998; 98WO-US25108.

PR 05-JAN-1999; 99WO-US00106.

PR 08-MAR-1999; 99WO-US05028.

PR 02-JUN-1999; 99WO-US12252.

PR 15-SEP-1999; 99WO-US21090.

PR 30-NOV-1999; 99WO-US21547.

PR 01-DEC-1999; 99WO-US28313.

PR 16-DEC-1999; 99WO-US28634.

PR 20-DEC-1999; 99WO-US30095.

PR 05-JAN-2000; 2000WO-US00219.

PR 06-JAN-2000; 2000WO-US00376.

PR 11-FEB-2000; 2000WO-US03565.

PR 18-FEB-2000; 2000WO-US04341.

PR 24-FEB-2000; 2000WO-US04914.

PR 24-FEB-2000; 2000WO-US05004.

PR 02-MAR-2000; 2000WO-US05841.

PR 10-MAR-2000; 2000WO-US06319.

PR 15-MAR-2000; 2000WO-US06884.

PR 30-MAR-2000; 2000WO-US07377.

PR 30-MAR-2000; 2000WO-US08439.

PR 15-MAY-2000; 2000WO-US13358.

PR 17-MAY-2000; 2000WO-US13705.

PR 22-MAY-2000; 2000WO-US14042.

PR 30-MAY-2000; 2000WO-US14941.

PR 02-JUN-2000; 2000WO-US15264.

PR 28-JUL-2000; 2000WO-US20710.

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PR 23-AUG-2000; 2000WO-US23522.

PR 24-AUG-2000; 2000WO-US23328.

PR 08-NOV-2000; 2000WO-US30952.

PR 01-DEC-2000; 2000WO-US32678.

PR 28-FEB-2001; 2001WO-US06520.

PR 01-JUN-2001; 2001WO-US18800.

PR 20-JUN-2001; 2001WO-US19692.

PR 29-JUN-2001; 2001WO-US21066.

PR 09-JUL-2001; 2001WO-US21735.

PR 16-JUN-1997; 97US-049787P.

PR 17-OCT-1997; 97US-062250P.

PR 12-NOV-1997; 97US-065186P.

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PR 05-JUN-1998; 98US-088217P.

PR 09-JUN-1998; 98US-088655P.

PR 10-JUN-1998; 98US-088734P.

PR 10-JUN-1998; 98US-088742P.

PR 10-JUN-1998; 98US-088748P.

PR 10-JUN-1998; 98US-088810P.

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PR 10-JUN-1998; 98US-088826P.

PR 11-JUN-1998; 98US-088858P.

PR 11-JUN-1998; 98US-088861P.

PR 12-JUN-1998; 98US-089105P.

PR 16-JUN-1998; 98US-089440P.

PR 16-JUN-1998; 98US-089512P.

PR 17-JUN-1998; 98US-089532P.

PR 17-JUN-1998; 98US-089538P.

PR 17-JUN-1998; 98US-089598P.

PR 17-JUN-1998; 98US-089600P.

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PR 18-JUN-1998; 98US-089801P.

PR 18-JUN-1998; 98US-089907P.

PR 19-JUN-1998; 98US-089947P.

PR 19-JUN-1998; 98US-089948P.

PR 22-JUN-1998; 98US-089952P.

PR 22-JUN-1998; 98US-090246P.

PR 22-JUN-1998; 98US-090252P.

PR 23-JUN-1998; 98US-090349P.

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PR 24-JUN-1998; 98US-090431P.

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PR 24-JUN-1998; 98US-090452P.

PR 24-JUN-1998; 98US-090472P.

PR 24-JUN-1998; 98US-090535P.

PR 24-JUN-1998; 98US-090540P.

PR 24-JUN-1998; 98US-090557P.

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PR 01-JUL-1998; 98US-091250P.

PR 01-JUL-1998; 98US-091544P.

PR 02-JUL-1998; 98US-091747P.

PR 02-JUL-1998; 98US-091519P.  
PR 02-JUL-1998; 98US-091626P.  
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PR 02-JUL-1998; 98US-091646P.  
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PR 07-JUL-1998; 98US-091978P.  
PR 07-JUL-1998; 98US-0921982P.  
PR 10-JUL-1998; 98US-092472P.  
PR 20-JUL-1998; 98US-093339P.  
PR 30-JUL-1998; 98US-094651P.  
PR 04-AUG-1998; 98US-095282P.  
PR 04-AUG-1998; 98US-095285P.  
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PR 04-AUG-1998; 98US-095318P.  
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PR 04-AUG-1998; 98US-095325P.  
PR 10-AUG-1998; 98US-095916P.  
PR 10-AUG-1998; 98US-095929P.  
PR 10-AUG-1998; 98US-096012P.  
PR 11-AUG-1998; 98US-096143P.  
PR 11-AUG-1998; 98US-096144P.  
PR 12-AUG-1998; 98US-096152P.  
PR 17-AUG-1998; 98US-096173P.  
PR 17-AUG-1998; 98US-096766P.  
PR 17-AUG-1998; 98US-096768P.  
PR 17-AUG-1998; 98US-096773P.  
PR 17-AUG-1998; 98US-096791P.  
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PR 18-AUG-1998; 98US-096897P.  
PR 18-AUG-1998; 98US-096949P.  
PR 18-AUG-1998; 98US-096950P.  
PR 18-AUG-1998; 98US-096959P.  
PR 18-AUG-1998; 98US-096960P.  
PR 18-AUG-1998; 98US-097022P.  
PR 19-AUG-1998; 98US-097141P.  
PR 20-AUG-1998; 98US-097218P.  
PR 24-AUG-1998; 98US-097661P.  
PR 26-AUG-1998; 98US-097952P.  
PR 26-AUG-1998; 98US-097955P.  
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PR 26-AUG-1998; 98US-097974P.  
PR 26-AUG-1998; 98US-097978P.  
PR 26-AUG-1998; 98US-097986P.  
PR 26-AUG-1998; 98US-098014P.  
PR 31-AUG-1998; 98US-098525P.  
PR 31-AUG-1998; 98US-100634P.  
PR 16-SEP-1998; 98US-100958P.  
PR 17-SEP-1998; 98US-113566P.  
PR 22-DEC-1998; 98US-123957P.  
PR 12-MAR-1999; 99US-141037P.  
PR 23-JUN-1999; 99US-143048P.  
PR 07-JUL-1999; 99US-143048P.

Query Match 24.1%; Score 78; DB 25; Length 570;  
Best Local Similarity 100.0%; Pred. No. 1.5e-07;  
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 246 GCGAGACCGGATATAGAGCTCGTGGCTTGGCCGGGCGAGCCGCGAGTTCCCGGGC 305  
DB 1 GCGAGACCGGATATAGAGCTCGTGGCTTGGCCGGGCGAGCCGCGAGTTCCCGGGC 60  
OY 306 GCGCGAGCGCCCGCGCC 323  
DB 61 GCGCGAGCGCCCGCGCC 78

RESULT 15  
ABX79570  
ID ABX79570 standard; cDNA; 570 BP.  
XX  
AC ABX79570;  
XX  
DT 17-APR-2003 (first entry)  
XX  
DE Human secreted/transmembrane protein cDNA, #163.  
XX  
KW Human; gene; ss; PRO; secreted; transmembrane; signal peptide;  
KW Pharmaceutical; diagnostic; biosensor; bioreactor; tumour; therapeutic;  
KW colon cancer; lung cancer; breast cancer; cancer; gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN US2002142961-A1.  
XX  
PD 03-OCT-2002.  
XX  
PF 19-NOV-2001; 2001US-0989721.  
XX  
XX 05-NOV-1997; 97WO-US20069.  
XX 17-SEP-1998; 98WO-US19437.  
XX 07-OCT-1998; 98WO-US21141.  
XX 01-DEC-1998; 98WO-US25108.  
XX 05-JAN-1999; 99WO-US00106.  
XX 08-MAR-1999; 99WO-US05028.  
XX 02-JUN-1999; 99WO-US12252.  
XX 15-SEP-1999; 99WO-US21090.  
XX 15-SEP-1999; 99WO-US21547.  
XX 30-NOV-1999; 99WO-US28313.  
XX 01-DEC-1999; 99WO-US28301.  
XX 16-DEC-1999; 99WO-US28634.  
XX 20-DEC-1999; 99WO-US30095.  
XX 05-JAN-2000; 99WO-US30911.  
XX 06-JAN-2000; 2000WO-US00376.  
XX 11-FEB-2000; 2000WO-US03565.  
XX 18-FEB-2000; 2000WO-US04341.  
XX 24-FEB-2000; 2000WO-US04914.  
XX 02-MAR-2000; 2000WO-US05841.  
XX 10-MAR-2000; 2000WO-US06319.  
XX 15-MAR-2000; 2000WO-US06884.  
XX 20-MAR-2000; 2000WO-US07377.  
XX 30-MAR-2000; 2000WO-US08439.  
XX 15-MAY-2000; 2000WO-US13358.  
XX 17-MAY-2000; 2000WO-US13705.  
XX 22-MAY-2000; 2000WO-US14042.  
XX 30-MAY-2000; 2000WO-US14941.  
XX 02-JUN-2000; 2000WO-US15264.  
XX 28-JUN-2000; 2000WO-US20710.  
XX 11-AUG-2000; 2000WO-US22031.  
XX 23-AUG-2000; 2000WO-US23522.  
XX 24-AUG-2000; 2000WO-US23528.  
XX 08-NOV-2000; 2000WO-US30952.  
XX 01-DEC-2000; 2000WO-US32678.  
XX 28-FEB-2001; 2001WO-US06520.  
XX 01-JUN-2001; 2001WO-US17800.  
XX 20-JUN-2001; 2001WO-US19692.  
XX 09-JUL-2001; 2001WO-US21066.  
XX 16-JUN-1997; 97US-049787P.  
XX 17-OCT-1997; 97US-062250P.  
XX 12-NOV-1997; 97US-065186P.  
XX 13-NOV-1997; 97US-065311P.  
XX 24-NOV-1997; 97US-066770P.  
XX 25-FEB-1998; 98US-075945P.  
XX 20-MAR-1998; 98US-078910P.  
XX 28-APR-1998; 98US-083322P.  
XX 07-MAY-1998; 98US-084600P.

PR 28-MAY-1998; 98US-087106P.  
 PR 02-JUN-1998; 98US-087607P.  
 PR 02-JUN-1998; 98US-087609P.  
 PR 02-JUN-1998; 98US-087659P.  
 PR 03-JUN-1998; 98US-087827P.  
 PR 04-JUN-1998; 98US-088021P.  
 PR 04-JUN-1998; 98US-088025P.  
 PR 04-JUN-1998; 98US-088026P.  
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 PR 04-JUN-1998; 98US-088033P.  
 PR 05-JUN-1998; 98US-088157P.  
 PR 05-JUN-1998; 98US-088202P.  
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 PR 10-JUN-1998; 98US-088738P.  
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 PR 11-JUN-1998; 98US-088858P.  
 PR 11-JUN-1998; 98US-088861P.  
 PR 11-JUN-1998; 98US-088876P.  
 PR 12-JUN-1998; 98US-089105P.  
 PR 12-JUN-1998; 98US-089440P.  
 PR 16-JUN-1998; 98US-089512P.  
 PR 16-JUN-1998; 98US-089514P.  
 PR 17-JUN-1998; 98US-089532P.  
 PR 17-JUN-1998; 98US-089538P.  
 PR 17-JUN-1998; 98US-089598P.  
 PR 17-JUN-1998; 98US-089599P.  
 PR 17-JUN-1998; 98US-089600P.  
 PR 17-JUN-1998; 98US-089653P.  
 PR 18-JUN-1998; 98US-089801P.  
 PR 18-JUN-1998; 98US-089907P.  
 PR 18-JUN-1998; 98US-089908P.  
 PR 28-AUG-2001; 2001US-0941992.  
 XX  
 XX (GETH ) GENENTECH INC.  
 XX  
 XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,  
 PI Ferrera N, Fong S, Gerber H, Gertlesen ME, Goddard A, Godowski PJ,  
 PI Grimaldi JC, Gurley AL, Kijavini TJ, Napier MA, Pan J, Paoni NF,  
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,  
 PI Zhang Z;  
 XX  
 XX WPI; 2003-155950/15.  
 DR P-PSDB; ABUS9026.  
 XX  
 XX New secreted and transmembrane PRO polypeptides (e.g. PRO183, PRO184,  
 PT PRO361 or PRO846) useful as targets for therapeutic intervention in  
 PT cancers (e.g. lung or breast cancers), or for diagnosing these cancers  
 PT  
 PT  
 XX  
 XX Claim 2; Fig 289; 647pp; English.  
 XX  
 XX The invention discloses isolated PRO secreted/transmembrane polypeptides  
 CC comprising a sequence without signal peptide and the nucleic acid  
 CC encoding them. The polypeptides can be used to raise antibodies that  
 CC specifically bind to the PRO polypeptide, for linking a bioactive  
 CC molecule to a cell expressing a PRO protein and for modulating at least  
 CC one biological activity of a cell. The PRO polypeptides or  
 CC polynucleotides are also useful as pharmaceutical diagnostics.  
 CC biosensors or bioreactors, for detecting or treating e.g. tumours in  
 CC mammals, e.g. humans, dogs, cats, cattle, horses, sheep, pigs, goats or  
 CC rabbits as targets for therapeutic intervention in certain cancers (e.g.  
 CC colon, lung or breast cancers) and diagnostic determination of the  
 CC presence of these cancers. The PRO polypeptides are also useful as  
 CC molecular weight markers or for chromosome identification. The PRO genes

CC are useful as hybridisation probes or for screening libraries of human  
 CC cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene  
 CC therapy, particularly for replacing a defective gene. The sequences  
 CC presented in ABX79290-ABX79675 are the genes encoding, the primers  
 CC amplifying and the probes detecting the PRO polynucleotides of the  
 CC invention.  
 CC Note: The sequence data for this patent is also available in electronic  
 CC format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).  
 XX  
 XX Sequence 570 BP; 129 A; 190 C; 170 G; 81 T; 0 other;  
 SO  
 Query Match 24.1%; Score 78; DB 25; Length 570;  
 Best local similarity 100.0%; Pred. No. 1.5e-07; Mismatches 0; Gaps 0;  
 Matches 78; Conservative 0; Indels 0; Gaps 0;  
 OY 246 GCGAGACCGGCTTTAGAGAGCTTCTGCTTCCCGGACCGGAGATTCCCGCC 305  
 Db 1 GCGAGACCGGCTTTAGAGAGCTTCTGCTTCCCGGACCGGAGATTCCCGCC 60  
 OY 306 GCGCGAGCGCCCGCGCC 323  
 Db 61 GCGCGAGCGCCCGCGCC 78  
 RESULT 16  
 ABX64209  
 ID ABX64209 standard; cDNA; 570 BP.  
 XX  
 XX ABX64209;  
 AC  
 XX 26-FEB-2003 (first entry)  
 DT  
 DE cDNA encoding human PRO1245 polypeptide.  
 XX  
 XX Human; PRO polypeptide; secreted protein; transmembrane protein;  
 KW genetic disorder; antibacterial; immunosuppressive; transgenic;  
 KW gene therapy; gene; ss.  
 XX  
 XX Homo sapiens.  
 OS  
 PV US2002103125-A1.  
 XX  
 XX 01-AUG-2002.  
 PD  
 XX 20-NOV-2001; 2001US-0989731.  
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 XX 05-NOV-1997; 97WO-US20069.  
 PR 16-SEP-1998; 98WO-US19350.  
 PR 17-SEP-1998; 98WO-US19437.  
 PR 07-OCT-1998; 98WO-US21141.  
 PR 01-DEC-1998; 98WO-US25108.  
 PR 05-JAN-1999; 99WO-US00106.  
 PR 08-MAR-1999; 99WO-US05028.  
 PR 02-JUN-1999; 99WO-US21252.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 16-DEC-1999; 99WO-US28634.  
 PR 20-DEC-1999; 99WO-US30095.  
 PR 06-JAN-2000; 2000WO-US00219.  
 PR 11-FEB-2000; 2000WO-US00376.  
 PR 18-FEB-2000; 2000WO-US03565.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US04914.  
 PR 10-MAR-2000; 2000WO-US05004.  
 PR 12-MAR-2000; 2000WO-US05841.  
 PR 15-MAR-2000; 2000WO-US06319.  
 PR 20-MAR-2000; 2000WO-US06854.  
 PR 30-MAR-2000; 2000WO-US08439.

PR 15-MAY-2000; 2000MO-US13358.  
 PR 17-MAY-2000; 2000MO-US13705.  
 PR 22-MAY-2000; 2000MO-US14042.  
 PR 30-MAY-2000; 2000MO-US14941.  
 PR 02-JUN-2000; 2000MO-US15264.  
 PR 28-JUL-2000; 2000MO-US20710.  
 PR 11-AUG-2000; 2000MO-US22031.  
 PR 23-AUG-2000; 2000MO-US23522.  
 PR 24-AUG-2000; 2000MO-US23328.  
 PR 08-NOV-2000; 2000MO-US30952.  
 PR 01-DEC-2000; 2000MO-US32678.  
 PR 28-FEB-2001; 2001MO-US06520.  
 PR 01-JUN-2001; 2001MO-US17800.  
 PR 20-JUN-2001; 2001MO-US19692.  
 PR 29-JUN-2001; 2001MO-US21066.  
 PR 09-JUL-2001; 2001MO-US21735.  
 PR 16-JUN-1997; 97US-049787P.  
 PR 17-OCT-1997; 97US-062250P.  
 PR 12-NOV-1997; 97US-065311P.  
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 PR 25-FEB-1998; 98US-075945P.  
 PR 20-MAR-1998; 98US-078910P.  
 PR 28-APR-1998; 98US-083322P.  
 PR 07-MAY-1998; 98US-084600P.  
 PR 28-MAY-1998; 98US-087106P.  
 PR 02-JUN-1998; 98US-087607P.  
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 PR 04-JUN-1998; 98US-088028P.  
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 PR 05-JUN-1998; 98US-088217P.  
 PR 09-JUN-1998; 98US-088655P.  
 PR 10-JUN-1998; 98US-088734P.  
 PR 10-JUN-1998; 98US-088738P.  
 PR 10-JUN-1998; 98US-088742P.  
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 PR 10-JUN-1998; 98US-088824P.  
 PR 10-JUN-1998; 98US-088826P.  
 PR 11-JUN-1998; 98US-088858P.  
 PR 11-JUN-1998; 98US-088861P.  
 PR 11-JUN-1998; 98US-088876P.  
 PR 12-JUN-1998; 98US-089105P.  
 PR 16-JUN-1998; 98US-089440P.  
 PR 16-JUN-1998; 98US-089512P.  
 PR 16-JUN-1998; 98US-089514P.  
 PR 17-JUN-1998; 98US-089532P.  
 PR 17-JUN-1998; 98US-089538P.  
 PR 17-JUN-1998; 98US-089598P.  
 PR 17-JUN-1998; 98US-089599P.  
 PR 17-JUN-1998; 98US-089600P.  
 PR 17-JUN-1998; 98US-089653P.  
 PR 18-JUN-1998; 98US-089801P.  
 PR 18-JUN-1998; 98US-089907P.  
 PR 18-JUN-1998; 98US-089908P.  
 PR 28-AUG-2001; 2001US-0941992.  
 XX  
 XX (GETH) GENENTECH LTD.  
 XX  
 PI Ashkenazi AJ, Baker KP, Bolstein D, Deanyers L, Eaton DL,  
 PI Ferreira N, Fong S, Geisler H, Geisleren ME, Goddard A,  
 PI Grimaldi UC, Gurney AL, Kijavini IU, Nadler MA, Pan J, Paoni NF,  
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams FW, Wood WI;

PI Zhang Z;  
 XX WPI; 2003-102117/09.  
 DR P-PSDB; ABU13986.  
 XX  
 XX Novel secreted and transmembrane polypeptide for modulating biological  
 PT activity of cell expressing the polypeptide, identifying agonists or  
 PT antagonists of polypeptide, and as molecular weight markers  
 XX  
 PS Claim 2; Fig 289; 649pp; English.

CC The present invention relates to the isolation of novel human PRO  
 CC polypeptides, and the polynucleotide sequences encoding them. The  
 CC PRO polypeptides are secreted and transmembrane proteins. The PRO  
 CC polypeptides are useful for detecting other PRO polypeptides for  
 CC linking bioactive molecules to cells expressing PRO polypeptides,  
 CC for modulating biological activities of cells expressing PRO  
 CC polypeptides, and for identifying agonists or antagonists.  
 CC The polynucleotide sequences encoding PRO polypeptides are useful as  
 CC hybridisation probes, in chromosome and gene mapping, in the generation  
 CC of antisense RNA and DNA, in the preparation of PRO polypeptides, for  
 CC generating transgenic animals or knockout animals, to construct  
 CC hybridisation probes for mapping the gene which encodes the PRO  
 CC polypeptide, and for the genetic analysis of individuals with genetic  
 CC disorders, in gene therapy, for chromosome identification, as  
 CC chromosome markers, and for generating probes for PCR, Northern  
 CC analysis, Southern analysis and Western analysis. The present  
 CC sequence encodes a human PRO polypeptide of the invention.  
 CC Note: The sequence data for this patent was obtained in electronic  
 CC format directly from the USPRO web site at  
 CC seqdata.uspro.gov/peptideentry.html.  
 XX

SQ Sequence 570 BP; 129 A; 190 C; 170 G; 81 T; 0 other;

Query Match 24.1%; Score 78; DB 25; Length 570;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-07;  
 Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 GCGAGGACGGGTATAGAGCTGCTGCTGCGCGGAGCGCAGATTCCCGGCC 305  
 DB 1 CCGAGGACCGGCTATAGAGCTGCTGCTGCGCGGAGCGCAGATTCCCGGCC 60

QY 306 GCGCGGAGCGCGCGGCC 323  
 DB 61 GCGCGGAGCGCGCGGCC 78

#### RESULT 17

ABX17173  
 ID ABX17173 standard; cDNA, 570 BP.

AC ABX17173;

DT 04-FEB-2003 (first entry)

XX Human PRO polynucleotide #127.

XX Human; PRO; gene; ss; secreted polypeptide; transmembrane polypeptide;  
 KW toxin; radiolabel; cell death; gene mapping; chromosome mapping;  
 KW protein electrophoresis; genetic disorder; immunosuppressive; cytostatic;  
 KW antibacterial.

XX Homo sapiens.

PN US2002123463-A1.

PD 05-SEP-2002.

BP 19-NOV-2001; 2001US-0989732.

XX 05-NOV-1997; 97MO-US20069.  
 XX 16-SEP-1998; 98MO-US19350.  
 XX 17-SEP-1998; 98MO-US19437.

PR 07-OCT-1998; 98WO-US21141.  
 PR 01-DEC-1998; 98WO-US25108.  
 PR 05-JAN-1999; 99WO-US00106.  
 PR 08-MAR-1999; 99WO-US05028.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 30-NOV-1999; 99WO-US21547.  
 PR 01-DEC-1999; 99WO-US28313.  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 16-DEC-1999; 99WO-US30095.  
 PR 20-DEC-1999; 99WO-US30911.  
 PR 06-JAN-2000; 2000WO-US00219.  
 PR 11-FEB-2000; 2000WO-US00376.  
 PR 18-FEB-2000; 2000WO-US03565.  
 PR 22-FEB-2000; 2000WO-US04341.  
 PR 24-FEB-2000; 2000WO-US04414.  
 PR 02-MAR-2000; 2000WO-US05841.  
 PR 10-MAR-2000; 2000WO-US06319.  
 PR 15-MAR-2000; 2000WO-US06834.  
 PR 30-MAR-2000; 2000WO-US07377.  
 PR 15-MAY-2000; 2000WO-US08439.  
 PR 17-MAY-2000; 2000WO-US13358.  
 PR 22-MAY-2000; 2000WO-US13705.  
 PR 30-MAY-2000; 2000WO-US14042.  
 PR 02-JUN-2000; 2000WO-US14941.  
 PR 28-JUL-2000; 2000WO-US15264.  
 PR 11-AUG-2000; 2000WO-US20710.  
 PR 23-AUG-2000; 2000WO-US23522.  
 PR 24-AUG-2000; 2000WO-US23328.  
 PR 08-NOV-2000; 2000WO-US30952.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 28-FEB-2001; 2001WO-US06520.  
 PR 01-JUN-2001; 2001WO-US17800.  
 PR 20-JUN-2001; 2001WO-US19692.  
 PR 29-JUN-2001; 2001WO-US21066.  
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 PR 13-NOV-1997; 97US-065311P.  
 PR 24-NOV-1997; 97US-066770P.  
 PR 25-FEB-1998; 98US-075945P.  
 PR 20-MAR-1998; 98US-078910P.  
 PR 28-APR-1998; 98US-083322P.  
 PR 07-MAY-1998; 98US-084608P.  
 PR 28-MAY-1998; 98US-087106P.  
 PR 02-JUN-1998; 98US-087607P.  
 PR 02-JUN-1998; 98US-087609P.  
 PR 03-JUN-1998; 98US-087759P.  
 PR 04-JUN-1998; 98US-087827P.  
 PR 04-JUN-1998; 98US-088021P.  
 PR 04-JUN-1998; 98US-088025P.  
 PR 04-JUN-1998; 98US-088026P.  
 PR 04-JUN-1998; 98US-088028P.  
 PR 04-JUN-1998; 98US-088029P.  
 PR 04-JUN-1998; 98US-088030P.  
 PR 04-JUN-1998; 98US-088033P.  
 PR 04-JUN-1998; 98US-088326P.  
 PR 05-JUN-1998; 98US-088167P.  
 PR 05-JUN-1998; 98US-088202P.  
 PR 05-JUN-1998; 98US-088212P.  
 PR 05-JUN-1998; 98US-088217P.  
 PR 09-JUN-1998; 98US-088655P.  
 PR 10-JUN-1998; 98US-088734P.  
 PR 10-JUN-1998; 98US-088738P.  
 PR 10-JUN-1998; 98US-088742P.  
 PR 10-JUN-1998; 98US-088810P.  
 PR 10-JUN-1998; 98US-088824P.  
 PR 10-JUN-1998; 98US-088826P.

PR 11-JUN-1998; 98US-088858P.  
 PR 11-JUN-1998; 98US-088861P.  
 PR 11-JUN-1998; 98US-088876P.  
 PR 12-JUN-1998; 98US-089105P.  
 PR 16-JUN-1998; 98US-089440P.  
 PR 16-JUN-1998; 98US-089512P.  
 PR 16-JUN-1998; 98US-089512P.  
 PR 17-JUN-1998; 98US-089513P.  
 PR 17-JUN-1998; 98US-089538P.  
 PR 17-JUN-1998; 98US-089598P.  
 PR 17-JUN-1998; 98US-089599P.  
 PR 17-JUN-1998; 98US-089600P.  
 PR 17-JUN-1998; 98US-089653P.  
 PR 18-JUN-1998; 98US-089801P.  
 PR 18-JUN-1998; 98US-089907P.  
 PR 18-JUN-1998; 98US-089908P.  
 PR 28-AUG-2001; 2001US-0941992.  
 (GERTH ) GENENTECH INC.  
 PR XX Ashkenazi AJ, Baker KP, Borstein D, Deanyers L, Eaton DL,  
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ,  
 PI Grimaldi JC, Gurley AL, Kljavin JU, Napier MA, Pan U, Paoni NF,  
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PW, Wood WI,  
 PI Zhang Z;  
 XX WPI; 2003-066810/06.  
 DR P-PSDB; ABU10941.  
 XX  
 PT Novel secreted and transmembrane polypeptide for modulating biological  
 PT activity of cell expressing the polypeptide, identifying agonists or  
 PT antagonists of polypeptide, and as molecular weight markers  
 XX  
 XX Claim 2; Fig 289; 655pp; English.  
 XX  
 CC The invention relates to a secreted and transmembrane polypeptide, termed  
 CC PRO polypeptide, and the polynucleotide encoding it. The polypeptide is  
 CC useful for detecting PRO polypeptides and for linking a bioactive  
 CC molecule to a cell expressing the above polypeptides, where the bioactive  
 CC molecule is a toxin, radiolabel or an antibody. The bioactive material  
 CC causes the death of the cell. The polypeptide is useful for identifying  
 CC agonists or antagonists of the PRO polypeptide, for preparing variants of  
 CC PRO, as a molecular weight marker for protein electrophoresis purposes  
 CC and the PRO polynucleotide is also useful as a hybridisation probe, in  
 CC markers. The polynucleotide is also useful for recombinantly expressing those  
 CC markers. The preparation of PRO polypeptide, in generation of antisense RNA and DNA, in  
 CC the preparation of PRO polypeptide, for generating transgenic animals or  
 CC knockout animals which in turn are useful in the development and  
 CC screening of therapeutically useful reagents, to construct hybridisation  
 CC probes for mapping the gene which encodes PRO, and for the genetic  
 CC analysis of individuals with genetic disorders, in gene therapy, for  
 CC chromosome identification, as a chromosome marker, and for generating  
 CC probes for PCR, Northern analysis, Southern analysis and Western  
 CC analysis. This sequence represents a human PRO polynucleotide of the  
 CC invention.  
 XX  
 SQ Sequence 570 BP; 129 A; 190 C; 170 G; 81 T; 0 other;  
 XX  
 Query Match 24.1%; Score 78; DB 25; Length 570;  
 Beat Local Similarity 100.0%; Pred. No. 1.5e-07;  
 Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 246 GCGAGGACCGGGTATAGAAGCTCGTGGCTTCCCGGACCGCAGGTTCCCGCGC 305  
 DB 1 GCGAGGACCGGGTATAGAAGCTCGTGGCTTCCCGGACCGCAGGTTCCCGCGC 60  
 QY 306 GCGCGGAGCCCGCGCGC 323  
 DB 61 GCGCGGAGCCCGCGCGC 78  
 RESULT 18  
 AAV54617



DT 13-AUG-2002 (first entry)  
XX Gene #3953 used to diagnose liver cancer.  
DE  
XX Gene: liver cancer; dr; hepatocellular carcinoma; hepatotropic;  
KM metastatic liver tumor; cytosolic; expression profile; disease state;  
KW disease progression; drug toxicity; drug efficacy; drug metabolism.  
XX  
XX Homo sapiens.  
OS  
XX WO200229103-A2.  
PN  
XX 11-APR-2002.  
PD  
XX 02-OCT-2001; 2001WO-US30589.  
PF  
XX 02-OCT-2000; 2000US-237054P.  
PR  
XX (GENE-) GENE LOGIC INC.  
XX  
XX Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;  
PI WPI; 2002-426119/45.  
DR  
XX  
XX Diagnosing and detecting the progression of liver cancer,  
PT hepatocellular carcinoma or metastatic liver tumor in a patient,  
PT involves detecting the level of expression of two or more genes in a  
liver tissue sample  
Claim 1; SEQ ID NO 3953; 298bp; English.  
XX  
XX The invention relates to a novel method for diagnosing and detecting the  
XX progression of liver cancer hepatocellular carcinoma or metastatic liver  
XX tumor in a patient, and differentiating metastatic liver cancer from  
XX hepatocellular carcinoma in a patient, involving detecting the level of  
XX expression of two or more genes represented in ABN93503-ABN97455 in a  
XX tissue sample. The method of the invention has hepatotropic, and  
XX cytosolic activity. The method is useful for diagnosing and detecting  
XX the progression of liver cancer, hepatocellular carcinoma and metastatic  
XX liver carcinoma in a patient. The method is useful for identifying  
XX expression profiles which serve as useful diagnostic markers as well as  
XX markers that can be used to monitor disease states, disease progression,  
XX drug toxicity, drug efficacy and drug metabolism.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
XX Sequence 43058 BP; 10264 A; 11643 C; 12243 G; 8908 T; 0 other;  
SQ  
Query Match 16.9%; Score 54.6; DB 24; Length 43058;  
Best Local Similarity 50.2%; Pred. No. 0.0095;  
Matches 161; Conservative 0; Mismatches 159; Indels 1; Gaps 1;  
QY 1 GCGCGTGGGTCAGACCGCGAAGGAGGAGTGGGGCGGGTGGGCTCCGCGAGACAA 60  
DB 25561 GCGGTCGGCG 25620  
QY 61 GCGCGGCGTCTCTCAAGGCGCCCGAGCGCTCGCGAAGAGTCTCGAGGCGC 120  
DB 25621 GCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 25680  
QY 121 GCGCGAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180  
DB 25681 GCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 25740  
QY 181 GCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 239  
DB 25741 GCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 25800  
QY 240 GCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 299  
DB 25801 GCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 25860

QY 300 CCG 320  
DB 25861 GCG 25881  
RESULT 21  
ID ABL64982 standard; DNA; 43058 BP.  
XX  
XX ABL64982;  
XX  
XX 15-MAY-2002 (first entry)  
XX  
XX  
XX Lung cancer related gene sequence SEQ ID NO:3319.  
XX  
XX Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;  
XX stomach; lung; prostate; pancreas; carcinoma; antitumor; cancerous;  
XX cytotoxic; gene therapy; antineoplastic; Wilms tumor; adenocarcinoma;  
XX gene; dr.  
XX  
XX Homo sapiens.  
XX  
XX WO200194629-A2.  
XX  
XX 13-DEC-2001.  
XX  
XX 30-MAY-2001; 2001WO-US10838.  
XX  
XX 05-JUN-2000; 2000US-209473P.  
XX 05-JUN-2000; 2000US-209531P.  
XX 18-SEP-2000; 2000US-233133P.  
XX 18-SEP-2000; 2000US-233617P.  
XX 20-SEP-2000; 2000US-234009P.  
XX 20-SEP-2000; 2000US-234034P.  
XX 20-SEP-2000; 2000US-234052P.  
XX 22-SEP-2000; 2000US-234509P.  
XX 22-SEP-2000; 2000US-234567P.  
XX 22-SEP-2000; 2000US-234923P.  
XX 22-SEP-2000; 2000US-234924P.  
XX 25-SEP-2000; 2000US-235077P.  
XX 25-SEP-2000; 2000US-235082P.  
XX 25-SEP-2000; 2000US-235134P.  
XX 25-SEP-2000; 2000US-235280P.  
XX 25-SEP-2000; 2000US-235637P.  
XX 25-SEP-2000; 2000US-235638P.  
XX 26-SEP-2000; 2000US-235711P.  
XX 27-SEP-2000; 2000US-235720P.  
XX 27-SEP-2000; 2000US-235840P.  
XX 27-SEP-2000; 2000US-235863P.  
XX 28-SEP-2000; 2000US-236028P.  
XX 28-SEP-2000; 2000US-236032P.  
XX 28-SEP-2000; 2000US-236033P.  
XX 28-SEP-2000; 2000US-236034P.  
XX 28-SEP-2000; 2000US-236109P.  
XX 28-SEP-2000; 2000US-236111P.  
XX 29-SEP-2000; 2000US-236842P.  
XX 29-SEP-2000; 2000US-236891P.  
XX 02-OCT-2000; 2000US-237112P.  
XX 02-OCT-2000; 2000US-237173P.  
XX 02-OCT-2000; 2000US-237278P.  
XX 02-OCT-2000; 2000US-237294P.  
XX 02-OCT-2000; 2000US-237295P.  
XX 02-OCT-2000; 2000US-237316P.  
XX 02-OCT-2000; 2000US-237425P.  
XX 03-OCT-2000; 2000US-237598P.  
XX 03-OCT-2000; 2000US-237604P.  
XX 03-OCT-2000; 2000US-237606P.  
XX 03-OCT-2000; 2000US-237608P.  
XX 01-NOV-2000; 2000US-244867P.  
XX 01-NOV-2000; 2000US-245084P.  
XX  
XX (AVAIL-) AVAILON PHARM.







XX 07-MAR-2002.  
 PD 01-SEP-2001; 2001WO-EPI0074.  
 PF 01-SEP-2000; 2000DE-1043826.  
 PR 05-SEP-2000; 2000DE-1044543.  
 XX (EPIC-) EPICENOMICS AG.  
 PA  
 PI Olek A, Piepenbrock C, Berlin K, Guetig D,  
 DR WPI; 2002-371829/40.  
 XX  
 PT Determining the degree of cytosine methylation in genomic DNA, useful  
 PT for diagnosis and prognosis, comprises selective hybridization of  
 PT amplicons from chemically treated DNA -  
 XX  
 PS Claim 12; 56pp + Sequence Listing; 56pp; German.

CC This invention describes a novel method for determining the degree of  
 CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a  
 CC genomic sample of DNA. The sample is treated chemically to convert  
 CC cytosine (C) but not methylated C, to uracil, then part of the genomic  
 CC DNA that contains the target C is amplified to form a labeled amplicon.  
 CC The amplicon is hybridized to two classes, each with at least one  
 CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers  
 CC and the degree of hybridization to both classes is determined from the  
 CC label on the amplicon. From the ratio of labels hybridized to the two  
 CC classes of oligomers, the degree of methylation is calculated. The method  
 CC is used: (i) for diagnosis and/or prognosis of side effects of  
 CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders  
 CC of the central nervous, cardiovascular, gastrointestinal and respiratory  
 CC systems etc.; particularly by detecting mutations or single nucleotide  
 CC polymorphisms (SNPs) and (ii) for differentiation of cell or tissue  
 CC types and for investigating cell differentiation. The method allows the  
 CC methylation status of many C residues to be determined simultaneously.  
 CC AB013410-AB054121 represent genomic DNA sequences used to illustrate the  
 CC method for determining the degree of cytosine methylation described in  
 CC the disclosure of the invention.

XX Sequence 629 BP; 164 A; 319 C; 100 G; 46 T; 0 other;

Query Match 16.2%; Score 52.2; DB 24; Length 629;  
 Best Local Similarity 50.2%; Pred. No. 0.033;  
 Matches 129; Conservative 0; Mismatches 128; Indels 0; Gaps 0;

QY 1 GCGCGTGGGTCAACCCGCAAGGAGTGCAGGCGCGGCTGCGCGGAGACAA 60  
 DB 347 GCGGTGCGGGCGGGCGGGCGGGGTGCGGGCGGGCGGGGTGCGGGCGGGGTGCGG 288  
 QY 61 GCGCGGCTGCTCTCTCAAGAGGCGCCAGCGCTGCAAGAGGAAGTCTCTGAGAGCC 120  
 DB 287 GCGCGGGCGGGGTGCGGGGTGCGGGCGGGGTGCGGGCGGGGTGCGGGCGGGGTGCGG 228  
 QY 121 GCGGAGGAGAGGCGGCGGCTTCCAGAGGCGCGCGCGCGAGCAGAAAGTTGGCCAG 180  
 DB 227 GCGGCGGGCGGGGTGCGGGGTGCGGGCGGGGTGCGGGCGGGGTGCGGGCGGGGTGCGG 168  
 QY 181 GGCACGCGCTGAGCGGAGCGGCGGAGGCTTTCTCAGAGACCGGCGGAGAGCGCGGCTG 240  
 DB 167 GCGCGGGCGGGGTGCGGGGTGCGGGGTGCGGGGTGCGGGGTGCGGGGTGCGGGGTGCGG 108  
 QY 241 GAGGCGGAGAGAGCGGG 257  
 DB 107 CGGGGCGCGGGCGGGG 91

RESULT 25  
 AAX53491/c  
 ID AAX53491 standard; DNA; 114955 BP.  
 XX AC AAX53491;

XX 05-JUL-1999 (first entry)  
 DT Human adenosine A1 receptor antisense oligonucleotide fragment.  
 DE Antisense oligonucleotide; multiple target; antisense treatment;  
 XX impaired respiration; inflammation; lung disease;  
 XX pulmonary vasoconstriction; inflammation; allergic rhinitis;  
 XX acute asthma; allergy; asthma; impeded respiration;  
 XX respiratory distress syndrome; pain; cystic fibrosis;  
 XX pulmonary hypertension; pulmonary vasoconstriction; emphysema;  
 XX chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;  
 XX colon cancer; breast cancer; lung cancer; pancreatic cancer;  
 XX hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;  
 XX prostate cancer; ss.  
 XX  
 OS Synthetic.  
 XX  
 XX WO9913886-A1.  
 XX  
 XX 25-MAR-1999.  
 XX  
 XX 17-SEP-1998; 98WO-US19419.  
 XX  
 XX 09-JUN-1998; 98US-0093972.  
 XX  
 XX 17-SEP-1997; 97US-0059160.  
 XX  
 XX (UYEC-) UNIV EAST CAROLINA.  
 XX  
 XX Nye JW;  
 XX WPI; 1999-229400/19.

CC The specification describes antisense oligonucleotides (AAX52869-X55271)  
 CC directed against at least 2 mRNAs selected from target genes, coding and  
 CC non-coding regions of RNA corresponding to target genes, gene  
 CC initiating regions, genomic flanking regions, intron/exon borders, the  
 CC 5'-end, the 3'-end and the juxta-section between coding and non-coding  
 CC regions and all segments of RNAs encoding proteins associated with one  
 CC or more diseases, conditions or mixtures. The antisense oligonucleotides  
 CC may be derived from sequences AAX5272-74. These multiple target  
 CC oligonucleotides (specifically AAX5180-271) can be used for the  
 CC antisense treatment of diseases and conditions. Typical diseases and  
 CC conditions are those associated with impaired respiration and  
 CC inflammation, including lung diseases, pulmonary vasoconstriction,  
 CC inflammation, allergic rhinitis, acute asthma, allergic asthma, impeded  
 CC respiration, respiratory distress syndrome, pain, cystic fibrosis,  
 CC pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic  
 CC obstructive pulmonary disease (COPD), and cancers such as leukemia,  
 CC lymphomas, carcinomas, hepatocellular carcinoma, kidney cancer, lung cancer,  
 CC pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma,  
 CC hepatic metastasis, as well as all types of cancers which may metastasize  
 CC or have metastasized to the lungs, including breast and prostate cancer.

XX Sequence 114955 BP; 6071 A; 29417 C; 36712 G; 21328 T; 21427 other;  
 Query Match 14.8%; Score 47.8; DB 20; Length 114955;  
 Best Local Similarity 45.3%; Pred. No. 0.24;  
 Matches 126; Conservative 9; Mismatches 140; Indels 3; Gaps 1;

QY 8 GGGTCAAGCCGCAAGGAGTGCAGGCGGGGTGCGGCTTCCGAGAGCAAGGCGCGG 67  
 DB 107160 GGGCGGGCGGGCAAGCGGGCGGGCGGGCGGAGCCNNNNNNCCCGGGCC--GGCGGG 107104  
 QY 68 CCGCTCTCTCAAGAGGCGCCAGCGCTTCCGAGAGGAAGTCTCTGAGAGCGCGGCGAG 127  
 DB 107103 CAAAGCGGGCGGGCGGGCGAGCCANNNNNNCCGGGCGGGCGGGCAAGCGGGCGCGG 107044

QY	128	GAAGGGGAGACGGGCTTCCAGAGGCGCGCGGAGAGAAATTGGCCAGAGCACGG	187
DB	107043	GGCGCGAGCCACNNHNNHNNCCGGGCGGGCGGAGAGCCGGGCGCGGGCCAGGCAAG	106984
QY	188	CCGTGAGCGGACCGGAGCGGCTTTTTCAGAGACCGGAGCGGAGCGGCGCTGAGAGGC	247
DB	106983	NNHNNNSCCGGGCGCGGCGGAGAGCCGGGCGCGGGCGGAGCCAGGNNHNNNSCCCG	1069224
QY	248	GAGGACCGGCGTATAGAAAGCCCTCGTGGCCCTTGCCCGGG	285
DB	106923	GCGGCGCGGAGAGCCGGGCGCGGGCGGAGGCAAGG	106886
RESULT 26			
ABN81321/G			
ID	ABN81321	standard, cDNA, 3743 BP.	
XX	ABN81321;		
AC			
XX	30-AUG-2002	(first entry)	
DT			
XX			
DE	Human mast cell related gene F10317 SEQ ID NO 6.		
XX			
KW	Human; mast cell; MC; antiallergic; antiinflammatory; antiasthmatic;		
KW	vasotropic; dermatological; allergy; hypersensitivity; rhinitis; asthma;		
KW	gene; ss.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	377..1951	
FT		/tag= a	
FT		/product= "MC17"	
XX			
PV	WO200246389-A2.		
XX			
PD	13-JUN-2002.		
XX			
PE	07-DEC-2001; 2001WO-US46180.		
XX			
FR	08-DEC-2000; 2000US-251835P.		
FR	14-MAR-2001; 2001US-275479P.		
FR	28-MAR-2001; 2001US-279115P.		
PR	02-APR-2001; 2001US-280143P.		
XX			
PA	(UNIO ) UCB SA.		
XX			
PI	Nocka K, Pirozzi G, Einstein R;		
XX			
XX	WPI, 2002-508560/54.		
DR	P-PsDB; ABB77572.		
XX			
PT	Novel isolated nucleic acids that are differentially expressed in mast		
PT	cells in patients with allergic hypersensitivity, encoding proteins		
PT	associated with mast cell regranulation and allergic hypersensitivity		
XX			
PS	Claim 1, Page 104-108; 11pp; English.		
XX			
CC	The invention relates to isolated nucleic acid (ABN81319-ABN81324),		
CC	corresponding to genes differentially expressed in mast cells following		
CC	activation or in patients with allergic hypersensitivity disease, (I)		
CC	that encodes proteins (ABB77569-ABB77575) (II) or a protein fragment of		
CC	(II) if at least 6 amino acids. (II) is useful for identifying binding		
CC	partners. (I) or (II) is useful for diagnosing or treating a disease		
CC	state (e.g. allergic hypersensitivity, seasonal rhinitis, asthma,		
CC	urticaria or atopic dermatitis or mastocytosis) in a subject which		
CC	involves determining the level of expression of (I) or (II). A computer		
CC	system, comprising a database containing information identifying the		
CC	expression level in a tissue or at least one mast cell of (I), is useful		
CC	for presenting information to identify the relative expression level of		
CC	(I). (II) is used as a marker to detect, diagnose or identify an allergic		
CC	response in a patient. The protein can also serve as a target that		

CC	module/ gene expression or activity and as an antigen to raise
CC	polyclonal or monoclonal antibodies. (ii) is useful for identifying
CC	agents that modulate expression of the protein or agents, such as
CC	agonists or antagonists. The agonists or antagonists are useful for
CC	modulating biological activity and function of (ii) and thus are useful
CC	for alleviating disease conditions such as allergic hypersensitivity,
CC	seasonal rhinitis, asthma, urticaria, atopic dermatitis or mastocytosis.
XX	
XX	Sequence 3743 BP; 778 A; 1088 C; 1134 G; 743 T; 0 other;
XX	
XX	Query Match 14.7%; Score 47.6; DB 24; Length 3743;
XX	Best Local Similarity 46.9%; Pred. No. 0.28; Indels 0; Gaps 0;
XX	Matches 149; Conservative 0; Mismatches 169;
QY	3 GCGTGGGGTCAGACCGCAAAAGCGAAGTGGGGGCGGGGCTTCGCGGACAAAGG 62
DB	381 GCCATGGCGCCCGGGCG 322
QY	63 CCGGGGCGCTGCTCTCTGAGAGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 122
DB	321 CCGGGGCGCTGCG 262
QY	123 GCAGGGAAGGGGGGACCGGGCTTCCACAGGGCGCGCGCGCGCGCGCGCGCGCGCGCG 182
DB	261 GCCCG 202
QY	183 CACGGCGCGTACCGGAGCGGGGACGGGCTTCTGAGAGCGCGGGCGAGGCGCGGCGTGGGA 242
DB	201 GAAAGCGCGCTCTGAGAGCTCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 142
QY	243 GGGGCGAGGAACGGGGTATTAAGAAAGCTCTGAGGCGCTTGGCGCGGAGCGGAGTTCGCGG 302
DB	141 GCGGGGCTCTGAGAGGGGGGACCCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 82
QY	303 CGCGCGCGCGAGCG 320
DB	81 CG 64
XX	
XX	RESULT 27
XX	AAFA44725
ID	AAFA44725 standard; cDNA; 2461 BP.
AC	AAFA44725;
DT	27-MAR-2001 (first entry)
DE	Novel protein kinase cDNA, SEQ ID NO: 106.
XX	
XX	Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;
XX	immunopressive; cardiac; renal; antiinflammatory; antisthmatic;
XX	dermatological; antidiabetic; antifertility; gene therapy; vaccine;
XX	immune disorder; cardiovascular disease; neurodegenerative disease;
XX	cancer; autoimmune disorder; stroke; inflammatory bowel disease;
XX	inflammatory pelvic disease; multiple sclerosis; psoriasis; ss.
OS	Homo sapiens.
XX	
XX	WO200073469-A2.
XX	07-DEC-2000.
XX	
XX	26-MAY-2000; 2000WO-US14842.
XX	
XX	28-MAY-1999; 99US-0136503.
XX	
XX	(SUGG-) SUGEN INC.
XX	
XX	Plowman GD, Martinez R, Whyte D, Sudersanam S,
XX	WFI; 2001-032161/04.
XX	P-PSDB; AAB65697.
XX	

PT Nucleic acids encoding kinase polypeptides, useful for diagnosing and  
PT treating immune-related diseases and disorders, cardiovascular disease,  
XX neurodegenerative diseases and/or cancers -  
XX  
XX Example 1; Fig 2; 310p; English.  
XX  
XX The present sequence encodes a novel protein kinase. The nucleic acids  
CC and the protein kinases they encode may be used in the treatment and  
CC diagnosis of diseases associated with inappropriate kinase expression  
CC such as immune-related diseases and disorders, cardiovascular disease,  
CC neurodegenerative diseases and/or cancers. The nucleic acids and  
CC complementary sequences may also be used as DNA probes in diagnostic  
CC assays. The kinase polypeptides may be used as antigens in the production  
CC of antibodies of kinase expression and activity. Anti-kinase antibodies  
CC and kinase antagonists may also be used to down regulate kinase  
CC expression and activity. Diseases related to down regulate kinase  
CC activity include rheumatoid arthritis, atherosclerosis, autoimmune  
CC disorders, complications of organ transplantation, myocardial infarction,  
CC immune disorders, cardiomyopathies, strokes, renal failure,  
CC oxidative-stress related disorders, chronic inflammatory bowel disease,  
CC chronic inflammatory pelvic disease, multiple sclerosis, asthma,  
CC osteoarthritis, psoriasis, rhinitis, autoimmunity, diabetes, cancers and  
CC reproductive disorders.  
XX  
XX Sequence 2461 BP; 426 A; 771 C; 811 G; 453 T; 0 other;  
SQ  
Query Match 14.6%; Score 47; DB 22; Length 2461;  
Best Local Similarity 47.7%; Pred. No. 0.38;  
Matches 137; Conservative 0; Mismatches 150; Indels 0; Gaps 0;  
OY 37 CGGGTGGGCTTCGCGAGACAAGCCCGGCTGCTCTCTCAAGAGGCCCGCCAGCGCT 96  
DB 224 CGGGTTCGAGGCTTCGAGCGAGGCACTCCCTTAGAGCTTCGCGCGCCCGGGTGGG 283  
OY 97 GCCAAGAGAGATCTCTCGAGCGCCCGGCGAGGAGGCGGCAAGGCTTCCAGGCGCCG 156  
DB 284 GCGGTGCGGGGGGCGCGGGGAGCTGGCCCGGCAATCGGGCGGCTACGAGAGTGC 343  
OY 157 CGGCGGACAGAGAGATTGGCCAGGCGACGCGCGTGAAGCGGCGGCGGCTTTCA 216  
DB 344 AGCGGTATTCGCGCGGGGCGCCCGGGCGGGCGGGCGGCGAGCGGCGCGCTGA 403  
OY 217 GGAGGCGGCGGCGAGCGCGCGCTGAGAGGCGGCGAGACCGGGTAAAGAGCTCTGGCC 276  
DB 404 TGGACTGTGCTCGGGGCGGCGCGCTGCGCGCTCGCGCCCGCCCTTGGGCTCGGCC 463  
OY 277 TTGCGCGGCGAGCGGAGGTTCCCGGCGCGCCCGAGCCCGCGCGC 323  
DB 464 TGTCCGACGCGCGCCCGAGGCTGGCCCCGCGCTCCGCGCCAGAGCTTC 510  
RESULT 28  
ABI9477  
ID ABI9477 standard; cDNA; 1729 BP.  
XX  
XX ABI9477;  
XX  
XX 07-MAR-2002 (first entry)  
XX  
XX Mouse ischaemic condition related cDNA sequence SEQ ID NO:435.  
XX  
XX Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;  
XX vasoospastic ischaemia; ischaemic condition; ischaemic disease; ss.  
XX  
XX Mus musculus.  
XX  
XX WO20018188-A2.  
XX  
XX 22-NOV-2001.  
XX  
XX 18-MAY-2001; 2001WO-TP04192.  
XX  
XX 18-MAY-2000; 2000JP-0145977.  
XX  
XX PR

XX  
XX (UYN1-) UNIV NIHON SCHOOL JURIDICAL PERSON.  
XX  
XX Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;  
XX  
XX WPI; 2002-034733/04.  
XX  
XX P-PSDB; ABB57179.  
XX  
XX Examining the ischemic condition (e.g. occlusive ischemia) by measuring  
PT expression levels of particular genes defined in the specification or  
PT by determining the expression profile of a gene group comprising these  
PT genes -  
XX  
XX Claim 2; Page 1194-1197; 2690p; English.  
XX  
XX The present invention describes a method for examining ischaemic  
CC conditions, comprising measuring the expression levels of particular  
CC genes (I) in a test sample or determining the expression profile of a  
CC gene group in the sample comprising genes selected from (I). The method  
CC is useful for examining the ischaemic condition (e.g. compressive  
CC ischaemia, occlusive ischaemia or vasoospastic ischaemia) by measuring  
CC expression levels of particular genes (ABI99202 to ABI99912, encoding  
CC the protein sequences in ABB57020 to ABB57374) or by determining the  
CC expression profile of a gene group comprising these genes. The  
CC expression levels or expression profiles produced by these genes are  
CC used as an indicator when screening for ischaemic condition-improving  
CC drugs or therapeutics for ischaemic diseases. ABI9913 and ABI9914  
CC represent PCR primers for a mouse ischaemic condition related sequence,  
CC which are used in the exemplification of the present invention.  
XX  
XX Sequence 1729 BP; 367 A; 548 C; 529 G; 283 T; 2 other;  
SQ  
Query Match 14.1%; Score 45.4; DB 24; Length 1729;  
Best Local Similarity 51.2%; Pred. No. 0.83;  
Matches 103; Conservative 1; Mismatches 97; Indels 0; Gaps 0;  
OY 122 GGCAGGGAAGGGGCAAGGCTTCCAGAGCCCGCGCGCGAGCAAGTTGGCCAGG 181  
DB 104 GGCAGGCGGAGGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 163  
OY 182 GCAAGCGCGTGAAGCGAGCGGCGGCTTTCTCAAGAGCGGCGGAGCGGCGCGCTGG 241  
DB 164 GCGGCGGCGGAGCGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGGCGGAG 223  
OY 242 AGGCGCGAGAGACCGGCTAATGAAGCTCTGCTGCTTCCCGGCGAGCCGCAAGTTCCC 301  
DB 224 GAGCGGAGACCGGAGCGCGAGCGAGCGAGCGCGCGCTGCGGCTTGGCTTGGCGCG 283  
OY 302 GCGGCGCGCGAGCG 322  
DB 284 CCGGCTTCGCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 304  
RESULT 29  
AAT75036/c  
ID AAT75036 standard; cDNA; 3937 BP.  
XX  
XX AAT75036;  
XX  
XX 07-OCT-1997 (first entry)  
XX  
XX Chick fringe A (radical) protein cDNA.  
XX  
XX Fringe A; radical fringe; fate specification; neural tube;  
XX apical ectodermal ridge; cell proliferation; vasculature;  
XX atherosclerosis; tumour; wound healing; therapy; ss.  
XX  
XX Gallus sp.  
XX  
XX Key Location/Qualifiers  
XX  
XX mIsq\_difference 42..43  
XX  
XX /\*tag= a  
XX  
XX /note= "there may be an additional nucleotide  
XX  
XX FT





```
XX AC ABT01503;
XX 07-NOV-2002 (first entry)
XX DT
XX DE Human neuregulin 1 gene.
XX KM Human; neuregulin 1; neuregulin-1-associated gene 1; NRGL1, NRGL1G1,
XX schizoprenia; chromosome 6p12; single nucleotide polymorphism; SNP;
XX KM neuroleptic; gene therapy; gene; dg.
XX OS Homo sapiens.
XX FH
XX FH Location/Qualifiers
XX Key 244312..1369465
XX CDS /*tag= a
XX FT /product= "neuregulin 1"
XX FT /note= "this sequence contains introns"
XX FT 244205..244348
XX FT /*tag= b
XX FT /number= 1
XX FT 244349..244640
XX FT /*tag= c
XX FT /number= 1
XX FT 244641..245646
XX FT /*tag= d
XX FT /number= 2
XX FT 245647..826009
XX FT /*tag= e
XX FT /number= 2
XX FT 826010..826101
XX FT /*tag= f
XX FT /number= 3
XX FT 826102..826307
XX FT /*tag= g
XX FT /number= 3
XX FT 826308..826355
XX FT /*tag= h
XX FT /number= 4
XX FT 826356..1034242
XX FT /*tag= i
XX FT /number= 4
XX FT 1034243..1034321
XX FT /*tag= j
XX FT /number= 5
XX FT 1034322..1153294
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XX FT /number= 5
XX FT 1153295..1153886
XX FT /*tag= l
XX FT /number= 6
XX FT 1153887..1200721
XX FT /*tag= m
XX FT /number= 6
XX FT 1200722..1201065
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XX FT /number= 7a
XX FT 1153887..1200887
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XX FT /number= 7a
XX FT 1200888..1201065
XX FT /*tag= p
XX FT /number= 7b
XX FT 1201066..1210622
XX FT /*tag= q
XX FT /number= 7b
XX FT 1210623..1210744
XX FT /*tag= r
XX FT /number= 8
XX FT 1210745..1219542
XX FT /*tag= s
XX FT /number= 8
XX FT 1219543..1219593
XX FT exon

FT FT /*tag= t
FT FT /number= 9
FT FT 1219594..1221863
FT FT /*tag= u
FT FT /number= 9
FT FT 1221864..1221914
FT FT /*tag= v
FT FT /number= 10
FT FT 1221915..1252253
FT FT /*tag= w
FT FT /number= 10
FT FT 1252254..1253413
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FT FT /number= 11
FT FT 1253414..1326781
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FT FT /number= 11
FT FT 1326782..1327071
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FT FT /number= 12
FT FT 1327072..1332977
FT FT /*tag= aa
FT FT /number= 12
FT FT 1332978..1333107
FT FT /*tag= ab
FT FT /number= 13a
FT FT 1333108..1347039
FT FT /*tag= ac
FT FT /number= 13a
FT FT 1332978..1333652
FT FT /*tag= ad
FT FT /number= 13b
FT FT 1333653..1347039
FT FT /*tag= ae
FT FT /number= 13b
FT FT 1347040..1347107
FT FT /*tag= af
FT FT /number= 14
FT FT 1347108..1347706
FT FT /*tag= ag
FT FT /number= 14
FT FT 1347707..1347765
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FT FT /number= 15a
FT FT 1347766..1354620
FT FT /*tag= aj
FT FT /number= 15a
FT FT 1347707..1348257
FT FT /*tag= ak
FT FT /number= 15b
FT FT 1348258..1354620
FT FT /*tag= al
FT FT /number= 15b
FT FT 1354621..1354644
FT FT /*tag= am
FT FT /number= 16
FT FT 1354645..1359431
FT FT /*tag= an
FT FT /number= 16
FT FT 1359432..1359534
FT FT /*tag= ao
FT FT /number= 17
FT FT 1359535..1361462
FT FT /*tag= ap
FT FT /number= 17
FT FT 1361463..1361589
FT FT /*tag= aq
FT FT /number= 18
FT FT 1361590..1364362
FT FT /*tag= ar
FT FT /number= 18
FT FT 1364363..1364493
FT FT /*tag= as
FT FT exon
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FT      intron          /number= 19
FT      1364494..1365256
FT      /*cag=| ac
FT      /number= 19
FT      exon           /number= 19
FT      1365257..1365463
FT      /*cag=| au
FT      /number= 20a
FT      1365464..1368280
FT      /*cag=| av
FT      /number= 20a
FT      1365257..1366044
FT      /*cag=| aw
FT      /number= 20b
FT      1366045..1368280
FT      /*cag=| ax
FT      /number= 20b
FT      1368281..1368422
FT      /*cag=| ay
FT      /number= 21
FT      1368423..1368810
FT      /*cag=| az
FT      /number= 21
FT      1368811..1369656
FT      /*cag=| ba
FT      /number= 22
FT      629728..744437
FT      /*cag=| db
FT      /product="neuregulin-1-associated gene 1"
FT      /note="this sequence contains introns"
FT      *
FT      exon           /number= 1
FT      629728..629804
FT      /*cag=| dc
FT      /number= 1
FT      629805..630974
FT      /*cag=| dd
FT      /number= 1
FT      630975..631187
FT      /*cag=| de
FT      /number= 2
FT      631188..631282
FT      /*cag=| df
FT      /number= 2
FT      631283..631320
FT      /*cag=| dg
FT      /number= 3
FT      631321..634334
FT      /*cag=| dh
FT      /number= 3
FT      634335..634441
FT      /*cag=| bi
FT      /number= 4a
FT      634442..635331
FT      /*cag=| bj
FT      /number= 4a

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	Query Match	13.7%	Score 44.4	DB 24	Length 1503841
	Best Local Similarity	50.0%	Pred. No. 1.1		
	Matches 111	Conservative 0	Mismatches 111	Indels 0	Gaps 0
Qy	2	CGGCTGGGCTCAACCGCAGAAAGCGAGAGTGGCGGCGGGGTGGGGCTTCGCGGAGACAAAG	61		
Db	244224	CTCGGGCGCAGACAGAGAGGAGAGGCGCGCGGGAGACGGGAGACCCCAAGAGACCAATC	244285		
Qy	62	GCGCGGCTGGCTCTCTCTCAAGAGGCGCCGACCGCTCCCAAGAGAAATCTTCAGAGCCG	121		
Db	244284	GCGGGTCCCGCTCGCTTCGCGACAGCATGAGGAGAAAGACCGCGCGGCGCAATTTGGAC	244344		
Qy	122	GCGAGGAGAGGGGCGACAGGGCTTCCAGAGGCGCCCGCGCTCCAGACAGAAAGTTGGCCAG	181		
Db	244344	CACAGGTAACACAGGCTGGCGAGCGAGGAGACGCTGTGCGCGCGCGCGGCCACCCAGCGATT	244403		
Qy	182	GCAAGGCGCTGAGCGGAGCGGAGCGGCTTTCTCAGAGCGC	223		
Db	244404	TTCAGGACAGCAATCCGCGCTTCAGGAGCTCTCTCTCCCTCGCG	244445		

ID	AAK95240	standard; DNA; 1503900 BP.
XX	AAK95240;	
XX	17-DEC-2001	(first entry)
XX	Human neuregulin-1 gene.	
XX	Human neuregulin-1 associated gene 1, NRX1A1; Schizophrenia gene;	
XX	gene therapy; ds.	
XX	Homo sapiens.	
XX	MO200164876-A2.	
XX	07-SEP-2001.	
XX	28-FEB-2001; 2001WO-US06376.	
XX	28-FEB-2000; 2000US-0515715.	
XX	(DECO-) DECODE GENETICS EMF.	
XX	Stefansson H, Steinthorsdottir V, Gulcher JR;	
XX	WPI; 2001-550179/61.	
XX	P-PSD; AAG67900, AAG67901, AAG67902, AAG67903, AAG67904, AAG67905,	
XX	DR AAG67906, AAG67907, AAG67908, AAG67909, AAG67910, AAG67911, AAG67912,	
XX	DR AAG67913, AAG67914, AAG67915, AAG67916, AAG67917, AAG67918, AAG67919,	
XX	DR AAG67920, AAG67921, AAG67922, AAG67923, AAG67924, AAG67925, AAG67926,	
XX	DR AAG67927, AAG67928, AAG67929, AAG67930, AAG67931, AAG67932, AAG67933,	
XX	DR AAG67934, AAG67935, AAG67936, AAG67937.	
XX	Neuregulin-1 associated gene 1 nucleic acids and fragments, useful for	
XX	preventing diagnosing and treating schizophrenia -	
XX	Disclosure; Page 90-501; 750pp; English.	
XX	Disclosure; Page 90-501; 750pp; English.	
XX	This sequence represents the human neuregulin-1 associated gene 1	
XX	(NRX1A1) of the invention. The NRX1A1 gene is also referred to as the	
XX	human Schizophrenia gene. The invention also relates to fragments or	
XX	variants of the gene and the NRX1A1 polypeptides they encode. The	
XX	NRX1A1 nucleic acids and polypeptides may be used in the prevention,	
XX	diagnosis and treatment of diseases associated with inappropriate NRX1A1	
XX	expression. For example, they may be used to treat disorders associated	
XX	with decreased expression by rectifying mutations or deletions in a	
XX	patient's genome that affect the activity of NRX1A1 by expressing of	
XX	inactive proteins or to supplement the patients own production of	
XX	NRX1A1. Additionally, the gene may be used to produce NRX1A1	
XX	polypeptides, by inserting the nucleic acids into a host cell and	
XX	culturing the cell to express the protein. The gene may also be used as	
XX	DNA probes and primers in diagnostic assays to detect and quantitate the	
XX	presence of similar nucleic acids in samples, and therefore which	
XX	patients may be in need of restorative therapy. The NRX1A1 polypeptides	
XX	may also be used as antigens in the production of antibodies against	
XX	NRX1A1 and in assays to identify modulators of NRX1A1 expression and	
XX	activity. Anti-NRX1A1 antibodies and antagonists may also be used to	
XX	down regulate expression and activity. Anti-NRX1A1 antibodies may	
XX	also be used as diagnostic agents for detecting the presence of NRX1A1	
XX	polypeptides in samples. NRX1A1 is associated with schizophrenia which	
XX	may be prevented, diagnosed and/or created by the above methods.	
XX	Sequence 1503900 BP; 452487 A; 281874 C; 288074 G; 480092 T; 1373 other;	
XX	Query Match 13.7%; Score 44.4; DB 22; Length 1503900;	
XX	Best Local Similarity 50.0%; Freq. No. 1.1.	
XX	Matches 111; Conservative 0; Mismatches 111; Indels 0; Gaps 0	







XX 20-JUL-1999 .(first entry)  
XX  
DE Human 3-OST-4 encoding DNA.  
KM Heparan sulfate D-glucosaminyl 3-O-sulfotransferase; anticoagulant;  
KW saccharide; glycosaminoglycan; proteoglycan; antithrombin; 3-OST;  
RM heparan sulfate; thrombotic disorder; deep vein thrombosis;  
KM pulmonary embolism; coagulation enzyme inactivation; ss.  
XX  
OS Homo sapiens.  
XX  
PN MO9922005-A2.  
PD 06-MAY-1999.  
PF 23-OCT-1998; 98WO-US22597.  
PR 31-OCT-1997; 97US-0065437.  
PP 24-OCT-1997; 97US-0062762.  
XX  
PI (MASI ) MASSACHUSETTS INST TECHNOLOGY.  
PI Fritze LMS, Liu J, Rosenberg RD, Schwartz JU, Shworak NW;  
PI Zhang L;  
XX WPI; 1999-312968/26.  
DR P-PsDB; AAY17067.  
XX  
PT Heparan sulfate D-glucosaminyl 3-O-sulfotransferase and related  
PT polynucleotides  
XX  
PS Claim 5; Page 86-89; 95pp; English.  
XX  
CC The invention relates to nucleic acid molecules (AMX37245-X37250)  
CC encoding heparan sulfate D-glucosaminyl 3-O-sulfotransferases (3-OSTs).  
CC The 3-OST proteins can be used for 3-O-sulfating saccharide residues  
CC within a preparation of glycosaminoglycan or proteoglycan  
CC polysaccharides. 3-OST-1 can be used for enriching the  
CC antithrombin-binding fraction in a preparation of heparan sulfates (HS).  
CC 3-OST-1 can also convert HS proteoglycan anticoagulant precursor to the  
CC HS anticoagulant (HAcC). The 3-OSTs (optionally lacking enzymatic  
CC function) can be used to determine partial sequence information for  
CC complex polysaccharides. The 3-OST proteins, genes and antibodies are  
CC also useful for diagnosis of disorders involving HS biosynthesis. 3-OSTs  
CC are especially used to generate anticoagulant pentasaccharides, which may  
CC be used to treat thrombotic disorders such as deep vein thrombosis and  
CC pulmonary embolism. Cosuglation enzyme inactivation by antithrombin is  
CC enhanced by complexing of antithrombin with endothelial cell surface HS  
CC proteoglycans. This is responsible for the non-thrombogenic properties  
CC of blood vessels. The present sequence represents a human 3-OST-4  
CC encoding DNA.

Sequence 3658 BP; 771 A; 1085 C; 1107 G; 695 T; 0 other;

Query Match 13.6%; Score 44; DB 20; Length 3658;  
Best Local Similarity 50.5%; Pred.No. 1.6;  
Matches 107; Conservative 0; Mismatches 105; Indels 0; Gaps 0.

111 CTCGAGCGCCCGGGACGGAAGGGGGGCACGAGGCTTCCCAAGGCCCGCCGCGCACAGAGA 170  
Db CTCGGCGGGACAGCGTGAGGGGGGGGGCATGCGCGCGGCTTCCTTCGAGAGCGCGGGCAG 679  
620 CTCGGCGGGACAGCGTGAGGGGGGGGGCATGCGCGCGGCTTCCTTCGAGAGCGCGGGCAG 679  
171 AGTTGGCCAGAGGCACAGCGCGTAGAGCGAGCGGGCAGAGGCTTCTCAGAGAGCGCGGGCAG 230  
Db CAGCGCGCCAGAGGCCCGGGGGCGCAGCGGTGCTTCATGACGCGGGGGCGGTGGCGAGC 739  
680 CAGCGCGCCAGAGGCCCGGGGGCGCAGCGGTGCTTCATGACGCGGGGGCGGTGGCGAGC 739  
CY GCCGCGCGCTGAGAGGGGGCGCAGAGCGGGGTATAAGAGCCTCGGTGGCGCTTGCCTCGGGCAGCG 290  
CY 221 GCCGCGCGCGCTGAGAGGGGGCGCAGAGCGGGGTATAAGAGCCTCGGTGGCGCTTGCCTCGGGCAGCG 290  
Db GGCTAAACAATGTCTCGGGCAGCG 799  
CY 291 GAAGTTCCCCCG 322

DB	800	CCGGGAGCTGCCCGCCGCGCCGCCGCSC	931
RESULT 37			
ID	AAX37251		
AC	AAX37251 standard; DNA; 4045 BP.		
XX			
XX	AAX37251;		
DT	20-JUL-1999	(first entry)	
DE	Human 3-OST-4 5' promoter and exon sequence.		
KM	Heparan sulfate D-glucosaminyl 3-O-sulfotransferase; anticoagulant;		
KM	saccharide; glycosaminoglycan; proteoglycan; antithrombin; 3-Ost;		
KW	heparan sulfate; chromocytic disorder; deep vein thrombosis;		
KW	pulmonary embolism; coagulatic enzyme inactivation; ss.		
OS	Homo sapiens.		
XX			
PN	WO922005-A2.		
PD	06-MAY-1999.		
PF	23-OCT-1998; 98WO-US22597.		
PR	31-OCT-1997; 97US-0065437.		
PR	24-OCT-1997; 97US-0062762.		
PA	(MASI ) MASSACHUSETTS INST TECHNOLOGY.		
XX			
PI	Filtze LMB, Liu J, Rosenberg RD, Schwartz JJ, Shworak NW;		
PI	Zhang L;		
DR	WPI, 1999-312968/26.		
XX			
PT	Heparan sulfate D-glucosaminyl 3-O-sulfotransferase and related		
PT	polynucleotides		
PS	Claim 60; Page 93-95; 95pp; English.		
CC	The invention relates to nucleic acid molecules (AAX37245-X37250)		
CC	encoding heparan sulfate D-glucosaminyl 3-O-sulfotransferases (3-Osts).		
CC	The 3-Ost proteins can be used for 3-O-sulfating saccharide residues		
CC	within a preparation of glycosaminoglycan or proteoglycan		
CC	polyasaccharides. 3-Ost-1 can be used for enriching the		
CC	antithrombin-binding fraction in a preparation of heparan sulfates (HS).		
CC	3-Ost-1 can also convert HS proteoglycan anticoagulant precursor to the		
CC	HS anticoagulant (HSact). The 3-Osts (optionally lacking enzymatic		
CC	function) can be used to determine partial sequence information for		
CC	complex polyasaccharides. The 3-Ost proteins, genes and antibodies are		
CC	also useful for diagnosis of disorders involving HS biosynthesis. 3-Osts		
CC	are especially used to generate anticoagulant pentasaccharides, which may		
CC	be used to treat thrombotic disorders such as deep vein thrombosis and		
CC	pulmonary embolism. Coagulation enzyme inactivation by antithrombin is		
CC	enhanced by complexing of antithrombin with endothelial cell surface HS		
CC	proteoglycans. This is responsible for the non-thrombogenic properties		
CC	of blood vessels. The present sequence represents a human 3-Ost-4		
CC	5' promoter and exon sequence.		
SQ	Sequence 4045 BP; 823 A; 1150 C; 1277 G; 795 T; 0 other;		
Query Match	13.6%; Score 44; DB 20; Length 4045;		
Best Local Similarity	50.5%; Pred. No. 1.6;		
Matches 107; Conservative	0; Mismatches 105; Indels 0; Gaps 0;		
Gy	111 CTGAGGCCCGGAGGAAGGGGCAAGGGCTTCCAGAGGCCCGCGCGCAGCAGGA 170		
Db	2619 CTCGGCGGCGACGCTGGGCGCGGGCGCCTTCGGCTCCCGCTTGCGCGAGCGGA 2678		
Gy	171 AGTTGGCAGAGCACCGCCGTGACGCGAGCGGAGAGGAGGCTTTCTACAGAACGCGGGCGAG 230		
Db	2679 CAGCGGCGGAGGCGCGGCGCGCAGCGAGCTTCCTTACGACGCGGAGCGGCGCTGAGGAGC 2738		

QY 231 GCCGCGCTGAGAGGCGAGAGACCGGCTATTAAAGCCTCTGAGCCTTCCCGGACGCG 290  
 DB 2739 GCGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGAACCATATGCTCCGCGACGCG 2798  
 QY 291 GCAGCTTCCCG 322  
 DB 2799 CCGGCGCGCTGCG 2830

RESULT 39  
 ABV24463/C  
 ID ABV24463 standard; cDNA; 5134 BP.

ABV24463;

16-SEP-2002 (first entry)

Human prostate expression marker cDNA 24454.

Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
 pharmacogenomic marker; gene; ss.

Homo sapiens.

WO200160860-A2.

23-AUG-2001.

20-FEB-2001; 2001WO-US05171.

17-FEB-2000; 2000US-183319P.

16-MAR-2000; 2000US-189862P.

25-MAY-2000; 2000US-207454P.

09-JUN-2000; 2000US-211314P.

18-JUL-2000; 2000US-219007P.

13-DEC-2000; 2000US-255281P.

(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Schlegel R, Endege WO, Monahan JE;

WPI; 2001-662795/76.

Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer -

Claim 1; Page 4618-4619; 11750pp; English.

The invention relates to an isolated nucleic acid molecule (1) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (1) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;  
 (b) monitoring the progression of prostate cancer in a patient;  
 (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;  
 (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;  
 (e) selecting a composition for inhibiting prostate cancer in a patient;  
 (f) assessing the prostate cell carcinogenic potential of a compound;  
 (g) determining whether prostate cancer has metastasized in a patient;  
 (h) assessing the aggressiveness or indolence of prostate cancer in a patient;

(1) is also useful as a pharmacodynamic or pharmacogenomic marker.

Sequence 5134 BP; 1498 A; 1184 C; 1186 G; 1262 T; 4 other;

Query Match 13.6%; Score 44; DB 23; Length 5134;

Best Local Similarity 48.8%; Pred. No. 1.6;

Matches 119; Conservative 0; Mismatches 125; Indels 0; Gaps 0;

80 AGAGGCGCCGCGCTGCGCAAGAGAGTCTCGAGCGCGCGAGGAGGAGGCGGACG 139

DB 402 AGAGGCGCGCTGCGCGGAGAGCGGCGCGCGCGCTGCGCGCGGAGAGGCGCAC 343  
 QY 140 GCGTTCAGAGGCG 199  
 DB 342 GCGCTGCGCGGAGAGGCGCTCTCAGCGGCGAGCGGCAACCGGCATGCGCGCTAGGCGCG 283  
 QY 200 CCGGCGAGGCGCTTCTCAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 259  
 DB 282 GCGGAGCGCGCGCTTCTAGGAGACAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 223  
 QY 260 TAAAGAGCTGCGCGCTTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 319  
 DB 222 GCGGCTGCG 163  
 QY 320 CGCC 323  
 DB 162 AGCC 159

RESULT 39  
 AAK52977/C  
 ID AAK52977 standard; cDNA; 2834 BP.

AAK52977;

06-NOV-2001 (first entry)

Human polynucleotide SEQ ID NO 2506.

Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
 vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
 tissue growth factor; immunomodulatory; cancer; leukaemia;  
 nervous system disorder; arthritis; inflammation; ss.

Homo sapiens.

WO200157190-A2.

09-AUG-2001.

05-FEB-2001; 2001WO-US04098.

03-FEB-2000; 2000US-0496914.

27-APR-2000; 2000US-0560875.

20-JUN-2000; 2000US-0598075.

19-JUL-2000; 2000US-0620325.

01-SEP-2000; 2000US-0654936.

15-SEP-2000; 2000US-0663561.

20-OCT-2000; 2000US-0693325.

30-NOV-2000; 2000US-0728422.

(HYSE-) HYSEQ INC.

Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;  
 Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZM;  
 Xue AJ, Yang Y, Wehrman T, Goodrich R;

WPI; 2001-476283/51.

Nucleic acids encoding polypeptides with cytokine-like activities,  
 useful in diagnosis and gene therapy -

Claim 1; Page 4784; 6221pp; English.

The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating

	CC	activity; tissue growth factor activity; immunomodulatory activity and
	CC	activin/inhibin activity and may be useful in the diagnosis and/or
	CC	treatment of cancer, leukaemia, nervous system disorders, arthritis and
	CC	inflammation.
	CC	Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
	CC	(AAM80020) are omitted as the relevant pages from the sequence listing
	CC	were missing at the time of publication.
XX	SQ	Sequence 2834 BP; 540 A; 1007 C; 919 G; 368 T; 0 other;
	Query Match	13.6%; Score 43.8; DB 22; Length 2834;
	Best Local Similarity	51.0%; Pred No. 1.7; Mismatches 122; Indels 5; Gaps 1;
	Matches 132; Conservative	0; Mismatches 122; Indels 5; Gaps 1;
OY	55	GACAAAGCGGGGCTCCTCTCTCTCAAGAGGCCGCCAGGCTTGCACAAGAAATCTTCG 114
DB	1887	GACACCACCTTGAGGGGCCCCGCTCTCGTGGAGACAGGCCCTCTTGACAGCCAGAGACTCC 1828
OY	115	AGGCCGGGACAGGAAGGGGACACAGGCTTTCCACAGGGCCCAGCCAGACAGGAATT 174
DB	1827	TGCTCTCGTGGGGTAGATGTGTGCGCTTGACATGAGTGCGCGCTGTGACTGACGCC 1768
OY	175	GCGCCAGGGCACCGGCCGTGAGCGGAGCGGAGCGGCTTTCTCAGAACCGG-----GGCGA 229
DB	1767	GCGCCGCCCGCGGGGCTGGAATGGGGCGCTGCGGGGTGACTCCGCGCTCCCATGACAGA 1708
OY	230	GCGCCGCGCTTGAGAGGGCGAGACCGGGTATAAGAGCCTCGTGCTTGCCTGGGAGCG 289
DB	1707	GCGTGGGCGCATGTGCGGCGGCGCGTGGGGCGGCACTCTGGGAGTGGCTCTCTCCAGC 1648
OY	290	CGCAGATTCCCGCGCGCGCC 308
DB	1647	CGCTTCTCTCTCGCGCTGCC 1629
<hr/>		
	RESULT 40	
	AAK51993/C	
XX	ID	AAK51993 standard; cDNA; 4809 BP.
AC	AAK51993;	
XX	DT	06-NOV-2001 (first entry)
DE	Human polynucleotide SEQ ID NO 538.	
XX	Human; cytokine; cell proliferation; cell differentiation; gene therapy;	
KW	vaccine; peptide therapy; stem cell growth factor; haematopoiesis;	
KW	tissue growth factor; immunomodulatory; cancer; leukaemia;	
KW	nervous system disorder; arthritis; inflammation; ss.	
XX	Homo sapiens.	
OS		
XX	WO200157190-A2.	
PN	09-AUG-2001.	
PD		
PF	05-FEB-2001; 2001MO-US04098.	
XX		
PR	03-FEB-2000; 2000US-0496914.	
PR	27-APR-2000; 2000US-0560875.	
PR	20-JUN-2000; 2000US-0598075.	
PR	19-JUL-2000; 2000US-0620325.	
PR	01-SEP-2000; 2000US-0624932.	
PR	15-SEP-2000; 2000US-0623561.	
PR	20-OCT-2000; 2000US-0693325.	
PR	30-NOV-2000; 2000US-0728422.	
XX		
PA	(HISE-) HISEQ INC.	
XX		
F1	Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y,	
PI	Zhao QJ, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW,	
PI	Xue AJ, Yang Y, Wejberman T, Goodrich R,	
XX		

DR	WPI; 2001-476283/51.
DR	P-PsDB; AAM78860.
XX	
PT	Nucleic acids encoding polypeptides with cytokine-like activities,
XX	useful in diagnosis and gene therapy -
PS	
XX	Claim 1; Page 1939-1944; 6221pp; English.
CC	The invention relates to polynucleotides (AAK51456-AAK51435) and the
CC	encoded polypeptides (AAM78732-AAM80020) that exhibit activity elating to
CC	cytokine cell proliferation or cell differentiation or which may induce
CC	production of other cytokines in other cell populations. The
CC	polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC	peptide therapy. The polypeptides have various cytokine-like activities,
CC	e.g. stem cell growth factor activity, haematopoiesis regulating
CC	activity, tissue growth factor activity, immunomodulatory activity and
CC	activin/inhibin activity and may be useful in the diagnosis and/or
CC	treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC	inflammation.
CC	Note: Records for SEQ ID NO 2110 (AAKS2581), 2111 (AAKS2582) and 3666
CC	(AAM80020) are omitted as the relevant pages from the sequence listing
CC	were missing at the time of publication.
XX	
XX	
SO	Sequence 4809 BP; 955 A; 1595 C; 1467 G; 792 T; 0 other;
	Query Match            13.6%; Score 43.8; DB 22; Length 4809;
	Best Local Similarity    51.0%; Pred. No. 1.7;
	Matches 132; Conservative 0; Mismatches 122; Indels 5; Gaps 1.
OY	55 GACAAAGGCCGGGCGTGCCTCTCTCAGAGGGCCCCAGCGGCTGCAAGAAGMAGTCCTCG 114 
Db	1938 GACAACAGACTTGAGAGGCCCGCTGTGCGTAGGAACAAGCCCTCTGTGACAGCGACGAGAGCTCC 1872 
OY	115 AGGCGCGGGGAGAGGAAGGGGGGACAGGGCTTCCAGAGGGCGCGCGGCGCACAGGAATTT 174 
Db	1878 TGCTTCGTGGGGTAGTAGTGTGGCGCGCTTGACATGACGTGCCGTGCTGTGGACGCC 1815 
OY	175 GGCCAGGCGACAGCGCGCTGAGAGGGAGCGGACAGGCTTCTCTAGAGACGCG-----GGGA 229 
Db	1818 GCCGCCGCCCGGCGCTGAGATGGGGCGCTGGCGGGTATCTCGGCTGCCCATAGACGAGA 1755 
OY	230 GGCCTGGCGCTTGAAGAGGCGAGAGACGGGTATTAAAGCTCTGTGCGCTTGGCGGGAGCG 289 
Db	1758 GAGCTGGGCGCAAGTGGGGGGCGGCGCGCTGGAGCGGACAGTCTCTGGGAGGAGCTCTCTCCAGC 1693 
OY	290 CGCAGATTCCCAGCGCGCC 308 
Db	1698 GCCTCTCTCTCGGCGTGGC 1680 

Search completed: November 6, 2003, 07:07:42  
Job time : 242.409 secs

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PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 24.1%; Score 78; DB 4; Length 570;  
Best Local Similarity 100.0%; Pred. No. 9e-03; 0; Indels 0; Gaps 0;  
Matches 78; Conservative 0; Mismatches 0

QY 246 GCGAGACCGGCTATTAAGAGCTCTGCTGCTTCCCGGCGACCCGAGTTCCCGCGC 305  
DB 1 GCGAGACCGGCTATTAAGAGCTCTGCTGCTTCCCGGCGACCCGAGTTCCCGCGC 60

QY 306 GCCCGGAGCCCGCGCGC 323  
DB 61 GCCCGGAGCCCGCGCGC 78

## RESULT 2

US-08-586-165-8/c  
Sequence 8, Application US/08586165  
Patent No. 6054298

## GENERAL INFORMATION:

APPLICANT: Laufer, Edward M.  
APPLICANT: Orozco, Olivia E.  
APPLICANT: Tabin, Clifford J.  
TITLE OF INVENTION: F-inge Proteins and Pattern Formation  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: US  
ZIP: 02173

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/586,165  
FILING DATE: 16-JAN-1996

## CLASSIFICATION: 800

## ATTORNEY/AGENT INFORMATION:

NAME: Granahan, Patricia

REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: HU95-05

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 861-9540

TELEFAX: (617) 861-9540

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 3937 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-08-586-165-8

Query Match 14.1%; Score 45.4; DB 3; Length 3937;  
Best Local Similarity 51.4%; Pred. No. 0.095; 121; Indels 2; Gaps 1;  
Matches 130; Conservative 0; Mismatches 121

QY 63 CCGGCTGCTCTCTCAAGAGGCGCCCAAGGCTCTCAAGAGGCTCTCAAGGCGCG 122  
DB 371 CCGGCTGCTCTCTCAAGAGGCGCCCGCGCTCTCAAGAGGCTCTCAAGGCGCG 312  
QY 123 GCAG-GGAAGGGGCGACCGGCTTCCAGGCGCCCGCGCGACGAGAGTTGGCCAG 180  
DB 311 GCGGCG 252

QY 181 GGCACGGCCCTGTAGCGGAGCGGCGGAGGCTTCTCAGAGCGCGCGGCGCGCTG 240  
DB 251 GAGAAGCGCGCGCGCGCGCGGAGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 192  
QY 241 GAGGGGCGAGAGCGGCTATTAAGAGCTCTGCTGCTTCCCGGCGACCCGAGTTCC 300  
DB 191 GCTGCTCATGTGCGGCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 132  
QY 301 GCGGCGCCCGAG 313  
DB 131 GCGAGCCCGCG 119

## RESULT 3

US-08-232-463-14/c  
Sequence 14, Application US/08232463  
Patent No. 5670367

## GENERAL INFORMATION:

APPLICANT: DORNER, F.

APPLICANT: SCHIEFLINGER, F.

APPLICANT: FALKNER, F. G.

TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 1800 Diagonal Road, Suite 500

CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: 22313-0299

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,463  
FILING DATE: 26-AUG-1991

## CLASSIFICATION: 435

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/935,313

FILING DATE: 26-AUG-1991

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 30472/114 IMMU

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-9300

TELEFAX: (703) 683-4109

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 7218 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

CLONE: PTZ9pt-F18

US-08-232-463-14

Query Match 13.5%; Score 43.6; DB 1; Length 7218;  
Best Local Similarity 4.5%; Pred. No. 0.24; 111; Indels 0; Gaps 0;  
Matches 13; Conservative 162; Mismatches 111

QY 7 GGGGTGACGCGGAG 66  
DB 1327 GGGGTGACGCGGAG 1268  
QY 67 GCTGCTCTCTCAAGAGGCGCCCGCGCGCTTCCCAAGAGAGAGAGAGAGAGAG 126

[illegible]

RESULT 4  
 US-08-572-951-1/c  
 Sequence 1, Application US/08572951  
 Patent No. 5824790  
 GENERAL INFORMATION:  
 APPLICANT: KEELING, PETER L.  
 APPLICANT: KNIGHT, MARY E.  
 APPLICANT: GUAN, HANPING  
 TITLE OF INVENTION: MODIFICATION OF STARCH  
 TITLE OF INVENTION: SYNTHESIS IN PLANTS  
 NUMBER OF SEQUENCES: 41  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: CUSHMAN DABRY & CUSHMAN  
 ADDRESSEE: Intellectual Property Group of  
 ADDRESSEE: Pillsbury Madison & Sutro LLP  
 STREET: 1100 New York Avenue, N.W.  
 CITY: Washington  
 STATE: DC  
 COUNTRY: USA  
 ZIP: 20005-3918  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy/disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/572,951  
 FILING DATE: 15-DEC-1995  
 CLASSIFICATION: 800  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/346,602  
 FILING DATE: 29-NOV-1994  
 CLASSIFICATION: 800  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/263,921  
 FILING DATE: 21-JUN-1994  
 CLASSIFICATION: 800  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Paul N. Kokulise  
 REGISTRATION NUMBER: 16,773  
 REFERENCE/DOCKET NUMBER: 222957/1.02.15C  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 861-3000  
 TELEFAX: (202) 822-0944  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2990 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: both  
 TOPOLOGY: linear  
 MOLECULE TYPE: CDNA  
 US-08-572-951-1

Query Match	13.4%	Score 43.4	DB 1	Length 2990
Best Local Similarity	49.3%	Pred. No. 0.25		
Matches 113	Conservative 0	Mismatches 110	Indels 0	Gaps 0

Position	Sequence	Position	Sequence
Db	CGCGGGCGCAGGAAGCCCGGCA	813	CGCGGGCGCAGGAGCCCGCCAGCAGCGCGTGGCAGCGGGCG
Qy	GGCCCCAGCGCTTGC	84	GGCCCCAGCGCTTGC
Db	CGCGGGGGCCCTCTCTCAGTTCG	753	CGCGGGGGCCCTCTCTCAGTTCG
Qy	TCCAGGACCGCGGCGCAGCAGGAATTGGCAGGCGCA	144	TCCAGGACCGCGGCGCAGCAGGAATTGGCAGGCGCA
Db	CTTCGCGGGCGCGCCGCTCGCAGCGCGGCGCGCAGGCGCGCGCGCAGGAGG	693	CTTCGCGGGCGCGCCGCTCGCAGCGCGGCGCGCAGGCGCGCGCGCAGGAGG
Qy	CAGGCGCTTCTCAGAGCGCGGCGAGCGCGCGCTGAGGGGGAGGA	204	CAGGCGCTTCTCAGAGCGCGGCGAGCGCGCGCGCTGAGGGGGAGGA
Db	CAGCGGCGCCACCGCCGAGGCGCTCGCATTTGGAGAGGAGAGCA	633	CAGCGGCGCCACCGCCGAGGCGCTCGCATTTGGAGAGGAGAGCA

```

RESULT 5
US-09-128-155-16/C
Sequence 16, Application US/09128155
Patent No. 6117654
GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128, 155
EARLIER FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PasteSeq for Windows Version 3.0
SEQ ID NO 16
LENGTH: 152331
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(152331)
OTHER INFORMATION: n = A,T,C or G
US-09-128-155-16

```

[illegible]

RESULT 6  
US-08-031-538-10/c  
; Sequence 10, Application US/08031538  
; Patent No. 5968817  
; GENERAL INFORMATION:

```

APPLICANT: Sutcliffe, J Gregor
APPLICANT: Exlander, Mark G
APPLICANT: Lovenberg, Timothy W
TITLE OF INVENTION: HUMAN SEROTONIN RECEPTORS, DNA ENCODING
TITLE OF INVENTION: THE RECEPTORS, AND USES THEREOF
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESSES:
ADDRESSES: The Scripps Research Institute, Office of
ADDRESSES: Patent Counsel
STREET: 10666 No. 5968817th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/031,538
FILING DATE: 19930315
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSP5099P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 2040 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-031-538-10

Query Match 12.8%; Score 41.4; DB 2; Length 2040;
Best Local Similarity 49.8%; Pred. No. 0.67; Indels 0; Gaps 0;
Matches 105; Conservative 0; Mismatches 106;

QY 28 GGTGCGGGCCGCGGGTGGGCTTCGCGAGAACAAAGCCGGGCTTCTCTCAGAGGGCC 87
DB 566 GGGGCTGGCCACTGCGGGGGCGCCGCGCTCGGCTCGGAGCCCGCAGGTCCAGAGGTCCC 507
QY 88 CCAAGCGCTGCGCAAGAGAGTCTTCGAGGCCCGGCGAGGAGAGGGGCAACGGGCTTCCC 147
DB 506 CCAAGCTCTGCGATGACGCGTGGGCGAGACTCCCGCGGAGGAGGACCAAGCGGTCCC 447
QY 148 AGGGCCCGCGCGCGCGAGAGATTGGCCAGGGCAAGCGCGCTGAGCGAGCGGGCAGG 207
DB 446 ACGGCGACGAGAGAGAGAGAGGAGGAGGAGCGAGCCGAGCTGGCGGCTTGGCCAGCCG 387
QY 208 GCTTTCTCAGAGCGCGCGCGAGCGCGCGCGC 238
DB 386 CCGCGACGATGCCCGCGCGCGCGGAGC 356

RESULT 7
US-09-602-877A-78/c
Sequence 78, Application US/09602877A
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Xu, Jianshun
APPLICANT: Dillon, David C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.446CS

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CURRENT APPLICATION NUMBER: US/09/602,877A
CURRENT FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 107
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 78
LENGTH: 1574
TYPE: DNA
ORGANISM: Homo sapiens
US-09-602-877A-78.

Query Match 12.5%; Score 40.4; DB 4; Length 1574;
Best Local Similarity 45.8%; Pred. No. 1.1;
Matches 140; Conservative 0; Mismatches 166; Indels 0; Gaps 0;

QY 17 GCGAAGGAGAGGTGCGGGCGCGGGGTGGGCTTCGCGGAGCAAGAGCCGGGCTGCTCT 76
DB 351 CCGACCGGCTGGGCGAGACCCGAGACCGAGAGTTGAAGAGTGAAGCGCCGCGCGCC 292
QY 77 CTCAGAGGCGCCGAGCGGCTGCGCAAGAGAGTCTCTGAGGCCCGGCGAGGAGGGGCG 136
DB 291 TCGTCAGAGAGCTGCGCGGAGACCCAGCATCTGAGGCTGCCAGGGTCTGCGGGTCC 232
QY 137 ACGGCTTCCAGGGCCCGCGCGCGCGCGAGCAAGATTGCGCAAGGCAACGCGCTGAGCG 196
DB 231 CCGAACCCCGCGGGCGCGCACCGGGCGAGCAACAGAGAGCGCAGACCGCGGCG 172
QY 197 GAGCGGAGAGGCTTCTCAGAGAGCGGCGAGGCGCGCGCTGAGGGCGAGAGACCGG 256
DB 171 GTGGGGCGGGGCGCCCTGGGCGCGGACAGAGGAGCGGACCGCTTGGCGGGGCTGC 112
QY 257 GTATAGAGAGCTCTGCGCTTGGCCCGGCGAGCGCGAGATTCCCGCGCGCCGAGGCC 316
DB 111 ATGAGCGCAGAGAAAGTTGGCTCGGACCCGACCGAGACAGACAGGAGCTCGAGCGGAGTGGC 52
QY 317 CCGCGC 322
DB 51 GCGCTC 46

RESULT 8
US-08-836-329-1/c
Sequence 1, Application US/08836329
Patent No. 6090546
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Method for the Detection of Ras Oncogenes,
TITLE OF INVENTION: In Particular the K-Ras Oncogene
NUMBER OF SEQUENCES: 16
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,329
FILING DATE:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3918 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: exon
LOCATION: 825..947
NAME/KEY: exon
LOCATION: 1388..1567
FEATURE:
NAME/KEY: exon

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QY	168	GGAA	GTGG	CGCAG	GGCAG	CGGCGG	CGCTTT	CTCAG	AGAC	CGCGGC	227
Db	12511	GTCCG	GAAG	CTAT	CAAC	CGCGCC	CGAC	CGCGGT	GTGTGG	CGTCC	CGAAC
QY	228	GAGC	CGCG	CGCT	GTGA	GGGG	GAA	AGAC	CGCGT	ATTAA	AACT
Db	12451	GCGG	GTCT	CAAC	CGCGGT	GTCTGG	CGCG	CGCGAG	CGTCC	AGC	AGTAC
QY	288	GCGC	AGGT	TCCC	CGCG	CGCGCC	CGAG	CCCC	CGCG	321	
Db	12391	GGA	GTAC	GTG	GG	CA	GGT	CA	CGCG	GTG	CGCCCG
<p>RESULT 12  US-09-320-878-19/c  Sequence 19, Application US/09320878A  Patent No. 6117659  GENERAL INFORMATION:  APPLICANT: ASHLEY, Gary  APPLICANT: BETLACH, Melanie C.  APPLICANT: BETLACH, Mary C.  APPLICANT: MCDANIEL, Robert  APPLICANT: TANO, Li  TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE  FILE REFERENCE: 300622002120  CURRENT APPLICATION NUMBER: US/09/320,878A  CURRENT FILING DATE: 1999-05-27  EARLIER APPLICATION NUMBER: CIP OF 09/141,908  EARLIER FILING DATE: 1998-08-28  EARLIER APPLICATION NUMBER: CIP OF 09/073,538  EARLIER FILING DATE: 1998-05-06  EARLIER APPLICATION NUMBER: CIP OF 08/846,247  EARLIER FILING DATE: 1997-04-30  EARLIER APPLICATION NUMBER: 60/119,139  EARLIER FILING DATE: 1998-02-08  EARLIER APPLICATION NUMBER: 60/100,880  EARLIER FILING DATE: 1998-09-22  EARLIER APPLICATION NUMBER: 60/087,080  EARLIER FILING DATE: 1998-05-28  NUMBER OF SEQ ID NOS: 34  SOFTWARE: PatentIn Ver. 2.0  SEQ ID NO 19  LENGTH: 38506  TYPE: DNA  ORGANISM: Streptomyces venezuelae  US-09-320-878-19</p>											
QY	108	GTCT	CTCG	AGCG	CGCG	CGAG	GGA	AGGG	GCAC	AGG	CTT
Db	10713	GTCC	CGCG	AGCC	CGG	GTGG	GTGCC	CA	GGAG	AGG	CGCG
QY	168	GGA	AGTT	GGC	AGG	GCAC	AGCG	CGCT	GTG	AGC	CGG
Db	10653	GTCC	GGAA	GGCT	GTG	AC	AGCG	CGCG	AG	GGG	GTG
QY	228	GAG	CGCG	CGCG	GTGA	GGGG	GCAG	AGCG	GGAT	TA	AA
Db	10533	GAG	CGT	CTCA	CCCG	GTGT	GGCG	CGCG	CGCT	CTCA	AG
QY	288	GCG	CA	GGT	TCCC	CGCG	CGCGCC	CGAC	CCCC	CGCG	321
Db	10533	GGA	GTAC	GTG	GG	CA	GGT	CA	CGCG	GTG	CGCCCG
<p>Query Match 12.3%, Score 39.6; DB 3; Length 38506;  Best Local Similarity 49.1%; Pred. No. 1.8;  Matches 105; Conservative 0; Mismatches 109; Indels 0; Gaps 0;</p>											

GENERAL INFORMATION:  
APPLICANT: ASHLEY, Gary  
APPLICANT: BETLACH, Melanie C.  
APPLICANT: BETLACH, Mary  
APPLICANT: MCDANIEL, Robert  
APPLICANT: TANG, Li  
TITLE OF INVENTION: Combinatorial Polyketide Libraries Produced Using a  
FILE REFERENCE: 300622002100  
CURRENT APPLICATION NUMBER: US/09/141,908  
CURRENT FILING DATE: 1998-08-28  
EARLIER APPLICATION NUMBER: CIP OF 09/073,538  
EARLIER FILING DATE: 1998-05-06  
EARLIER APPLICATION NUMBER: CIP OF 08/846,247  
EARLIER FILING DATE: 1997-04-30  
EARLIER APPLICATION NUMBER: PROV. 60/076,919  
EARLIER FILING DATE: 1998-03-05  
EARLIER APPLICATION NUMBER: PROV. 60/087,080  
NUMBER OF SEQ ID NOS: 31  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 38506  
TYPE: DNA  
ORGANISM: Streptomyces venezuelae

Query Match 12.3%; Score 39.6; DB 4; Length 38506;  
Best Local Similarity 49.1%; Pred. No. 1,8;  
Matches 105; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

Db 108 GTCTCGAGGCGCGGCGAGGAGGAGGCGCAGCGGCTTCCACAGGCGCCGCGCGCAGCA 167  
10713 GTCCGCGAGCCAGCGGGTGCGTGCAGGAGAGGCGCGCGGCGTACGACGAGCGCCGCCG 10554

QY 168 GGAAGTTGGCCAGGCGCAGCGCGCGTGAAGCGAGCGGCGCAGGCGCTTCTCAGAGCGCGCGCC 227  
Db 10653 GTCCGAGAGCTACACACCGCGCGCCGACAGCAGCGGCTGTGCGGCGTCCGAGACCGAGGCC 10594

QY 228 GAGCGCGCGCGCTGAGGAGCGGAGAGACCGGTTAATAAGACCTTCGTCGCGCGCGCA 287  
Db 10593 GCGCGTCTCACCGCGGTCGCGCGCGCGCGCGCTCCAGCAGTACGCGTCCGCGCGGA 10534

QY 288 GCGGACGTTCCCG 321  
Db 10533 GGAGTACGTGGCGCAGGTCCACGCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 10500

RESULT 14  
US-09-657-440-19/c  
; Sequence 19, Application US/09657440  
; Patent No. 6509455  
; GENERAL INFORMATION:  
APPLICANT: ASHLEY, Gary  
APPLICANT: BETLACH, Melanie C.  
APPLICANT: BETLACH, Mary C.  
APPLICANT: MCDANIEL, Robert  
APPLICANT: TANG, Li  
TITLE OF INVENTION: RECOMBINANT NARONOLIDE POLYKETIDE SYNTHASE  
FILE REFERENCE: 300622002120  
CURRENT APPLICATION NUMBER: US/09/657,440  
CURRENT FILING DATE: 2000-09-07  
PRIOR APPLICATION NUMBER: 09/320,878  
PRIOR FILING DATE: 1999-05-27  
PRIOR APPLICATION NUMBER: CIP OF 09/141,908  
PRIOR FILING DATE: 1998-08-28  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 19  
LENGTH: 38506  
TYPE: DNA  
ORGANISM: Streptomyces venezuelae  
US-09-657-440-19

Query Match	12.3%	Score 39.6	DB 4	Length 38506
Best Local Similarity	49.1%	Pred. No. 1.8		
Matches	105	Conservative	0	Mismatches 109; Indels 0; Gaps 0;
QY	108	GTCCTCAGAGCCCGGCGAGGAGAGGAGCCAGGCTTCCAGAGGCCCGCGCGGAGCA	167	
Db	10713	GTCGCGCGAGCCAGGCTGGGTGGCCAGGAGAGGCGCGCCGATGACAGCGCGCTGCCG	10654	
QY	168	GGAAGTTGGCCAGGAGCACGGCTGTGAGGGAGCGGAGGAGGCTTCTCAGAGACGGGGC	227	
Db	10653	GTCGCGAAGCTTGACACAGCGCGCCGAGCAGCGGTGTCCGCGTGCAGACCGAGGCC	10594	
QY	228	GAGGCGGCGGCTGTGAGGGGCGAGGACCGGGTATTAGAGGCTTCGTGGCTTTGCCCGAGCA	287	
Db	10593	GGCAGTGTCCACCCCGGTGTCTGCGCGCGCCGCGGCGCTCCAGCGCATGAGGTGTGCGCGGAA	10534	
QY	288	GCCGAGGTTCCCGCGCGGCCCCGAGGCCCGCGG	321	
Db	10533	GGAATACGTGGGCGAGCTTCACGCGGTGGCCCCG	10500	

RESULT 15  
 US-08-912-951-e/c  
 : Sequence 6, Application US/08912951  
 : Patent No. 6475789  
 : GENERAL INFORMATION:  
 : APPLICANT: Cech, Thomas R.  
 : APPLICANT: Lingner, Joachim  
 : APPLICANT: Nakamura, Toru  
 : APPLICANT: Chapman, Karen B.  
 : APPLICANT: Morin, Gregg B.  
 : APPLICANT: Harley, Calvin H.  
 : TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT.  
 : TITLE OF INVENTION: THERAPEUTIC METHODS  
 : NUMBER OF SEQUENCES: 335  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Townsend, and Townsend and Crew LLP  
 : STREET: Two Embarcadero Center, 8th Floor  
 : CITY: San Francisco  
 : STATE: California  
 : COUNTRY: United States of America  
 : ZIP: 94111  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: Patentin Release #1.0, Version #1.30  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/912,951  
 : FILING DATE: 14-AUG-1997  
 : CLASSIFICATION: 435  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 08/854,050  
 : FILING DATE: 09-MAY-1997  
 : CLASSIFICATION: 435  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 08/851,843  
 : FILING DATE: 06-MAY-1997  
 : CLASSIFICATION: 435  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 08/846,017  
 : FILING DATE: 25-APR-1997  
 : CLASSIFICATION: 435  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 08/844,419  
 : FILING DATE: 18-APR-1997  
 : CLASSIFICATION: 435  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 08/724,643  
 : FILING DATE: 01-OCT-1996  
 : CLASSIFICATION: 435

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?      ATTORNEY/AGENT INFORMATION:
?
?      NAME: Apple, Randolph T.
?      REGISTRATION NUMBER: 36,429
?      REFERENCE/DOCKET NUMBER: 015389-002600US
?      TELECOMMUNICATION INFORMATION:
?
?      TELEPHONE: (415) 576-0200
?      TELEFAX: (415) 576-0300
?      INFORMATION FOR SEO ID NO: 6:
?
?      SEQUENCE CHARACTERISTICS:
?
?      LENGTH: 4200 base pairs
?      TYPE: nucleic acid
?      STRANDEDNESS: single
?      TOPOLOGY: linear
?
?      MOLECULE TYPE: DNA (genomic)
?
?      US-08-912-951-6

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Query Match	12.0%;	Score 38.8;	DB 4;	Length 4200;
Best Local Similarity	48.0%;	Pred. No. 2.5;		
Matches 142; Conservative	0;	Mismatches 152;	Indels 2;	Gaps 1;

Oy	1	GC	GTG	GGG	GGT	CA	CAC	CG	CAA	AGG	AAG	TGT	CG	GGC	CG	GGG	AG	CA	AA	60											
Db	2430	GC	AC	CAC	CG	CG	CAC	CC	CT	CG	GGG	CC	CC	CA	GGC	CG	CA	CGA	AG	TC	GC	CG	CAC	ACT	2377						
Oy	61	GG	CC	GG	GC	CT	CT	CT	CA	GA	GGG	CC	CC	CA	GC	CT	TC	CA	AG	AA	GT	CT	CG	AG	GC	120					
Db	2370	CG	CG	TAG	TG	TG	CT	CG	CA	GAG	CG	CA	CG	CT	CG	CA	CG	GGG	AG	CG	CG	CG	CAT	CG	2311						
Oy	121	GG	CA	GG	AA	AG	GG	GG	CA	CG	GG	CT	CC	CA	-	GG	GC	CG	CG	CG	CG	CA	CG	AA	GT	TG	GC	178			
Db	2310	CG	GG	GG	GT	GG	CC	CG	GG	CC	CA	GG	CT	CC	CA	CG	TG	CG	CA	GAG	CA	CG	CA	GG	CG	CT	GC	CT	GA	AA	2251
Oy	179	AG	GG	CA	CG	CC	GT	TAG	CG	GA	CG	GG	CA	GG	CT	TT	CT	CA	GA	G	CG	CG	CG	CA	GG	CG	CG	CG	CG	238	
Db	2250	TC	CG	CG	CG	CA	AG	GA	GAG	CG	GG	CG	CG	CG	CG	CG	GA	AA	AG	GA	GG	GA	GG	GG	CT	GG	GA	GG	GG	CG	2191
Oy	239	TG	GA	GG	GG	CG	CA	GG	CA	CG	GG	GT	T	A	AA	GA	AG	CT	CG	TG	CG	CT	TG	CC	CG	CG	CA	GG	CG	CG	294
Db	2190	GG	AA	GG	GG	CT	GG	CG	CG	GA	CT	GT	GG	AA	AG	GT	TT	CG	GA	AC	GG	GG	CG	GG	GT	CG	CG	CG	CG	CG	2135

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RESULT 16
US-09-105-537-32/c
: Sequence 32, Application US/09105537A
: Patent No. 6255202
: GENERAL INFORMATION:
: APPLICANT: Sherman, D. H.
: APPLICANT: Liu, H.
: APPLICANT: Xue, Y.
: APPLICANT: Zhao, L.
: TITLE OF INVENTION: DNA encoding methymycin and pikromycin
: FILE REFERENCES: 600,438US1
: CURRENT APPLICATION NUMBER: US/09/105,537A
: CURRENT FILING DATE: 1998-06-26
: NUMBER OF SEQ ID NOS: 43
: SOFTWARE: Paetted for Windows Version 3.0
: SEQ ID NO 32
: LENGTH: 11220
: TYPE: DNA
: ORGANISM: Streptomyces venezuelae
: US-09-105-537-32

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	Query March Best Local Similarity Matches 109; Conservative	12.0%; Score 38.8; DB 3; 48.2%; Pred. No. 2.6; 0; Mismatches 117; Indels 0; Gaps 0;
QY	32 CGGCGCCGGGGTGGGCTTCGCGAGACCAAGGCGCGGCTTCCTTCAGAGGCGCCCGAC	91
Db	7453 CGACCTGGTCTCCCGCGCTCGGAGCGCAGCTTCACAGAGCGCTGTTCCGGAGCGACGCG	7394
QY	92 CGCCTTGCAGAGAGAACTCTCAGAGGCCCGGCGACGAGAAAGGGGACACGGGCTTCCCGAGG	151
Db	7393 TGGCCGGCACACGGGTGTCTCGCCAGCCACGAGGTGCTCAGAGAGGAAGAGCTCCCTCGTA	7334

QY 152 CCCGCGCGCGGAGAGAGAAATTGGCCAGAGGACCGCCCTGAGCGAGCGCGGAGGCTT 211  
DB 7333 GCAGGCGAGCGCTGAGGATCCGCGAGCGCCAGCGCGCGCTGCGGCTCGGCGG 7274  
QY 212 TCTCAGGAGCGCGGCGGAGCGCGCTGAGGAGGCGGAGACCGG 257  
DB 7273 CCCCAGAGACGCGCGGAGGATGATGTCACCGCGCGGAGAGGATCGGG 7228

RESULT 17  
PCT-US91-06532-1/C  
Sequence 1, Application PC/TUS9106532  
GENERAL INFORMATION:  
APPLICANT: Kozlman, Bernard  
TITLE OF INVENTION: Recombinant Herpes Simplex Viruses  
TITLE OF INVENTION: Vaccines and Methods  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
STREET: Two First National Plaza Suite 2100  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US91/06532  
FILING DATE: 19910910  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Gruber, Lewis S.  
REGISTRATION NUMBER: 30,060  
REFERENCE/DOCKET NUMBER: 27373/8235  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/346-5750  
TELEFAX: 312/984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1335 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
PCT-US91-06532-1

Query Match 12.0%; Score 38.6; DB 5; Length 1335;  
Best Local Similarity 48.1%; Pred. No. 2.6;  
Matches 139; Conservative 0; Mismatches 149; Indels 1; Gaps 1;

QY 4 CGTGGGCTCAACCGCAAGAGGAGGCGCGGCGGCTGCGCGGAGCAAAAGC 63  
DB 660 CGCGGGGTGTCGGGGGTGCGGGGGTTCGCGGGGGTTCGCGGGGGCTCCGG 601  
QY 64 CGGCGCTGCTCTCTCAAGAGGCGCCCAAGCGCTGCGCAAGAGAGTCTGAGCGCCGG 123  
DB 600 CGCCCTCTCCCGCGCGCTGCGAGGCGCGGCGCAAGGTCTCTCGGGTGAACGG 541  
QY 124 CAGGAAAGGAGGACCGGCTTCCAGGCGCCCGCGCGGCGAGAGAAATTGCGAGCG 183  
DB 540 CAGCGGAGGAGCGAGCGCGCGGAGGCGGAGAGGAGGAGGAGGAGGAGGAGGAGG 481  
QY 184 ACGGCGGTGAGCGAGCGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 242  
DB 480 AGCCCGG 421  
QY 243 GGGGCGAGGACGGGATATAGAGACCTTCGCGCTTCCCGGAGCGCG 291

DB 420 GGGCGGGGCTCTGCGCGCGCGCTTCGCGGGGAGGAGCTTCCGCGCAATCG 372

RESULT 18  
US-08-398-008A-1  
Sequence 1, Application US/08398008A  
Patent No. 5665588  
GENERAL INFORMATION:  
APPLICANT: Kornbluth, Jacki  
TITLE OF INVENTION: DNA Encoding Natural Killer Lytic Associated  
TITLE OF INVENTION: Protein  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Gilbreth & Adler, P.C.  
STREET: 8011 Candle Lane  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage  
COMPUTER: MACINTOSH Plus  
OPERATING SYSTEM: Macintosh  
SOFTWARE: Microsoft Word 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/398,008A  
FILING DATE: March 2, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/126,501  
FILING DATE: 24-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Adler, Dr. Benjamin Aaron  
REGISTRATION NUMBER: 35,423  
REFERENCE/DOCKET NUMBER: D5705CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (713) 777-2321  
TELEFAX: (713) 777-6908  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2823 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double-stranded  
TOPOLOGY: unknown  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: no  
AMBI-SENSE: no  
US-08-398-008A-1

Query Match 12.0%; Score 38.6; DB 1; Length 2823;  
Best Local Similarity 47.8%; Pred. No. 2.7; Indels 1; Gaps 1;  
Matches 142; Conservative 0; Mismatches 154;

QY 28 GGTGGGGCGCGGGGCTCTGCGGAGCAAAAGCGCGGCTCTCTCTCAAGAGGCG 87  
DB 335 GGGCCAAAGCGGAGGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 394  
QY 88 CCAGGCGCTGCGCAAGAGAGATCTCAAGGCGCGCGCGCGCGCGCGCGCGCGCGCTTCC 147  
DB 395 CTGCG 454  
QY 148 AGGCG 207  
DB 455 AGGCGGAGCG 514  
QY 208 GCTTCTCAAGAGCG 266  
DB 515 GCGGTGCG 574  
QY 267 CCTGTGCGCTTTCG 323





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NAME/KEY: exon
LOCATION: 22465..22537
OTHER INFORMATION: /function="non-translated"
OTHER INFORMATION: /gene="ACHE"
OTHER INFORMATION: /number= 1
FEATURE:
NAME/KEY: exon
LOCATION: 24090..25177
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /function="(translation start:
OTHER INFORMATION: 24110)"
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene="ACHE"
OTHER INFORMATION: /number= 2
FEATURE:
NAME/KEY: exon
LOCATION: 25524..26009
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene="ACHE"
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FEATURE:
NAME/KEY: exon
LOCATION: 27005..27274
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FEATURE:
NAME/KEY: exon
LOCATION: 27255..28007
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FEATURE:
NAME/KEY: terminator
LOCATION: 27385..27387
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LOCATION: complement (34528..34895)
OTHER INFORMATION: /function="arsenite resistance
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LOCATION: complement (33493..33591)
OTHER INFORMATION: /gene="AR"
OTHER INFORMATION: /number= 4
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OTHER INFORMATION: /gene="AR"
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LOCATION: complement (32959..33094)
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NAME/KEY: exon
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LOCATION: complement (30470..30626)
OTHER INFORMATION: /gene="AR"
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NAME/KEY: exon
LOCATION: complement (30187..30274)
OTHER INFORMATION: /gene="AR"
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NAME/KEY: exon
LOCATION: complement (29945..30073)
OTHER INFORMATION: /gene="AR"
OTHER INFORMATION: /number= 15
FEATURE:
NAME/KEY: exon
LOCATION: complement (29664..29856)
OTHER INFORMATION: /gene="ARS"
OTHER INFORMATION: /number= 16
US-08-814-095-7
Query Match 11.9%; Score 38.4; DB 3; length 35060;
Best Local Similarity 47.7%; Pred. No. 3.2;
Matches 143; Conservative 0; Mismatches 156; Indels 1; Gaps 1;
QY 23 GCGAAGTGGGCGGCGGCTCGCGAGACAAAGCCGGCTCTCTCAGA 82
DB 22726 GCGTGGGCGTGGTGTGTGAGGCGCGCGGGAAGATTCCGGAAGAAGTGGCGGCGAGC 22667
QY 83 GGGCCCGAGCGCTGCGCAAGAGAGTCTCGAGGCGCGGCGAGGAGGCGAGCGGC 142
DB 22666 GAGAGCGCGCGCGGCGAGGCGCGGAGAGCGGAGCGCTCCGTTAGGCGGCGCTGAGC 22607
QY 143 TTCCAGGCGCGCGCGCGCGAGAGAGTGGCCAGGCGACGCGCGTGAAGCGGCGG 202

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Db 22606 CCCCTCGGGAGCCGACAGGTGCCCCCGGACCCCGGCTTTAAGAGAGTCCCGGCGGGAGG 22547  
QY 203 GCAGGGCTTTCTAGAGAGCGGGGCGAGCGCGGCGTGAAGGGGCGAGAGACCGGGTATATA 262  
Db 22546 G-AGACTACCTAGAGCGGCGCGAGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 22488  
QY 263 GAAGCTCGTGGCTTTGCCCCGAGAGCGCGAGGTTCCCGCGCGCGCGCGCGCGCGCGCGCG 322  
Db 22487 GCCGATGTTTCCCGCGCGCAGAGGTGAGCGGACTCTGACAGCGCGCGCGCTCCGCGCGCGCGCG 22428

RESULT 22  
US-08-781-802-7  
Sequence 7, Application US/08781802  
Patent No. 5969121  
GENERAL INFORMATION:  
APPLICANT: ALLEN, Larry  
APPLICANT: AIKENS, John  
APPLICANT: FONSTEIN, Michael  
APPLICANT: VONSTEIN, Veronika  
APPLICANT: DEMIRJIAN, David  
APPLICANT: CASADABAN, Malcolm  
TITLE OF INVENTION: Stable Biocatalysts for Ester Hydrolysis  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff  
STREET: 300 S. Wacker Drive 32nd Floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/781,802  
FILING DATE: 10-JAN-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/019,580  
FILING DATE: 12-JUN-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/009,704  
FILING DATE: 11-JAN-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/001,995  
FILING DATE: 01-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Chao, Mark  
REGISTRATION NUMBER: 37,293  
REFERENCE/DOCKET NUMBER: 95,963-E  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-913-0001  
TELEFAX: 312-913-0002  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3147 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 245..1231 /note="TspA E101 sequence longest  
OTHER INFORMATION: open reading frame; other possible start codons are TTG/leu9;  
OTHER INFORMATION: TTG/leu13; TTG/leu15; GTG/val43"

FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 245..1231  
US-08-781-802-7

Query Match 11.8%; Score 38.2; DB 2; Length 3147;  
Best Local Similarity 47.8%; Pred. No. 3.3;  
Matches 141; Conservative 0; Mismatches 153; Indels 1; Gaps 1;

QY 25 GAAGTGCAGGCGCGGGGTGGGCTTCGCGAGACAAAGCGCGGCTTCCTCTCTAGAGG 84  
Db 2386 GGAGGCGCTGAGAGGAGGAGGCGCGCGCTGCGCGGAGGCGAGGCTTCAAGCG 2445  
QY 85 GCCCAGAGCGCT-GCCAAAGAGAGTCTCCAGAGCGCGGCGAGGAGGCGGACAGGCT 143  
Db 2446 GTGGCTGCGCTTCGAGAGCGGAGAAAGCGAGAGGCGCGGCTTCCTCAAGCGCGG 2505  
QY 144 TCCAGAGGCGCGCGCGCGCAGCAGAGATTGGCCAGAGGCAAGCGCTTGAAGCGAGCGG 203  
Db 2506 CATTAATCGGCGCTTCCCAAGAGCGCCCTCTTGGGCGCTTGGGCGGTTGGAGGCGG 2565  
QY 204 CAGGCTTTCTAGAGAGCGCGGCGAGCGCGCGCTGAGAGGCGAGACCGGGTATTAAG 263  
Db 2566 CGCTCTTCCAGAGAGCGCTTGGCGCGGCGAGCGGCGGCGGCGGCGGCGGCGGCGG 2625  
QY 264 AAGCTCGTGGCTTCCCGGCGAGCGGAGGTTCCCGCGCGCGCGAGCGCGG 318  
Db 2626 CCTCTTAAGGAGCTTCTTCTCTGCGCCAGAGACCGCGGAGGCGGCGCGGCGGCGG 2680

RESULT 23  
US-08-694-078-7  
Sequence 7, Application US/08694078  
Patent No. 6218163  
GENERAL INFORMATION:  
APPLICANT: ALLEN, Larry  
APPLICANT: AIKENS, John  
APPLICANT: FONSTEIN, Michael  
APPLICANT: VONSTEIN, Veronika  
APPLICANT: DEMIRJIAN, David  
APPLICANT: CASADABAN, Malcolm  
TITLE OF INVENTION: Stable Biocatalysts for Ester Hydrolysis  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff, Ltd.  
STREET: 300 S. Wacker Drive 7th Floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/694,078  
FILING DATE: 07-AUG-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/019,580  
FILING DATE: 12-JUN-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/009,704  
FILING DATE: 10-JAN-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/001,995  
FILING DATE: 07-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Chao, Mark  
REGISTRATION NUMBER: 37,293  
REFERENCE/DOCKET NUMBER: 95,963-C  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-913-0001  
TELEFAX: 312-913-0002  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3147 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 245..1231  
OTHER INFORMATION: /note="TSPA E101 sequence longest  
OTHER INFORMATION: open reading frame; other possible start codons are TTG/Leu3,  
FEATUERE: TTG/Leu13; TTG/Leu15; GTG/Val43"  
NAME/KEY: mat\_peptide  
LOCATION: 245..1231  
US-08-694-078-7

Query Match 11.8%; Score 38.2; DB 3; Length 3147;  
Best Local Similarity 47.8%; Pred. No. 3.3;  
Matches 141; Conservative 0; Mismatches 153; Indels 1; Gaps 1;

QY 25 GAAGTGCAGGCGCGGCTGGGCTCGCGAGACAAAGCGCGCTGCTCTCTCAAGG 84  
DB 2386 GAGAGCCCTGAGAGGCGGCGCGCGCTCGCGAGAGGTGAGCGGCTCAAGG 2445

QY 85 GCGCCAGCGCTT-GCCAAAGAGAAAGTCTGAGGCGCGGCGAGGAGGCGCGGCT 143  
DB 2446 GTGCTGCGCTTGAAGGCGGAGAAAGCGCGAGAGCGCGCGCTTCAAGCGCGG 2505

QY 144 TCCAGAGGCGCGCGCGCGCGCGAGAAAGTTCGAGGCGCGCGCGAGAGCGCGGCT 203  
DB 2506 CATCTACTCGGCGCTTCCCAAGAGCGCGCTCTGCGCGCTTGAAGCGCGG 2565

QY 204 CAGGCTTTCTCAGAGAGCGCGCGAGCGCGCGCTGAGAGGCGCGAGAGCGGCTAAG 263  
DB 2566 CCGCTCTTCCAGAGAGCGCGCTGCGCGCGAGCGCGCGAGCGCGGCGAGCGCG 2625

QY 264 AAGCTCTGCGCTTGGCGCGCGCGAGCGCGGTTCCCGCGCGCGCGCGCGCG 318  
DB 2626 CCGCTTAAGGCGCTTCTCTCTGCGCGCGAGAGCGCGCGAGCGCGCGCGCG 2680

RESULT 24  
US-09-058-260-7  
Sequence 7, Application US/09058260B  
Patent No. 6218167  
GENERAL INFORMATION:  
APPLICANT: Allen, Larry  
APPLICANT: Atkins, John  
APPLICANT: Fontstein, Michael  
APPLICANT: Venerjian, Veronika  
APPLICANT: Demirjian, David  
APPLICANT: Casadaban, Malcolm  
TITLE OF INVENTION: Stable Biocatalysts for Ester Hydrolysis  
FILE REFERENCE: 95-963-H  
CURRENT APPLICATION NUMBER: US/09/058, 260B  
EARLIER FILING DATE: 1999-04-10  
EARLIER APPLICATION NUMBER: 60/001, 995  
EARLIER FILING DATE: 1996-08-07  
EARLIER APPLICATION NUMBER: 60/009, 704  
EARLIER FILING DATE: 1996-01-11  
EARLIER APPLICATION NUMBER: 60/019, 580  
EARLIER FILING DATE: 1996-06-12  
EARLIER APPLICATION NUMBER: 08/694, 078  
EARLIER FILING DATE: 1996-08-08  
EARLIER APPLICATION NUMBER: 08/781, 802  
EARLIER FILING DATE: 1997-01-10  
EARLIER APPLICATION NUMBER: 08/827, 810  
EARLIER FILING DATE: 1997-04-11  
NUMBER OF SEQ ID NOS: 37

SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 7  
LENGTH: 3147  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: cloned esterase  
OTHER INFORMATION: gene from bacteria E101  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (245) .. (1231)  
US-09-058-260-7

Query Match 11.8%; Score 38.2; DB 3; Length 3147;  
Best Local Similarity 47.8%; Pred. No. 3.3;  
Matches 141; Conservative 0; Mismatches 153; Indels 1; Gaps 1;

QY 25 GAAGTGCAGGCGCGGCTGGGCTCGCGAGACAAAGCGCGCTGCTCTCTCAAGG 84  
DB 2386 GAGAGCCCTGAGAGGCGGCGCGCGCTCGCGAGAGGTGAGCGGCTCAAGG 2445

QY 85 GCGCCAGCGCTT-GCCAAAGAGAAAGTCTGAGGCGCGGCGAGGAGGCGCGGCT 143  
DB 2446 GTGCTGCGCTTGAAGGCGGAGAAAGCGCGAGAGCGCGCGCTTCAAGCGCGG 2505

QY 144 TCCAGAGGCGCGCGCGCGCGCGAGAAAGTTCGAGGCGCGCGCGAGAGCGCGGCT 203  
DB 2506 CATCTACTCGGCGCTTCCCAAGAGCGCGCTCTGCGCGCTTGAAGCGCGG 2565

QY 204 CAGGCTTTCTCAGAGAGCGCGCGAGCGCGCGCTGAGAGGCGCGAGAGCGGCTAAG 263  
DB 2566 CCGCTCTTCCAGAGAGCGCGCTGCGCGCGAGCGCGCGAGCGCGGCGAGCGCG 2625

QY 264 AAGCTCTGCGCTTGGCGCGCGCGAGCGCGGTTCCCGCGCGCGCGCGCGCG 318  
DB 2626 CCGCTTAAGGCGCTTCTCTCTGCGCGCGAGAGCGCGCGAGCGCGCGCGCG 2680

RESULT 25  
US-09-103-840A-2  
Sequence 2, Application US/09103840A  
Patent No. 6284328  
GENERAL INFORMATION:  
APPLICANT: FLEISCHMAN, Robert D.  
APPLICANT: WHITE, Owen R.  
APPLICANT: FRASER, Claire M.  
APPLICANT: VENTER, John C.  
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
FILE REFERENCE: 24366-20007.00  
CURRENT APPLICATION NUMBER: US/09/103, 840A  
CURRENT FILING DATE: 1998-06-24  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 4403765  
TYPE: DNA  
ORGANISM: Mycobacterium tuberculosis  
FEATURE:  
OTHER INFORMATION: CDC 1551  
OTHER INFORMATION: "n" bases at various positions throughout the sequence  
OTHER INFORMATION: represent a, t, c or g  
US-09-103-840A-2

Query Match 11.8%; Score 38.2; DB 3; Length 4403765;  
Best Local Similarity 49.8%; Pred. No. 4.1; Indels 8; Gaps 1;  
Matches 150; Conservative 0; Mismatches 123;

QY 4 CCGTGGGTCAAGCCGGAAGCGAAGTGCAGGCGCGGCTCGCGAGACAAAGGC 63  
DB 841343 CCGCGGGGCGGAGAGCGCGGAGCGCTCGCACTGTATGCGCGCGCGGAGC 841402

QY 64 CCGGCTGCTCTCTCAAGAGGCGCGCGCTCGCAAGAGAAAGTCTTCAAGCGCGG 123



```

; ADDRESSER: THOMAS G. PLANT 1501
; STREET: LILLY CORPORATE CENTER
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: USA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: ASCII(DOS) Text only
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/804,227C
; FILING DATE: February 21, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Plant, Thomas, G.
; REGISTRATION NUMBER: 35,784
; REFERENCE/DOCKET NUMBER: X-8231
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-276-2459
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43280 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 816..14234
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 14351..19945
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 20010..31199
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 31232..36067
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 36249..41774
; US-08-804-227C-1

Query Match 11.7%; Score 37.8; DB 2; Length 43280;
Best Local Similarity 45.7%; Pred. No. 4.4;
Matches 132; Conservative 0; Mismatches 157; Indels 0; Gaps 0;

QY 33 GGGCGGGGTGGGCTCGCGGAGAAAGCGGGGCTCTCTCAGAGGGCCGAGC 92
DB 18673 GCGCGGGACCGTGCCTGCGGAGACCAATGCGGGCGCTCGCGCGAGGGCTGCGGT 18614

QY 93 GCGTCCCAAGAGAACTCTGAGAGCCCGGCGAGGAGAGGGGGCGACGGGCTTCCCAAGGC 152
DB 18613 GCGCCCAATGATCAGAGAGGTGCGCTGAGTGCAGGCGAGCCGGCGCGCGGCGAGACGT 18554

QY 153 CGCGCGCGCGAGCAGAGATTGCGCAGGGGCAACGCGCTGTAGCGGAGCGGGCAGGCTTT 212
DB 18553 GCGCAGGGTGTAGGGAGGGGGGAGAGAGGTGCGCTGTGCGAGTGTGAGCTCTCGGGCGT 18494

QY 213 CTCAGAGACGCGGGGCGAGCGCGCGCTGTGAGAGGGGCGAGAGACCGGATATAGAGACCTTGT 272
DB 18493 GCGCCCGACGCGTGTGCGAGAGATTGTCGGGAGACGGGGGAGAGTGTGTGCTGTGAGAGAGGC 18434

QY 273 GCGCTTGGCCCGGCGAGCGCGCAGATTCCCGCGCGCGCGCGCGAGCGCCCGCGG 321
DB 18433 GAAGCACCAGGGGTGCTGTGAGTGTGCGCGCGCGAGCAAGTCCCGCAGCG 18385

RESULT 29
US-08-965-048-5/c
; Sequence 5, Application US/08965048
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; Patent No. 6323244
; GENERAL INFORMATION:
; APPLICANT: Chen, Hong
; APPLICANT: Freilmer, Nelson
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF NEUROPSYCHIATRIC DISORDERS
; FILE REFERENCE: 7853-093
; CURRENT APPLICATION NUMBER: US/08/965,048
; CURRENT FILING DATE: 1997-11-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; LENGTH: 45716
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-08-965-048-5

Query Match 11.7%; Score 37.8; DB 4; Length 45716;
Best Local Similarity 50.8%; Pred. No. 4.4;
Matches 90; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY 117 GCGCGGCGAGGAGAGGGGCGACGGGCTTCCAGGGCCCGCGCGCGCAGAGAGATTGG 176
DB 5094 GCGGAGATCTCTGCGCGACCATGAGCCCTTGCGCCCTGTGCGCGGCGCCCGCGG 5035

QY 177 CCAGGCGACGCGCGCTGAGCGGAGCGGCGCAGGGCTTTCTCAGAGCGCGCGAGCGCGC 236
DB 5034 TCAGGACTGTGTGCGGATCTCCGAGCGCGCGGAGGGCGGAGGGCGGAGCGCGGCGAGC 4975

QY 237 GCTGAGGGGCGAGAGACCGGGATATAGAGCTTGTGCGCTTGTCCCGGAGCGCGCA 293
DB 4974 GCGCGAGCGGGGCGACGCTCAGGGCATAGAGGGCGCTCATTTGCGCGCGCGCA 4918

RESULT 30
US-08-965-048-6/c
; Sequence 6, Application US/08965048
; Patent No. 6323244
; GENERAL INFORMATION:
; APPLICANT: Chen, Hong
; APPLICANT: Freilmer, Nelson
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF NEUROPSYCHIATRIC DISORDERS
; FILE REFERENCE: 7853-093
; CURRENT APPLICATION NUMBER: US/08/965,048
; CURRENT FILING DATE: 1997-11-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 45989
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-08-965-048-6

Query Match 11.7%; Score 37.8; DB 4; Length 45989;
Best Local Similarity 50.8%; Pred. No. 4.4;
Matches 90; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY 117 GCGCGGCGAGGAGAGGGGCGACGGGCTTCCAGGGCCCGCGCGCGCAGAGAGATTGG 176
DB 5094 GCGGAGATCTCTGCGCGACCATGAGCCCTTGCGCCCTGTGCGCGGCGCCCGCGG 5035

QY 177 CCAGGCGACGCGCGCTGAGCGGAGCGGCGCAGGGCTTTCTCAGAGCGCGCGAGCGCGC 236
DB 5034 TCAGGACTGTGTGCGGATCTCCGAGCGCGCGGAGGGCGGAGGGCGGAGCGCGGCGAGC 4975

QY 237 GCTGAGGGGCGAGAGACCGGGATATAGAGCTTGTGCGCTTGTCCCGGAGCGCGCA 293
DB 4974 GCGCGAGCGGGGCGACGCTCAGGGCATAGAGGGCGCTCATTTGCGCGCGCGCA 4918

RESULT 31
US-08-483-533-37/c
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QY 241 GAGGCGAGGACCGGGTATAGAACCTGTGCGCTTCCCGGAGCCG 291  
DB 754 GTGGCGCGGGCTCTGGCGCGACTCGGGGGGGGCTGTCCGGCAGTGC 804

RESULT 37  
US-09-252-991A-13576  
; Sequence 13576, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 13576  
; LENGTH: 732  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-13576

Query Match 11.5%; Score 37.2; DB 4; Length 732;  
Best Local Similarity 48.6%; Pred. No. 5.2; Mismatches 108; Indels 0; Gaps 0;  
Matches 102; Conservative 0;

QY 107 AGTCTCGAGGCGCGGCGAGGAGGCGGCTTCCAGGCGCGCGCGCAGC 166  
DB 480 ACTTCTGCTGCGCGCGCGCGAGGCGGCTTCCAGGCGCGCGCGCAGC 539  
QY 167 AGGAATTGGCCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 226  
DB 540 TCGGAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 599  
QY 227 CGAGGCG 286  
DB 600 CTTTGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 659  
QY 287 AGCGGAGGTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 316  
DB 660 TGGGCGAGGCTCAGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCG 689

RESULT 38  
US-09-252-991A-13471  
; Sequence 13471, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 13471  
; LENGTH: 891  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-13471

Query Match 11.5%; Score 37.2; DB 4; Length 891;  
Best Local Similarity 48.6%; Pred. No. 5.2; Mismatches 108; Indels 0; Gaps 0;  
Matches 102; Conservative 0;

QY 107 AGTCTCGAGGCGCGGCGAGGAGGAGGCGGCTTCCAGGCGCGCGCGCAGC 166  
DB 22 ACTTCTGCTGCGCGCGCGCGCGAGGCGGCTTCCAGGCGCGCGCGCAGC 81  
QY 167 AGGAATTGGCCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 226  
DB 82 TCGGAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 141  
QY 227 CGAGGCG 286  
DB 142 CTTTGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 201  
QY 287 AGCGGAGGTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 316  
DB 202 TGGGCGAGGCTCAGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCG 231

RESULT 39  
US-09-252-991A-13766/c  
; Sequence 13766, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 13766  
; LENGTH: 1098  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-13766

Query Match 11.5%; Score 37.2; DB 4; Length 1098;  
Best Local Similarity 48.6%; Pred. No. 5.2; Mismatches 108; Indels 0; Gaps 0;  
Matches 102; Conservative 0;

QY 107 AGTCTCGAGGCGCGGCGAGGAGGAGGCGGCTTCCAGGCGCGCGCGCAGC 166  
DB 797 ACTTCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 738  
QY 167 AGGAATTGGCCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 226  
DB 737 TCGGAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 678  
QY 227 CGAGGCG 286  
DB 677 CTTTGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 618  
QY 287 AGCGGAGGTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 316  
DB 617 TGGGCGAGGCTCAGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCG 588

RESULT 40  
US-08-278-729A-32/c  
; Sequence 32, Application US/08278729A  
; Patent No. 5650276  
; GENERAL INFORMATION:  
; APPLICANT: SMART, JOHN  
; APPLICANT: OPERMANN, HERMAN  
; APPLICANT: OKAYAKI, ENGIN  
; APPLICANT: KUBERASAMPATH, THANGAVEL  
; APPLICANT: RUEGER, DAVID C.  
; APPLICANT: PANG, ROY H. L.  
; APPLICANT: COHEN, CHARLES M.

TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES  
STREET: 45 SOUTH STREET  
CITY: HOPKINTON  
STATE: MA  
COUNTRY: USA  
ZIP: 01748  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/278,729A  
FILING DATE: 20-JUL-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: PITCHER Esq., EDMUND R.  
REGISTRATION NUMBER: 27,829  
REFERENCE/DOCKET NUMBER: CRP-058CPFW  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (508) 435-9001  
TELEFAX: (508) 435-6951  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1247 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 84..1199  
OTHER INFORMATION: /product= "GDF-1"  
US-08-278-729A-32

Query Match 11.5%; Score 37.2; DB 1; Length 1247;  
Best Local Similarity 48.6%; Pred. No. 5.2; Mismatches 102; Conservative 0; Gaps 0;  
Matches 102; Indels 108; Gaps 0;  
QY 113 CGAGGCCCGGCGAGGAGGGGCGACGGGCTTCCAGAGCCCGCGCGCAGCAGGAAG 172  
DB 838 CGCGGCCGGGCGAGGGGTGCGACAGGCGGGGTGAGGAGTCAACAGCAGCGAGCGAGGCC 779  
QY 173 TTGGCTCAGGCGACGCGCGTGAAGGAGCGGGCGAGGCTTTCTCAGAGCGCGGGCGAGGC 232  
DB 778 TCGGCCAGGCGCGCGCAGGCGCGGAGGGGCCCGGGGGCGTAGCGCCAGCGCCAGGCGGAGG 719  
QY 233 CGAGCGCTGAGGGGCGAGGACCGGAGTATAGAAAGCTTCGTGAGCTTGCCCGGGCGAGCGCG 292  
DB 718 CTGCGCGGCGCATGAGGCGTTGGCAGGCCCAAGCGCGGCCCAAGCAGAGCTCCGCGGCACTGCG 659  
QY 293 AGGTTCCCGCGCGCGCGCGCGAGCGCGCGCGC 322  
DB 658 GCGCCCGAGGGCGGGCGACCAACTGCGCGAGGC 629

Search completed: November 6, 2003, 09:05:47  
Job time : 63.0256 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using SW model

Run on: November 6, 2003, 08:07:17 ; Search time 242.663 Seconds  
(Without alignments)  
4247.375 Million cell updates/sec

Title: US-10-081-817a-19\_COPY\_229\_551

Perfect score: 323

Sequence: 1 GCGCGTGGGAGTCCAGACGCA.....GCGCCCCGAGCCCCGCGCC 323

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 214154 seqs, 1595478879 residues

Total number of hits satisfying chosen parameters: 4282708

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications\_NA:\*

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3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	323	100.0	547	13 US-10-081-817-19	Sequence 19, Appl
2	316.4	98.0	1794	12 US-10-059-579-120	Sequence 120, Appl
3	116	35.9	561	14 US-10-237-435-6	Sequence 6, Appl
4	78	24.1	569	12 US-10-210-951-27	Sequence 27, Appl
5	78	24.1	569	12 US-10-211-884-27	Sequence 27, Appl
6	78	24.1	570	9 US-09-989-722-407	Sequence 407, Appl
7	78	24.1	570	9 US-09-989-723-407	Sequence 407, Appl
8	78	24.1	570	9 US-09-989-729-407	Sequence 407, Appl
9	78	24.1	570	9 US-09-989-731-407	Sequence 407, Appl
10	78	24.1	570	10 US-09-989-732-407	Sequence 407, Appl
11	78	24.1	570	10 US-09-989-733-407	Sequence 407, Appl
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13	78	24.1	570	10 US-09-990-442-407	Sequence 407, Appl
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17	78	24.1	570	10 US-09-989-721-407	Sequence 407, Appl
18	78	24.1	570	10 US-09-992-598-407	Sequence 407, Appl
19	78	24.1	570	10 US-09-989-293A-407	Sequence 407, Appl
20	78	24.1	570	10 US-09-989-735-407	Sequence 407, Appl
21	78	24.1	570	10 US-09-990-444-407	Sequence 407, Appl
22	78	24.1	570	10 US-09-991-181-407	Sequence 407, Appl
23	78	24.1	570	10 US-09-989-730-407	Sequence 407, Appl
24	78	24.1	570	10 US-09-990-436-407	Sequence 407, Appl
25	78	24.1	570	10 US-09-993-697-407	Sequence 407, Appl
26	78	24.1	570	11 US-09-989-734-407	Sequence 407, Appl
27	78	24.1	570	11 US-09-997-653-407	Sequence 407, Appl
28	78	24.1	570	11 US-09-993-667-407	Sequence 407, Appl
29	78	24.1	570	11 US-09-997-428-407	Sequence 407, Appl
30	78	24.1	570	11 US-09-997-666-407	Sequence 407, Appl
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33	78	24.1	570	11 US-09-990-711-407	Sequence 407, Appl
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36	78	24.1	570	11 US-09-990-437-407	Sequence 407, Appl
37	78	24.1	570	11 US-09-991-157-407	Sequence 407, Appl
38	78	24.1	570	11 US-09-997-514-407	Sequence 407, Appl
39	78	24.1	570	11 US-09-997-573-407	Sequence 407, Appl
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41	78	24.1	570	11 US-09-990-726-407	Sequence 407, Appl
42	78	24.1	570	11 US-09-987-559-407	Sequence 407, Appl
43	78	24.1	570	11 US-09-987-601-407	Sequence 407, Appl
44	78	24.1	570	11 US-09-991-854-407	Sequence 407, Appl
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## ALIGNMENTS

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RESULT 1
US-10-081-817-19
; Sequence 19, Application US/10081817
; Publication No. US20020183501A1
; GENERAL INFORMATION:
; APPLICANT: Polyak, Kornelia
; APPLICANT: Portier, Dale
; APPLICANT: Sgroi, Dennis
; APPLICANT: Krop, Ian
; TITLE OF INVENTION: HIN-1, A TUMOR SUPPRESSOR GENE
; FILE REFERENCE: 00530-094001
; CURRENT APPLICATION NUMBER: US/10/081,817
; PRIOR FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: 60/270,973
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/351,908
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 547
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 186
; OTHER INFORMATION: n = C or G
US-10-081-817-19
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Query Match 100.0%; Score 323; DB 13; Length 547;  
Best Local Similarity 100.0%; Pred. No. 6.2e-67;  
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GCGCGGGGAGTCCAGACGCAAGCGAAGGTGGGCGCGGAGTGGCGCTTCGCGGAGCAAA	60
Db	225	GCGCGGGGAGTCCAGACGCAAGCGAAGGTGGGCGCGGAGTGGCGCTTCGCGGAGCAAA	284
Qy	61	GCGCGGGGAGTCCAGACGCAAGCGAAGGTGGGCGCGGAGTGGCGCTTCGCGGAGCAAA	120

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Db      285 GGCCTGCTGCTCTCTCAGAGAGCCCGCAGCGCTGCGAAGAGAACTCTCGAGGCC 344
Qy      121 GGGGAGGAGAGGGGGGAGCGGGCTTCCAGAGCCCGCGCGCCGAGAGAGATTGGCCAG 180
Db      345 GGGGAGGAGAGGGGGGAGCGGGCTTCCAGAGCCCGCGCGCCGAGAGAGATTGGCCAG 404
Qy      181 GGCACGGCGCTGAGCGAGCGGGGCGAGGGCTTTCTCAGAGCGCGGGCGAGCGCGGCTG 240
Db      405 GGCACGGCGCTGAGCGAGCGGGGCGAGGGCTTTCTCAGAGCGCGGGCGAGCGCGGCTG 464
Qy      241 GAGGGGCGAGGACCGGGGTATTAAGAGCTTCGTGCGCTTCCGCGGAGCGGAGGTTCCC 300
Db      465 GAGGGGCGAGGACCGGGGTATTAAGAGCTTCGTGCGCTTCCGCGGAGCGGAGGTTCCC 524
Qy      301 GCGCGCGCCCGAGCGCCCGCGCGCC 323
Db      525 GCGCGCGCCCGAGCGCCCGCGCGCC 547

RESULT 2
; US-10-059-579-120
; Sequence 120, Application US/10059579
; Publication No. US20030138783A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: SUKUMAR, Sarabwati
; APPLICANT: EVRON, Elia
; APPLICANT: DOOLEY, William C.
; APPLICANT: DAVIDSON, Nancy Jo.
; TITLE OF INVENTION: ABERRANTLY METHYLATED GENES AS MARKERS OF BREAST MALIGNANCY
; FILE REFERENCE: JHU1630-1
; CURRENT FILING DATE: 2003-02-03
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 09/771,357
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 120
; LENGTH: 1794
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (359)..(359)
; OTHER INFORMATION: n is any nucleotide
US-10-059-579-120

Query Match      98.0%; Score 316.4; DB 12; Length 1794;
Best Local Similarity 99.7%; Pred. No. 1.6e-65;
Matches 317; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 TGGGCTCAGACCGGAAAGCGAGGTCGGCGGGCTGCGCTCCGAGAGCAAGAGCCG 65
Db      854 TGGGCTCAGACCGGAAAGCGAGGTCGGCGGGCTGCGCTCCGAGAGCAAGAGCCG 913
Qy      66 GGCCTGCTCTCTCAGAGGGCGCCGAGCGCTGCGAAGAGAGTCTTCGAGCGCCGAGCA 125
Db      914 GGCCTGCTCTCTCAGAGGGCGCCGAGCGCTGCGAAGAGTCTTCGAGCGCCGAGCA 973
Qy      126 GGGAGGGGGGACCGGGCTTCCAGAGCGCCCGCGCGGAGAGAGTTGGCGAGGCA 185
Db      974 GGGAGGGGGGACCGGGCTTCCAGAGCGCCCGCGCGGAGAGAGTTGGCGAGGCA 1033
Qy      186 GGCCTGAGCGAGGCGGCGAGGGCTTTCTCAGAGCGCGGGCGAGCGCGCTGAGAGG 245
Db      1034 GGCCTGAGCGAGGCGGCGAGGGCTTTCTCAGAGCGCGGGCGAGCGCGCTGAGAGG 1093
Qy      246 GCGAGAGCGGGGTATTAAGAGCTTCGTGCGCTTCCGCGGAGCGCGAGGTTCCCGCGC 305
Db      1094 GCGAGAGCGGGGTATTAAGAGCTTCGTGCGCTTCCGCGGAGCGCGAGGTTCCCGCGC 1153
Qy      306 GCGCGAGCGCCCGCGCGCC 323
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Db      1154 GCGCGAGCGCCCGCGCGCC 1171

RESULT 3
; US-10-237-435-6
; Sequence 6, Application US/10237435
; Publication No. US20030124580A1
; GENERAL INFORMATION:
; APPLICANT: Walker, Michael G.
; APPLICANT: Spiro, Peter A.
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: LONG SURFACTANT MOLECULES
; FILE REFERENCE: PB-0019 US
; CURRENT FILING DATE: 2002-09-06
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 60/317,822
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PERL Program
; SEQ ID NO: 6
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030124580A1 242745.1
US-10-237-435-6

Query Match      35.9%; Score 116; DB 14; Length 561;
Best Local Similarity 100.0%; Pred. No. 1.5e-18;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      208 GCTTCTCAGAGCGCGGCGAGCGCGCTGCGAGGGCGAGAGCCGGGTATTAAGAGC 267
Db      1 GCTTCTCAGAGCGCGGCGAGCGCGCTGCGAGGGCGAGAGCCGGGTATTAAGAGC 60
Qy      268 CTCGTGCGCTTGGCCCGGCGAGCGCGAGGTTCCCGCGCGCGCCCGAGCCCGCGCGCC 323
Db      61 CTCGTGCGCTTGGCCCGGCGAGCGCGAGGTTCCCGCGCGCGCCCGAGCCCGCGCGCC 116

RESULT 4
; US-10-210-951-27
; Sequence 27, Application US/10210951
; Publication No. US20030170228A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Pitti, Robert M.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stone, Donna M.
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR
; FILE REFERENCE: P2931R1C1
; CURRENT FILING DATE: 2002-08-02
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/014699
; PRIOR FILING DATE: 1996-04-01
; PRIOR APPLICATION NUMBER: 60/026943
; PRIOR FILING DATE: 1996-09-23
; PRIOR APPLICATION NUMBER: 60/059121
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/062037
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PRIOR FILING DATE: 1997-10-10  
PRIOR APPLICATION NUMBER: 60/063755  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063045  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063046  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/06511  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/066772  
PRIOR FILING DATE: 1997-11-24  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 258  
SEQ ID NO 27  
LENGTH: 569  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-210-951-27

Query Match 24.1%; Score 78; DB 12; Length 569;  
Best Local Similarity 100.0%; Pred. No. 1,1e-09;  
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 GCGAGACCGGGTATAGAGCTTGCGCTTGGCCGCGGACGCGAGTTCCCGCGCC 305  
DB 1 GCGAGACCGGGTATAGAGCTTGCGCTTGGCCGCGGACGCGAGTTCCCGCGCC 60  
QY 306 GCGCCGAGCCCGCGCGCC 323  
DB 61 GCGCCGAGCCCGCGCGCC 78

RESULT 5  
US-10-211-884-27  
Sequence 27, Application US/10211884  
Publication No. US20030175900A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Marsters, Scot A.  
APPLICANT: Pan, James  
APPLICANT: Pitti, Robert M.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Smith, Victoria  
APPLICANT: Stone, Donna M.  
APPLICANT: Metanabe, Colin K.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR  
FILE REFERENCE: P2931R1C1  
CURRENT APPLICATION NUMBER: US/10/211,884  
PRIOR APPLICATION NUMBER: 2002-08-02  
PRIOR FILING DATE: 1996-04-01  
PRIOR APPLICATION NUMBER: 60/026943  
PRIOR FILING DATE: 1996-09-23  
PRIOR APPLICATION NUMBER: 60/059121  
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PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/066511  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/066772

PRIOR FILING DATE: 1997-11-24  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 258  
SEQ ID NO 27  
LENGTH: 569  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-211-884-27

Query Match 24.1%; Score 78; DB 12; Length 569;  
Best Local Similarity 100.0%; Pred. No. 1,1e-09;  
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 GCGAGACCGGGTATAGAGCTTGCGCTTGGCCGCGGACGCGAGTTCCCGCGCC 305  
DB 1 GCGAGACCGGGTATAGAGCTTGCGCTTGGCCGCGGACGCGAGTTCCCGCGCC 60  
QY 306 GCGCCGAGCCCGCGCGCC 323  
DB 61 GCGCCGAGCCCGCGCGCC 78

RESULT 6  
US-09-989-722-407  
Sequence 407, Application US/09989722  
Patent No. US2002072067A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerlitsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kjaevin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Metanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C63  
CURRENT APPLICATION NUMBER: US/09/989,722  
PRIOR APPLICATION NUMBER: 2001-11-19  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/084600

Fri Nov 7 08:10:02 2003

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3 PRIOR FILING DATE: 1998-05-28  
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5 PRIOR FILING DATE: 1998-06-02  
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11 PRIOR FILING DATE: 1998-06-03  
12 PRIOR APPLICATION NUMBER: 60/088021  
13 PRIOR FILING DATE: 1998-06-04  
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73 PRIOR FILING DATE: 1998-06-17

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36 PRIOR FILING DATE: 1998-06-24  
37 PRIOR APPLICATION NUMBER: 60/090535  
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60 PRIOR FILING DATE: 1998-06-26  
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62 PRIOR FILING DATE: 1998-07-01  
63 PRIOR APPLICATION NUMBER: 60/091478  
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72 PRIOR FILING DATE: 1998-07-02  
73 PRIOR APPLICATION NUMBER: 60/091978

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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match      24.1%; Score 78; DB 9; Length 570;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      246 GCGAGACCGGGGTATAGAACCTTCCTGCGCCCGGCGAGCGAGTTCCCGCGC 305
        1 GCGAGACCGGGGTATAGAACCTTCCTGCGCCCGGCGAGCGAGTTCCCGCGC 60
Qy      306 GCGCGGAGCGCGCGCGCGC 323
        61 GCGCGGAGCGCGCGCGC 78
Db      61 GCGCGGAGCGCGCGCGC 78

RESULT 7
US-09-989-723-407
Sequence 407, Application US/09989723
Patent No. US20020072092A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Inc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tuma, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C62
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: US/09/989,723
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/049787
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US-09-989-279-407
Sequence 407, Application US/09989279
Patent No. US20020072496A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavyn, Ivar J.
APPLICANT: Nadiet, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: F2730P1C56
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PRIOR FILING DATE: 2001-11-19
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PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR APPLICATION NUMBER: 60/087609
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RESULT 9
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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnuyere, Luc
; APPLICANT: Eaton, Dan L.
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; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC65
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PRIOR FILING DATE: 1998-07-09

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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Borstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
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; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C70
; CURRENT FILING DATE: 2001-11-20
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RESULT 11  
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Patent No. US20020123463A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Bockstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gottlieb, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Goddard, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavik, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C57  
CURRENT FILING DATE: 2001-11-19  
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 Patent No. US2002012756A1  
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 APPLICANT: Zhang, Zemin  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: P2730P1C5  
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GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Bostein, David  
APPLICANT: Desnoyers, Luc  
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TITLE OF INVENTION: Acids Encoded and Transmembrane Polypeptides and Nucleic  
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QY      306 GCCCGAGGCCCGCCGCC 323
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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Kijavini, Ivar J.
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; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Thomas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C17
; CURRENT APPLICATION NUMBER: US/09/991,163
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; PRIOR APPLICATION NUMBER: 60/049787
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Query Match 24.1%; Score 78; DB 10; Length 570;  
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; Patent No. US20020137075A1  
; GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
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APPLICANT: Fong, Sherman  
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APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
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PRIOR FILING DATE: 1998-07-09

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QY      306 GCCCGGAGCCCCCGCGGCC 323
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; Sequence 407, Application US/09990456
; Patent No. US20020137890A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Gerritsen, Mary E.
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; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
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Query Match 24.1%; Score 78; DB 10; Length 570;
Best Local Similarity 100.0%; Pred.No. 1;le-09;
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RESULT 17
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Sequence 407, Application us/09989721
Patent No. US20020142961A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bostein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone

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APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Geriltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavir, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: 2730155  
CURRENT APPLICATION NUMBER: US/09/989,721  
PRIOR FILING DATE: 2001-11-19  
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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
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; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.

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; APPLICANT: Godowski, Paul J.
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; APPLICANT: Tunes, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
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Query Match 24.1%; Score 78; DB 10; Length 570;  
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RESULT 19  
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GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnuyers, Luc  
APPLICANT: Batoni, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerlitsen, Maty E.  
APPLICANT: Goddard, Audrey J.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher



APPLICANT: Gurney, Austin L.  
APPLICANT: KJavain, Ivar J.  
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APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
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PRIOR FILING DATE: 1998-07-09

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Query Match 24.1%; Score 78; DB 10; Length 570;  
Best Local Similarity 100.0%; Pred. No. 1.1e-09; Indels 0; Gaps 0;  
Matches 78; Conservative 0; Mismatches 0;

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OY 306 GCGCGAGCGCGCGCGCC 323
DB 61 GCGCGAGCGCGCGCGCC 78

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RESULT 20  
US-09-989-735-407.

Sequence 407, Application US/09989735  
Publication No. US20020193299A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deenoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerstein, Mary E.  
APPLICANT: Goddard, Bailey J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Guiney, Austin J.  
APPLICANT: Kljavin, Ivair J.  
APPLICANT: Napier, Mary A.

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APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P27301P1C1
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;; PRIOR FILING DATE: 1998-07-09

Query Match 24.1%; Score 78; DB 10; Length 570;  
Best local similarity 100.0%; Pred. No. 1,1e-09;  
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-09-980-444-407  
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;; PUBLICATION NO. US20020193300A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Ashkenazi, Avi J.  
;; APPLICANT: Baker, Kevin P.  
;; APPLICANT: Bocstein, David  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Bacon, Dan L.  
;; APPLICANT: Ferrara, Napoleone  
;; APPLICANT: Fong, Sherman  
;; APPLICANT: Gerber, Hanspeter  
;; APPLICANT: Gerritsen, Mary B.  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.  
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;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Kljavin, Ivar J.  
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;; APPLICANT: Pan, James  
;; APPLICANT: Paoni, Nicholas F.  
;; APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same  
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PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 24.1%; Score 78; DB 10; Length 570;  
Best Local Similarity 100.0%; Pred. No. 1.1e-09;  
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 246 GCGGAGACCGGCTTAAGAAGCCCTGCGCTTGCCTCCGCGGACCCGAGGTTCCCGCGCC 305  
Db 1 GCGGAGACCGGCTTAAGAAGCCCTGCGCTTGCCTCCGCGGACCCGAGGTTCCCGCGCC 60  
Qy 306 GCGCGAGACCCCGCGCGCC 323  
Db 61 GCGCGAGACCCCGCGCGCC 78

RESULT 22  
US-09-991-181-407  
Sequence 407, Application US/09991181  
Publication No. US2002019761SA1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Bostein, David  
APPLICANT: Deenoyers, Luc  
APPLICANT: Ealon, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltzen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secured and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC53  
CURRENT FILING DATE: 2001-11-16  
PRIOR APPLICATION NUMBER: US/09/991,181  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065186  
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PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/075945  
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;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 24.1%; Score 78; DB 10; Length 570;  
Best Local Similarity 100.0%; Pred. No. 1, 1e-09;  
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 246 GCGAGACCGGGTATTAAGAGCTTGTGACCTTGCCCGGAGCGGAGGTTCCCGGCC 305  
Db 1 GCGAGACCGGGTATTAAGAGCTTGTGACCTTGCCCGGAGCGGAGGTTCCCGGCC 60  
Qy 306 GCGCCGAGCCCGCGGCC 323  
Db 61 GCGCCGAGCCCGCGGCC 78

RESULT 23  
US-09-988-730-407  
; Sequence 407, Application US/09989730  
; Publication No. US20020197674A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC69  
CURRENT APPLICATION NUMBER: us/09/989,730  
PRIOR FILING DATE: 2001-11-20  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
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; PRIOR FILING DATE: 1998-07-07
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; PRIOR FILING DATE: 1998-07-09

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Query Match      24.1%; Score 78; DB 10; Length 570;
Best Local Similarity 100.0%; Pred. No. 1,1e-09;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      246 GCGAGACCGGGATATAGAACCTCGGCTTGGCCGGCAGCCAGTTCCCGCCG 305
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DB      1 GCGAGACCGGGATATAGAACCTCGGCTTGGCCGGCAGCCAGTTCCCGCCG 60
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QY      306 GCCCGAGCCCGCCGCC 323
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DB      61 GCCCGAGCCCGCCGCC 78
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RESULT 24
US-09-990-436-407
; Sequence 407, Application US/09990436
; Publication No. US20020198148A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferreira, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Guirney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C14

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; PRIOR APPLICATION NUMBER: 60/062250
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PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089908  
PRIOR FILING DATE: 1998-06-18  
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PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/089948  
PRIOR FILING DATE: 1998-06-19  
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PRIOR APPLICATION NUMBER: 60/090254  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090349  
PRIOR FILING DATE: 1998-06-23  
PRIOR APPLICATION NUMBER: 60/090355  
PRIOR FILING DATE: 1998-06-23  
PRIOR APPLICATION NUMBER: 60/090429  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090431  
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PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090444  
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PRIOR APPLICATION NUMBER: 60/090678  
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PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090694  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090695  
PRIOR FILING DATE: 1998-06-25

PRIOR APPLICATION NUMBER: 60/090696  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090862  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/090863  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/091360  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091478  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091544  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091519  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091626  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 24.1%; Score 78; DB 10; Length 570;  
Best Local Similarity 100.0%; Pred. No. 1,1e-09;  
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 246 GCGAGACCGGTTAAGAGCTTGTGCTGCTCCGCGGACGCGAGATTCCCGGCC 305  
DB 1 GCGAGACCGGTTAAGAGCTTGTGCTGCTCCGCGGACGCGAGATTCCCGGCC 60  
OY 306 GCGCGGACCGCGCGGCC 323  
DB 61 GCGCGGACCGCGCGGCC 78

RESULT 25  
US-09-993-687-407  
Sequence 407, Application US/09993687  
Publication No. US20020198149A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertelsen, Mary B.  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Guiney, Austin L.  
APPLICANT: Kijavlin, Ivar A.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C11  
CURRENT FILING DATE: 2002-11-14  
PRIOR FILING DATE: 2002-11-14  
PRIOR APPLICATION NUMBER: 60/049787

[illegible]

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PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
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PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match          24.1%  Score 78:  DB 10:  Length 570:
Best Local Similarity 100.0%  Prcd. No. 11e-09;
Matches 78;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY      246  GCGAGGACCGCGGTATAGAGCCTTCTGCGCTTCCCGCGGACCGCCAGCTTCCCGCGCC 305
Db      1    GCGAGGACCGCGGTATAGAGCCTTCTGCGCTTCCCGCGGACCGCCAGCTTCCCGCGCC 60
QY      306  GCGCGGAGCGCCCGCGCGCC 323
Db      61  GCGCGGAGCGCCCGCGCGCC 78

RESULT 26
US-09-989-734-407
Sequence 407, Application US/09989734
Publication No. US20030003531A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deaneviers, Luc
APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlesen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Goddowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gunney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Nadler, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Nunes, Daniel
APPLICANT: Matanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Acids Encoded and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C64
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
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PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
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PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
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;; PRIOR FILING DATE: 1998-06-17  
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;; PRIOR FILING DATE: 1998-06-17  
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;; PRIOR FILING DATE: 1998-06-17  
;; PRIOR APPLICATION NUMBER: 60/089801  
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;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090862  
;; PRIOR FILING DATE: 1998-06-26  
;; PRIOR APPLICATION NUMBER: 60/090863  
;; PRIOR FILING DATE: 1998-06-26

;; PRIOR APPLICATION NUMBER: 60/091360  
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;; PRIOR APPLICATION NUMBER: 60/091478  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091544  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091519  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091626  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091633  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 24.1%; Score 78; DB 11; Length 570;  
Best Local Similarity 100.0%; Pred. No. 1,1e-09;  
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 GCGAGACCGGATATAGAGCCTGCGCTTGGCCCGGACGCCGAGTTCCCGCGC 305  
|||  
Db 1 GCGAGACCGGATATAGAGCCTGCGCTTGGCCCGGACGCCGAGTTCCCGCGC 60

QY 306 GCCCGAGCCCCCGCGCC 323  
|||  
Db 61 GCCCGAGCCCCCGCGCC 78

RESULT 27  
US-09-997-653-407  
;; Sequence 407, Application US/0997653  
;; Publication No. US2003008297A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Ashkenazi, Avi J.  
;; APPLICANT: Baker, Kevin P.  
;; APPLICANT: Botstein, David  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Eaton, Dan L.  
;; APPLICANT: Ferrara, Napoleone  
;; APPLICANT: Fong, Sherman  
;; APPLICANT: Geisler, Hanspeter  
;; APPLICANT: Gerritsen, Mary E.  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Grimaldi, J. Christopher  
;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Kljavin, Ivar J.  
;; APPLICANT: Napier, Mary A.  
;; APPLICANT: Pan, James  
;; APPLICANT: Paoni, Nicholas F.  
;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE OF INVENTION: Acids Encoding the Same  
;; FILE REFERENCE: P2730PIC38  
;; CURRENT APPLICATION NUMBER: US/09/997.653  
;; PRIOR FILING DATE: 2001-11-15  
;; PRIOR APPLICATION NUMBER: 60/049787  
;; PRIOR FILING DATE: 1997-06-16  
;; PRIOR APPLICATION NUMBER: 60/062250  
;; PRIOR FILING DATE: 1997-10-17  
;; PRIOR APPLICATION NUMBER: 60/065186  
;; PRIOR FILING DATE: 1997-11-12  
;; PRIOR APPLICATION NUMBER: 60/065311



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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      24.1%; Score 78; DB 11; Length 570;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      246 GCGAGACCGGGATATAGAGCCTCGTGGCTTCCCGGCGAGCGGAGGTTCCCGCGCG 305
Db      1 GCGAGACCGGGATATAGAGCCTCGTGGCTTCCCGGCGAGCGGAGGTTCCCGCGCG 60
Qy      306 GCGCGGAGCGCGCGCGCGCG 323
Db      61 GCGCGGAGCGCGCGCGCGCG 78

RESULT 28
US-09-993-667-407
; Sequence 407, Application US/09993667
; Publication No. US20030022187A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Maty E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavlin, Ivar, J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C4
; CURRENT APPLICATION NUMBER: US/09/993,667
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
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; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
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; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
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; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
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PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
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PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
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PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090540
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090542
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PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090680
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
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PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01

PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 24.1% Score 78; DB 11; Length 570;
Best Local Similarity 100.0%; Pred. No. 1,le-09; Mismatches 0; Indels 0; Gaps 0;
Matches 78; Conservative 0;

QY 246 GCGAGCACCGGCTRTAGAGCTCGCTTGCCTGCGGACGCGCAGATTCCCGGCGC 305
DB 1 GCGAGCACCGGCTRTAGAGCTCGCTTGCCTGCGGACGCGCAGATTCCCGGCGC 60

QY 306 GCGCGAGCGCCCGCGCGC 323
DB 61 GCGCGAGCGCCCGCGCGC 78

RESULT 29
US-09-997-428-407
Sequence 407, Application US/09997428
Publication No. US20030027162A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavyn, Ivar J.
APPLICANT: Nadiet, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C44
CURRENT APPLICATION NUMBER: US/09/997,428
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
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[illegible]





;; PRIOR FILING DATE: 1998-06-17  
;; PRIOR APPLICATION NUMBER: 60/089653  
;; PRIOR FILING DATE: 1998-06-17  
;; PRIOR APPLICATION NUMBER: 60/089801  
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;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091626  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091633  
;; PRIOR FILING DATE: 1998-07-02

;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 24.1% Score 78; DB 11; Length 570;  
Best Local Similarity 100.0%; Pred. No. 1,1e-09; Indels 0; Gaps 0;  
Matches 78; Conservative 0; Mismatches 0;

QY 246 GCGAGACCGGGTATTAAGAGCTTCGTGCTTGCCTGCGGAGCGGAGGTTCCCGCGC 305  
DB 1 GCGAGACCGGGTATTAAGAGCTTCGTGCTTGCCTGCGGAGCGGAGGTTCCCGCGC 60

QY 306 GCGCGGAGCGCGCGCGCC 323  
DB 61 GCGCGGAGCGCGCGCGCC 78

## RESULT 31

US-09-990-438-407  
; Sequence 407, Application US/09990438  
; Publication No. US200302754A1

## GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi J.  
;; APPLICANT: Baker, Kevin P.  
;; APPLICANT: Botstein, David  
;; APPLICANT: Desnuyers, Luc  
;; APPLICANT: Eaton, Dan L.  
;; APPLICANT: Ferrara, Napoleone  
;; APPLICANT: Fong, Sherman  
;; APPLICANT: Gerber, Hanspeter  
;; APPLICANT: Gerritsen, Mary E.  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Grimaldi, J. Christopher  
;; APPLICANT: Gueney, Austin L.  
;; APPLICANT: Kljavin, Ivar J.  
;; APPLICANT: Napier, Mary A.  
;; APPLICANT: Pan, James  
;; APPLICANT: Paoni, Nicholas F.  
;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE REFERENCE: P2730P1C3  
;; CURRENT APPLICATION NUMBER: US/09/990,438  
;; PRIOR FILING DATE: 2001-11-14  
;; PRIOR APPLICATION NUMBER: 60/049787  
;; PRIOR FILING DATE: 1997-06-16  
;; PRIOR APPLICATION NUMBER: 60/062250  
;; PRIOR FILING DATE: 1997-10-17  
;; PRIOR APPLICATION NUMBER: 60/065186  
;; PRIOR FILING DATE: 1997-11-12  
;; PRIOR APPLICATION NUMBER: 60/065311  
;; PRIOR FILING DATE: 1997-11-13  
;; PRIOR APPLICATION NUMBER: 60/066770  
;; PRIOR FILING DATE: 1997-11-24  
;; PRIOR APPLICATION NUMBER: 60/075945  
;; PRIOR FILING DATE: 1998-02-25  
;; PRIOR APPLICATION NUMBER: 60/078910  
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;; PRIOR APPLICATION NUMBER: 60/083322  
;; PRIOR FILING DATE: 1998-04-28  
;; PRIOR APPLICATION NUMBER: 60/084600  
;; PRIOR FILING DATE: 1998-05-07  
;; PRIOR APPLICATION NUMBER: 60/087106



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/ PRIOR FILING DATE: 1998-07-07
/ PRIOR APPLICATION NUMBER: 60/092182
/ PRIOR FILING DATE: 1998-07-09

Query Match      24.1%; Score 78; DB 11; Length 570;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      246 GCGAGGACGGGGATAGAGACCTCGGCGCTTGCCGCGGACGCGGAGTTCCCGCGGC 305
DB      1 GCGAGGACGGGGATAGAGACCTCGGCGCTTGCCGCGGACGCGGAGTTCCCGCGGC 60

QY      306 GCGCGGAGCGCCCGCGCGCC 323
DB      61 GCGCGGAGCGCCCGCGCGCC 78

RESULT 32
US-09-990-562-407
/ Sequence 407, Application US/09990562
/ Publication No. US20030027985A1
/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi J.
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Botstein, David
/ APPLICANT: Desnovers, Luc
/ APPLICANT: Eaton, Dan L.
/ APPLICANT: Ferrara, Napoleone
/ APPLICANT: Feng, Sherman
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerlitsen, Maly E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Kijavlin, Ivar J.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ TITLE OF INVENTION: Acids Encoding the Same
/ FILE REFERENCE: P2730P1C18
/ CURRENT FILING DATE: 2001-11-14
/ PRIOR APPLICATION NUMBER: US/09/990,562
/ PRIOR FILING DATE: 1997-06-16
/ PRIOR APPLICATION NUMBER: 60/049787
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/ PRIOR FILING DATE: 1997-11-24
/ PRIOR APPLICATION NUMBER: 60/075945
/ PRIOR FILING DATE: 1998-02-25
/ PRIOR APPLICATION NUMBER: 60/078910
/ PRIOR FILING DATE: 1998-03-20
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/ PRIOR FILING DATE: 1998-05-28
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/ PRIOR FILING DATE: 1998-06-02
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/ PRIOR FILING DATE: 1998-06-17
/ PRIOR APPLICATION NUMBER: 60/089653
/ PRIOR FILING DATE: 1998-06-17
/ PRIOR APPLICATION NUMBER: 60/089801
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/089907
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PRIOR FILING DATE: 1998-06-18  
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PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089947  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/089948  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/089952  
PRIOR FILING DATE: 1998-06-19  
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PRIOR FILING DATE: 1998-07-01  
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PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091626  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 24.1% Score 78; DB 11; Length 570;  
Best Local Similarity 100.0%; Pred. No. 1.1e-09;  
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 246 GCGAGGACCGGGATATAGAAAGCTGTGGCTTGGCCGGGACAGCCGACAGTTCCCGGCC 305  
Db 1 GCGAGGACCGGGATATAGAAAGCTGTGGCTTGGCCGGGACAGCCGACAGTTCCCGGCC 60  
Qy 306 GCGCGGAGCCCGCGGCC 323  
Db 61 GCGCGGAGCCCGCGGCC 78  
RESULT 33  
US-09-990-711-407  
; Sequence 407, Application US/09990711  
; Publication No. US20030032023A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyer, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PIC3  
; CURRENT APPLICATION NUMBER: US/09/990, 711  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066770  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/075945  
; PRIOR FILING DATE: 1998-02-25  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
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; PRIOR APPLICATION NUMBER: 60/087609  
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; PRIOR APPLICATION NUMBER: 60/087759

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PRIOR FILING DATE:	1998-06-10
PRIOR APPLICATION NUMBER:	60/088924
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PRIOR APPLICATION NUMBER:	60/088826
PRIOR FILING DATE:	1998-06-10
PRIOR APPLICATION NUMBER:	60/088858
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PRIOR APPLICATION NUMBER:	60/088861
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PRIOR APPLICATION NUMBER:	60/089105
PRIOR FILING DATE:	1998-06-12
PRIOR APPLICATION NUMBER:	60/089440
PRIOR FILING DATE:	1998-06-16
PRIOR APPLICATION NUMBER:	60/089512
PRIOR FILING DATE:	1998-06-16
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PRIOR FILING DATE:	1998-06-17
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57	PRIOR APPLICATION NUMBER: 60/091633
58	PRIOR FILING DATE: 1998-07-02
59	PRIOR APPLICATION NUMBER: 60/091978
60	PRIOR FILING DATE: 1998-07-07
61	PRIOR APPLICATION NUMBER: 60/091982
62	PRIOR FILING DATE: 1998-07-07
63	PRIOR APPLICATION NUMBER: 60/092182
64	PRIOR FILING DATE: 1998-07-09

Query Match	24.1%;	Score 78;	DB 11;	Length 570;
Best Local Similarity	100.0%;	Pred. No. 1.1e-09;		

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Db 1 GCGAGGACCGGGTATAGAGCTCTGTGCGCTTCCCGGCGACCGCAGGTTCCCCGCGC 60
Qy 306 GCCCGGAGCCCCCGCGCC 323
Db 61 GCCCGGAGCCCCCGCGCC 78

RESULT 34
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; Publication No. US20030040473A1
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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
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; APPLICANT: Gertlisen, Mary E.
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; APPLICANT: Godowski, Paul J.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumaas, Daniel
; APPLICANT: Tumaas, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P730P160
; CURRENT APPLICATION NUMBER: US/09/989,726
; PRIOR FILING DATE: 2001-11-19
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; Sequence 407, Application US/09998156  
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; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
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; APPLICANT: Desnovers, Luc  
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; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
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;; PRIOR FILING DATE: 1998-07-09

Query Match 24.1%; Score 78; DB 11; Length 570;  
Best Local Similarity 100.0%; Pred. No. 1,le-09; Indels 0; Gaps 0;  
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Db 1 GCGAGACCGGCTATAGAGCTCGTGGCTTGGGCGAGCCGAGATTCCCGCGCC 60

Fri Nov 7 08:10:02 2003

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QY 306 GCGCCGAGCCCGCGCC 323  
Db 61 GCGCCGAGCCCGCGCC 78

RESULT 36  
US-09-990-437-407  
Sequence 407, Application US/09990437  
Publication No. US20030045463A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
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APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Seclected and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC49  
CURRENT APPLICATION NUMBER: US/09/990,437  
CURRENT FILING DATE: 2001-11-16  
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PRIOR APPLICATION NUMBER: 60/090246  
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PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 24.1%; Score 78; DB 11; Length 570;  
Best Local Similarity 100.0%; Pred. No. 1,1e-09;  
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 246 GCGAGGACCGGATATAGAGAGCTGTGCTTGGCCGCGAGCCGCGAGTTTCCCGCGCC 305  
DB 1 GCGAGGACCGGATATAGAGAGCTGTGCTTGGCCGCGAGCCGCGAGTTTCCCGCGCC 60  
OY 306 GCGCGAGCCCGCGCGCC 323  
DB 61 GCGCGAGCCCGCGCGCC 78

RESULT 37  
US-09-991-157-407  
Sequence 407, Application US/09991157  
Publication No. US20030049638A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Baton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Geisler, Hanspeter  
APPLICANT: Gerlstein, Mary E.  
APPLICANT: Goddard, Audrey J.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, T. Christopher  
APPLICANT: Gueney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C51  
CURRENT FILING DATE: 2001-11-16  
PRIOR APPLICATION NUMBER: 60/049787  
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PRIOR FILING DATE: 1998-07-09

Query Match 24.1%; Score 78; DB 11; Length 570;  
Best Local Similarity 100.0%; Pred. No. 1.1e-09;  
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 GCGAGGACGGGTATTAAGAGCTTCGCGCGGAGCGGAGGTTCCCGCGCC 305  
DB 1 GCGAGGACGGGTATTAAGAGCTTCGCGCGGAGCGGAGGTTCCCGCGCC 60  
QY 306 GCGCGGAGCGCGCGCGCC 323  
DB 61 GCGCGGAGCGCGCGCGCC 78

RESULT 38

US-09-997-514-407  
Sequence 407, Application US/09997514  
Publication No. US20030049681A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertlisen, Mary B.  
APPLICANT: Goddard, Audrey E.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavits, Ivar J.  
APPLICANT: Madier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Panti, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tuma, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C46  
CURRENT APPLICATION NUMBER: US/09/997,514  
CURRENT FILING DATE: 2001-11-15  
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29 PRIOR FILING DATE: 1998-06-25
30 PRIOR APPLICATION NUMBER: 60/090695
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35 PRIOR FILING DATE: 1998-06-26
36 PRIOR APPLICATION NUMBER: 60/090863
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38 PRIOR APPLICATION NUMBER: 60/091260
39 PRIOR FILING DATE: 1998-07-01
40 PRIOR APPLICATION NUMBER: 60/091478
41 PRIOR FILING DATE: 1998-07-02
42 PRIOR APPLICATION NUMBER: 60/091544
43 PRIOR FILING DATE: 1998-07-01
44 PRIOR APPLICATION NUMBER: 60/091519
45 PRIOR FILING DATE: 1998-07-02
46 PRIOR APPLICATION NUMBER: 60/091626
47 PRIOR FILING DATE: 1998-07-02
48 PRIOR APPLICATION NUMBER: 60/091633
49 PRIOR FILING DATE: 1998-07-02
50 PRIOR APPLICATION NUMBER: 60/091978
51 PRIOR FILING DATE: 1998-07-07
52 PRIOR APPLICATION NUMBER: 60/091982
53 PRIOR FILING DATE: 1998-07-07
54 PRIOR APPLICATION NUMBER: 60/092182
55 PRIOR FILING DATE: 1998-07-09

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	Query March	24.1%;	Score 78;	DB 11;	Length 570;
	Best Local Similarity	100.0%;	Pred. No. 1;	le 09;	
	Matches	78;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0
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Db	1 GCGAGGACCGGAGTATGAAGAGCTGTGGCCCTGCGCGGAGCGGAGGTCTCCCGCC	60			
QY	306 GCCCGGAGCCCGCGGCC	323			
Db	61 GCCCGGAGCCCGCGGCC	78			

RESULT 39  
US-09-997-573-407  
; Sequence 407, Application US/09997573  
; Publication No. US20030049682A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Baton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Geider, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Goddard, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gueney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas P.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zenlin

TITLE OF INVENTION: Seccited and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P27301C45  
CURRENT APPLICATION NUMBER: US/09/197,573  
CURRENT FILING DATE: 2001-11-15  
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PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
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PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
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PRIOR FILING DATE: 1998-05-07  
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;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 24.1%; Score 78; DB 11; Length 570;  
Best Local Similarity 100.0%; Pred. No. 1, 1e-09; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 GCGAGACCGGGTATTAAGCTGTGGCTTGGCCGGCGACGGCGAGTTCCCGCGCC 60  
QY 306 GCCCGAGCCCGCGCGCC 323  
Db 61 GCCCGAGCCCGCGCGCC 78

RESULT 40  
US-09-991-172-407  
; Sequence 407, Application US/09991172  
; Publication No. US20030050457A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Geritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secified and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C50  
CURRENT FILING DATE: 2001-11-16  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
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PRIOR APPLICATION NUMBER:	60/091982
PRIOR FILING DATE:	1998-07-07
PRIOR APPLICATION NUMBER:	60/092182
PRIOR FILING DATE:	1998-07-09

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 6, 2003, 06:45:57 ; Search time 1862.61 Seconds  
(without alignments)

4214.691 Million cell updates/sec

Title: us-10-081-817a-19\_COPY\_229\_551

Perfect score: 1 ggcgcgcgggggtcagaccgca.....ggcgcgcgcgcgcgcgcgcgc 323

Sequence: 1 ggcgcgcgcgggggtcagaccgca.....ggcgcgcgcgcgcgcgcgcgc 323

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: em\_estba:\*  
2: em\_esthm:\*  
3: em\_estlm:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hrc:\*  
9: gb\_estcl:\*  
10: gb\_estc2:\*  
11: gb\_estc3:\*  
12: gb\_estc4:\*  
13: gb\_estc5:\*  
14: gb\_estc6:\*  
15: em\_estom:\*  
16: em\_estom2:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vtc:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rpd:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gsscl:\*  
29: gb\_gsscl2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	ID	Description
C 1	72.4	22.4	982 13	BX415111
C 2	69	21.4	935 29	CNS006XK
C 3	64.6	20.0	526 9	AA742697
C 4	64.6	20.0	1009 29	CNS0105W

Result No.	Score	Query Match Length	ID	Description
C 5	63.6	19.7	982 13	BX415111
C 6	63.4	19.6	925 29	CNS0091P
C 7	63.2	19.6	1061 13	BX391246
C 8	63.2	19.6	1203 29	CNS015Y4
C 9	63	19.5	935 29	CNS006XK
C 10	61.8	19.1	932 29	CNS0072Q
C 11	61.4	19.0	1057 13	BX349688
C 12	61.4	19.0	1292 28	AZ673197
C 13	60.8	18.8	925 29	CNS0091P
C 14	60.4	18.7	1072 13	BX381336
C 15	59.8	18.5	1144 13	BX415926
C 16	59.8	18.5	840 29	AG043457
C 17	59.6	18.5	1000 29	BX407619
C 18	59.4	18.4	844 29	CNS0052P
C 19	59.4	18.4	1101 29	CNS0178Y
C 20	59	18.3	703 29	AG054687
C 21	58.8	18.2	1103 13	BX403654
C 22	58.8	18.2	1581 29	AG052690
C 23	58.4	18.1	932 29	CNS0072Q
C 24	58	18.0	515 13	BX424977
C 25	58	18.0	1201 29	CNS01523
C 26	57.8	17.9	693 13	BX381320
C 27	57.8	17.9	839 29	CNS004NB
C 28	57.8	17.9	881 13	BX368720
C 29	57.6	17.8	910 29	CNS006ON
C 30	57.4	17.8	723 28	BZ046906
C 31	57.4	17.8	776 29	CNS010RY
C 32	57.4	17.8	1019 13	BO957113
C 33	57.2	17.7	873 12	BG844318
C 34	57	17.6	828 29	AG136798
C 35	56.8	17.6	971 13	BO678466
C 36	56.4	17.5	1126 13	BU185501
C 37	56.4	17.5	1150 13	BO892481
C 38	56.2	17.4	810 29	AG060267
C 39	56.2	17.4	888 12	BG809572
C 40	56	17.3	978 29	AG042900
C 41	55.6	17.2	1030 29	AG126213
C 42	55.6	17.2	1048 13	BO928358
C 43	55.4	17.2	788 29	AG032923
C 44	55.4	17.2	828 28	AZ184464
C 45	55	17.0	1076 12	BM479703

#### ALIGNMENTS

RESULT 1  
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LOCUS  
DEFINITION  
5-PRIME, mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Unpublished  
Contact: Genoscope  
Genoscope Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Web : www.genoscope.cns.fr  
Email: segre@genoscope.cns.fr  
Library was constructed by Life Technologies, a division of Invitrogen, contact : Feng Liang Email : fliang@lifestech.com URL : http://fulllength.invitrogen.com/invitrogen Corporation 1600 Paraday Avenue Genoscope sequence ID : CS0CAP004B510QPL  
Location/Qualifiers  
1..982  
/organism="Homo sapiens"



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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1257654"
/rnause_type="pooled germ cell tumors"
/lab_host="DH10B"
/clone_1ib="NCI_GCAP_GC4"
/notes="Vector: p773D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from 3 pooled
germ cell tumors, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified p773
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo."
BASE COUNT      88 a      162 c      189 g      85 t      2 others
ORIGIN
Query Match      20.0%; Score 64.6; DB 9; Length 526;
Best Local Similarity 83.9%; Pred. No. 0.0016;
Matches 73; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 237 GCTGAGAGGCGGAGACCGGCTATAGAGCTTCGCTCCCGGACCGGAGGT 296
DB 526 GCACGAGGCGGACAGACCGGCTATAGAGCTTCGCTCCCGGACCGGAGGT 467
QY 297 TCCCGGCGGCGGCGGAGCGCGCGCC 323
DB 466 TCCCGGCGGCGGCGGAGCGCGCGGCC 440

RESULT 4
CNS010EW/c      1009 bp      DNA      linear      GSS 26-JUL-1999
LOCUS
DEFINITION
Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN03P19 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION
AL098882
GI:5610493
GSS.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1009)
Genoscope.
Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (ENGP) -
http://www.engp.ebi.ac.uk -. This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billard at CERH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
Project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
peloBAC11.
FEATURES
Source
1..1009
Location/Qualifiers
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACN03P19"
/clone_1ib="DrosBAC"
/plasmid="peloBAC11"
/notes="end : SP6"
BASE COUNT      147 a      377 c      178 g      64 t      243 others
ORIGIN
Query Match      20.0%; Score 64.6; DB 29; Length 1009;
Best Local Similarity 37.4%; Pred. No. 0.0017;
Matches 104; Conservative 64; Mismatches 103; Indels 7; Gaps 1;

```

```

QY 43 GGGCTTCGCGAGACAAAGCCGCGCTCTCTCAGAGGCCCGACGCTTGCCAG 102
DB 964 GCGGMSRARSAYTCGCGMCCGCGMSAGRCSCCGGGGSCSCSCSCSCSC 905
QY 103 AGAAGTCTCTGAGAGCCGCGGAGGAAAGGAGCAGGCTTCCAGAGCCCGCGCG 162
DB 904 CSSGCGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 845
QY 163 CAGCAGAGAGTTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 222
DB 844 CGAGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 792
QY 223 CGGCGGAGGCGGCGGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 282
DB 791 CGCAGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 732
QY 283 GGGGAGCGGAGGAGTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 320
DB 731 GGGCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 694

RESULT 5
BX415111
LOCUS
DEFINITION
5-PRIME, mRNA sequence.
ACCESSION
BX415111
GI:30765470
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 982)
L.I.W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0CAP004BE10P1.
FEATURES
Source
1..982
Location/Qualifiers
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0CAP004Y120"
/rnause_type="THYMUS"
/clone_1ib="Homo sapiens THYMUS"
/notes="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
BASE COUNT      177 a      257 c      323 g      18 t      207 others
ORIGIN
Query Match      19.7%; Score 63.6; DB 13; Length 982;
Best Local Similarity 34.2%; Pred. No. 0.0026;
Matches 110; Conservative 69; Mismatches 144; Indels 0; Gaps 0;

QY 2 CGCGTGGGCTTCAGACCGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 61
DB 259 CCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 318
QY 62 GCCGAGGCTCTCTCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 121
DB 319 GSGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 378

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QY 122 GCGAGGGAAGGGGCAACGGGCTTCCACAGGGCCCGCGCGCAGCAGAGAAATTGGCGACAG 181

Db 379 GCGGGSSSSGCGGGGSSGGGAGMSSSSGGCCCCCGCCSSGGGGSSSGGSCSSGGGSSGV 438

QY 182 GCACGGCCGTGAGCGGAGCGGCGAGGAGGCTTTCTAGAGCGCGGAGCGAGGCCGCGCTGG 241

Db 439 GCGSSSCGCGCCSCSGSGSGSGGSGGSGSCSSGSGGAGCCCGGGGSCCGGGGSGGCGSSCS 498

QY 242 AGGAGGGAAGACCCGGTATTAGAAACCTCTGAGCTTGGCCCGGCAAGCCGCAAGTTCCCC 301

Db 499 SGGGGGGGGGGGGSSGSGSCCGGCCCCGAGGCCCCGCGCCSCGCCCTCCCCCGCCCCACAG 558

QY 302 GCGCGCCCGGAGCCCGCGGCC 323

Db 559 ACGGAGCCCAACCCGAVAGSCS 580

RESULT 6	:
CNS0091P/c	:
LOCUS	:
DEFINITION	: CNS0091P 925 bp DNA linear GSS 03-JUN-1999
	: Drosophila melanogaster genome survey sequence TET3 end of BAC #
	: BACR3D916 of RPGI-98 library from Drosophila melanogaster (fruit
	: fly). genomic survey sequence.
	: AL053013
ACCESSION	: AL053013.1 GI:4934461
VERSION	: GSS
KEYWORDS	: Drosophila melanogaster (fruit fly)
SOURCE	: Drosophila melanogaster
ORGANISM	: Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
	: Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
	: Ephydraidae; Drosophilidae; Drosophila.
REFERENCE	: 1 (bases 1 to 925)

REFERENCE AUTHORS TITLE JOURNAL	COMMENT
1 (bases 1 to 925) Genoscope. Direct Submision Submitted (02-jun-1999) BP 191 91006 EVRY cedex - FRANCE (E-mail : secrete@genoscope.cns.fr - Web : www.genoscope.cns.fr)	Determination of this BAC-end sequence was carried out as part of a

melanogaster BAC library was prepared by Kazuhiro Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCL-98 and was constructed by partial *NotI* digestion of *Drosophila* DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the library p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

```

FEATURES
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    Location/Qualifiers
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        /organism="Drosophila melanogaster"
        /mol_type="genomic DNA"
        /db_xref="taxon:7227"
        /clone="BACR19D16"
        /clone_1fb="RPC1-98"
        /note="end : TET3"
  BASE COUNT      120 a      61 c      61 g      172 t      511 others
  BRIGIN

```

<b>Query Match</b>	19.6%	<b>Score 63.4</b>	<b>DB 29</b>	<b>Length 925</b>
<b>Best Local Similarity</b>	14.2%	<b>Pred. No. 0.0029</b>		
<b>Matches 44</b>	<b>Conservative 153</b>	<b>Mismatches 113</b>	<b>Indels 0</b>	<b>Gaps 0</b>

<b>QY</b>	1 GGCCTGTGGGTCAGACCGCAAAAGCGAAGTGTCCGGGCGCGGTGGGCTCTGCCGAACA	60
	::::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::	
<b>Db</b>	867 SSSSTGTSACVCKCNASSCGCGCGGMBPCMCSSSSSCGSABARVKRYRAGAGAGKRG	808
	::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::	
<b>OY</b>	61 GGCGGGCTGTGCTCTCTCAGAGAGGCCCCACGGCTCCCAAGAGAATGTCCTTGAGAGCCC	120

Db 807 GGGASASHSSSSBACBSSSSSSCSASCSWBSASSSSSASSSSRNSGGGAGGSGASSSRSSSS 748

Qy 121 GGGCAGAGGAGAGGGGGCAGCGGCTTCCCAAGGGCCCGCGCGCAGCAGAGAAATTGGCCAG 180

Db 747 SSASASSSVSSASSSSSSSCSSSVSCSSVASSMSCSBBSSASASASSSSSSSASACASC 688

Qy 181 GGCACGCGCGGTGAGCGAGCGGACGCGGCTTTCTCAGAGCGCGCGCGCAGCGCGCGCTG 240

Db 687 CCTWSGCSTSTASMSAARSSSSSSSSSCSSSSMSASASASASASSSSSSSGSSSSSCGAC 628

Qy 241 GAGGGGCGAGACCGGGTTAAGAAAGCTTCGTGCGCTTCCCGGAGCGCCGCAATTCCC 300

Db 627 GBSMSAGGSGSVASASGMSVSSGRRSGSGAGGAGVGGSGSSGSSGSGSGSVCS 568

Qy 301 CGCGCGCCCC 310

Db 567 CSGCGMCRCS 558

RESULT 7	1061 bp	mrna	linear	EST 13-MAY-2000
LOCUS	EX391246			
DEFINITION	EX391246 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA			
ACCESSION	clone CS00D10081N19 3-PRIME, mRNA sequence.			
VERSION	EX391246			
KEYWORDS	EX391246.1 GI:30615383			
SOURCE	EST.			
ORGANISM	Homo sapiens (human)			
	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	1. (bases 1 to 1061)			
AUTHORS	I.J.W.B., Gruber,C., Jesseee,J. and Polayes,D.			
TITLE	Full-length cDNA libraries and normalization			
JOURNAL	unpublished			
COMMENT	Contact: Genoscope			

BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 7394.f For  
more information about this cluster, see  
[http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CSDBAH012ZH06NP1&cluster=7394.f](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CSDBAH012ZH06NP1&cluster=7394.f). Contact :  
Peng Liang Email : [liang@lifetech.com](mailto:liang@lifetech.com) URL :  
<http://fulllength.invitrogen.com/>, Invitrogen Corporation 1600  
Faraday Avenue Genoscope sequence ID : CSDBAH012ZH06NP1.

FEATURES	Source	Location/Qualifiers
		1..1061
	/organism="Homo sapiens"	
	/mol_type="mRNA"	
	/db_xref="taxon:9606"	
	/clone="CSOD1008Y19"	
	/tissue_type="PLACENTA	COT 25-NORMALIZED"
	/clone_lib="Homo sapiens PLACENTA	COT 25-NORMALIZED"
	/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."	
BASE COUNT	225 a	153 c 229 g 289 t 165 others
ORIGIN		

Qy	3	GCCTGGGGCTCAACCGCAAGGTCGCGGCGCGGAGTGGGCTCTGCACGAGACAAAG	62
Dy	294	GGBBVAGCTNNNNSSBNNBSSSSGGGGGGSSGGSSSSGGAGGGGGGGGGGGG	353
Qy	63	CCGGGCTTGCCTCTCAAGAGGCCCGCCCGCTTGCCCAAGAGAAATCTTCGAGGCGCG	122

[illegible][illegible]

[illegible]

RESULT 10					
CNS0072Q					
LOCUS					
DEFINITION	CNS0072Q	932 bp	DNA	linear	GSS 03-JUN-1999
	Drosophila melanogaster genome survey sequence T7 end of BAC #				
	BACR48B9 of RPCR98 library from Drosophila melanogaster (fruit				
	fly), genomic survey sequence.				
ACCESSION	AL066742				
VERSION	AL066742.1	GI:4945205			
KEYWORDS	GSS.				
SOURCE	Drosophila melanogaster (fruit fly)				
ORGANISM	Drosophila melanogaster				

REFERENCE 1 (bases 1 to 932)  
AUTHORS Genoscope.  
TITLE Direct Submision  
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage

COMMENT

Submitted (02-JUN-1999) Genoscope - Centre National de Séquenage  
BP 191 91006 EVRY cedex - FRANCE (E-mail: sequef@genoscope.cns.fr  
- Web: [www.genoscope.cns.fr](http://www.genoscope.cns.fr))  
Determination of this BAC-end sequence was carried out as part of a  
collaboration with the Berkeley Drosophila Genome Project (BDGP).  
The BDGP is constructing a physical map of the Drosophila  
melanogaster genome using these BACs. For further information  
please see <http://www.fruitfly.org> The BDGP Drosophila  
melanogaster BAC library was prepared by Kazutoyo Oosagawa and  
Aaron Memmocer in Pierre de Jong's laboratory in the Department of  
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,  
NY. The library is named RPc1-98 and was constructed by Buffalo,  
Escotti digestion of Drosophila DNA provided by the BDGP from the  
isogenic strain, Y2; cn bw sp, the same strain used for the BDGP's  
p1 and EST libraries. A more detailed description of the library  
and how to order individual BAC clones, the entire library, or  
filters for hybridization from the BACPAC Resource Center can be  
found at <http://bacpac.med.buffalo.edu/drosophila.bac.htm>.

**FEATURES**  
**SOURCE**

```

BASE COUNT      155 a      202 c      241 g      91 t      243 others
BRGIN

```

[illegible][illegible]

RESULT 11	LOCUS EX349688	DEFINITION	EX349688 Homo sapiens p11.1 band 1057 bp cDNA, clone #300D1063YK05 3' PRIME, mRNA sequence.	ACCESSION	EX349688	VERSION	EX349688.1	KEYWORDS	EST.	SOURCE	1057 bp cDNA, clone #300D1063YK05 3' PRIME, mRNA sequence.	1 linear	EST 05-MAY-2000
										Homo sapiens (human)			

REFERENCE	1 (bases 1 to 1057)
AUTHORS	K4,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished
COMMENT	Contact: Genoscope

Genoscope - Centre National de Séquençage  
BP 191 91006 Evry cedex - France  
Email: [segreg@genoscope.cns.fr](mailto:segreg@genoscope.cns.fr), Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 7092.r. For  
more information on this cluster, see  
<http://www.genoscope.cns.fr/cluster/>.  
Pang-Liang Cluster: [cgs1.seg.cnsbah10152B03NP1.cluster.r.7092.r](http://cgs1.seg.cnsbah10152B03NP1.cluster.r.7092.r). Contact :  
[Peng-Liang.Cluster@life.technologies.com](mailto:Peng-Liang.Cluster@life.technologies.com) URL : <http://fulllength.invitrogen.com/>  
Invitrogen Corporation 1600  
Paraday Avenue Genoscope sequence ID : [cgsbah10152B03NP1](http://cgsbah10152B03NP1).

FEATURES  
SOURCE

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="cazon:3606"
/clone="CSOD1063YK05"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_1ib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-CGA (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT
188 a 194 c 358 g 197 t 120 others
ORIGIN

```

Query Match	19.0%	Score 61.4	DB 13	Length 1057
Best Local Similarity	30.7%	Pred. No. 0.0073		
Matches	91	Conservative 78	Mismatches 127	Indels 0
			Gaps 0	
QY	28	GGTGGGGCCGGGGGTGTGGGCTTCGGGAGACAAAGCCGGGCTTGTCTTCAAGAGAGCC	87	
DB	337	SSNNBNKGGGGGKXGGGSSGGSSCGGGGCGGCGCCGGGGGGGAGAGGGSSGGGGCCGGAG	396	
QY	88	CCAGCGCCCTGACCAAGGAGAGTCTCTGAGGCTCGGCGAGAAAGGGGCGACGGGCTTCCC	147	
DB	397	SGGSSSSGGGGGCGSSGGGGGGGGGGCGGGGCGGGGCGGGSSGSSCGSSGGGCGG	456	
QY	148	AGGCGCCGCGCGCGCCGACAGACAGAAATTGGCCAGGGGCACGGCTGTGAGCCGAGCGGACAG	207	
DB	457	GGGGGAGGGGGGSSGGSSGCGSSCGGGGSSSSCCGSCGSSSCSSSSSCSSSSSS	516	



Qy 208 GCTTTCAGAGCGCGGAGCGCGCTGAGGCGGAGACCGGATTATAGAGC 267  
Db 517 SSGGCGSSGCGGCGGSSGSSGCGSSGSSGSSGSSGSSGSSGCGGCGGSS 576  
Qy 268 CTCCTGAGCGCGGCGGAGCGGAGTTCCCGCGCGCGCGCGCGCGCGC 323  
Db 577 SGGGCGCGSSGSSGSSGSSGSSGSSGSSGSSGSSGSSGSSGSSGSSG 632

RESULT 12  
LOCUS A2673197 1292 bp DNA linear GSS 14-DEC-2000  
DEFINITION ENT1K77R Entamoeba histolytica Sheared DNA Entamoeba histolytica  
ACCESSION A2673197  
VERSION A2673197.1 GI:11810343  
KEYWORDS GSS.  
SOURCE Entamoeba histolytica  
ORGANISM Entamoeba histolytica  
REFERENCE 1 (bases 1 to 1292)  
AUTHORS Loftus, B., Van Aken, S. and Fraser, C.  
TITLE Determination of clone end sequences from Entamoeba histolytica  
JOURNAL HML:IMSS, sheared DNA library  
COMMENT Unpublished  
Contact: Brendan J Loftus  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0208  
Fax: 301 838 3543  
Email: b.loftus@tigr.org  
Clones are derived from the Entamoeba histolytica HML:IMSS sheared  
DNA library  
Seq primer: M13-Reverse  
Class: Shotgun  
High quality sequence start: 282  
High quality sequence stop: 610.  
Location/Qualifiers  
1..1292  
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/mol\_type="genomic DNA"  
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/db\_xref="taxon:5759"  
/clone\_lib="Entamoeba histolytica Sheared DNA"  
/note="Vector: pBOS1, Site 1. Bst I. Constructed at The  
Institute for Genomic Research (TIGR), Rockville, MD.  
Genomic DNA isolated from broth cultures of E. histolytica  
using a method described by Clark and Diamond (Clark,  
C.G., and Diamond, V.S. (1993) Entamoeba histolytica: a  
method for isolate identification. Exp. Parasitol.  
77:450.). The DNA was mechanically sheared to give a  
tight size distribution (~2 kb). The v + 1 method used for  
the library construction is described in detail in Smith,  
H.O. and Venter, J.C. (Making small insert libraries for  
whole genome shotgun sequencing projects. In Genome  
Sequencing: A Practical Approach, eds. M. Vaudin and B.  
Bartell, Oxford University Press, 1999)."

BASE COUNT 265 a 307 c 537 g 183 t  
ORIGIN

Query Match 19.0%; Score 61.4; DB 28; Length 1292;  
Best Local Similarity 49.5%; Pred. No. 0.0073;  
Matches 158; Conservative 0; Mismatches 161; Indels 0; Gaps 0;

Qy 5 GTGGAGGTTCAGACCGCAAGAGTGTGCGGCGGCTTCGCGAGCAAGAGCC 64  
Db 745 GGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 804  
Qy 65 GGGCGTGTCTCTTCAGAGGCGCCAGCGCTGTGCAAGAGAGTCTCTGAGGCGCGGCG 124  
Db 805 GGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 864

Qy 125 AGGAGAGGAGGCAAGGCTTCCAGAGCGCGCGCGCGAGAGAGTTGCGCAGAGCA 184  
Db 865 GGGGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 924  
Qy 185 CGGCGTGTGAGCGGAGCGGAGAGGCTTCTTCAGAGCGCGGCGGAGAGCGCGCTGAGAG 244  
Db 925 GCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 984  
Qy 245 GCGAGAGCGCGGCGGATTAAGAGCTGTGCGCGCGCGCGGAGCGCGAGTTCCCGCG 304  
Db 985 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1044  
Qy 305 CGCCCGGAGCGCGCGCGCGC 323  
Db 1045 CGGCGGCGGCGCGCGCGCGC 1063

RESULT 13  
LOCUS CDS0091P 925 bp DNA linear GSS 03-JUN-1999  
DEFINITION Drosophila melanogaster genome survey sequence TERT end of BAC #  
BACR19D16 of RPL1-98 library from Drosophila melanogaster (fruit  
fly), genomic survey sequence.  
ACCESSION AL053013  
VERSION AL053013.1 GI:4934461  
KEYWORDS GSS.  
SOURCE Drosophila melanogaster (fruit fly)  
ORGANISM Drosophila melanogaster  
REFERENCE 1 (bases 1 to 925)  
AUTHORS Neoptera; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Ephidra; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidae; Drosophilidae; Drosophila.  
TITLE Direct Submission  
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage;  
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
Determination of this BAC-end sequence was carried out as part of a  
collaboration with the Berkeley Drosophila Genome Project (BDGP).  
The BDGP is constructing a physical map of the Drosophila  
melanogaster genome using these BACs. For further information  
please see <http://www.fruitfly.org> The BDGP Drosophila  
melanogaster BAC library was prepared by Kazuhiro Ogasawara and  
Aaron Mammeter in Peter de Jong's laboratory in the Department of  
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,  
NY. The library is named RPL1-98 and was constructed by partial  
EcoRI digestion of Drosophila DNA provided by the BDGP from the  
isogenic strain y2; cn bw sp; the same strain used for the BDGP's  
P1 and Bst libraries. A more detailed description of the library  
and how to order individual BAC clones, the entire library, or  
filters for hybridization from the BACPAC Resource Center, can be  
found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).  
Location/Qualifiers  
1..925  
/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7227"  
/clone="BACR19D16"  
/clone\_lib="RPL1-98"  
/note="end : TERT"

BASE COUNT 120 a 61 c 172 t 511 others  
ORIGIN

Query Match 18.8%; Score 60.8; DB 29; Length 925;  
Best Local Similarity 10.4%; Pred. No. 0.0096;  
Matches 33; Conservative 169; Mismatches 116; Indels 0; Gaps 0;

Qy 2 GCGGTGAGGTTCAGACCGCAAGAGTGTGCGGCGGCTTCGCGAGCAAG 61  
Db 597 SSVCCSSBSBSKSSSBSBSBSBSBSBSBSBSBSBSBSBSBSBSBSBSBS 656  
Qy 62 GCGGCGTGTCTCTTCAGAGGCGCCAGCGCTGTGCAAGAGAGTCTCTGAGGCGCG 121

Db 657 SSSSSSSSSSSSYTTTSSKTSASGSGSWAGGSGSSTGSSSSSSSSSSSTSSSSSSSSSVSSGK 716  
Qy 122 GCGAGGAGGAGGCGGCGCTTCCACAGGCCCCCGCGCGACGAGAAATTGGCCAG 181  
Db 717 SSTSBSGSS 776  
Qy 182 GCACGCGCTTGTAGAGCGGAGCGGCGCTTCTCAGAGCGCGCGCGCGCGCGCTG 241  
Db 777 SSTSBSGSS 836  
Qy 242 AGGCGCGGAGCGGCGCTTGTAGAGCGGCGCTTGTAGAGCGGCGCGCGCGCGCTG 301  
Db 837 KGGTTCGCGCGCGGCTTGTAGAGCGGCGCTTGTAGAGCGGCGCGCGCGCGCTG 896  
Qy 302 GCGGCG 319  
Db 897 SSS 914

RESULT 14  
BX381336 1072 bp mRNA linear EST 08-MAY-2003  
LOCUS BX381336 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
DEFINITION clone CS0D1064YV14 3-PRIME, mRNA sequence.

ACCESSION BX381336  
VERSION BX381336.1 GI:30452937  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polyes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished  
COMMENT Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 674.r For  
more information about this cluster, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CS0D1064BA07NP1&cluster=674.r. Contact :  
Feng Liang Email : filiang@lifetech.com URL :  
http://fulllength.invitrogen.com/Invitrogen Corporation 1600  
Faraday Avenue Genoscope sequence ID : CS0D1064BA07NP1.

FEATURES  
source  
Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0D1064YV14"  
/issue\_type="PLACENTA COT 25-NORMALIZED"  
/clone\_id="Homo sapiens PLACENTA COT 25-NORMALIZED"  
/note="1st strand cDNA was primed with a NotI-oligo(dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and EcoRV sites of the pCMVSPORT 6 vector.  
Library was normalized."  
BASE COUNT 172 a 324 c 268 g 231 t 77 others  
ORIGIN

Query Match 18.7%; Score 60.4; DB 13; Length 1072;  
Best Local Similarity 44.7%; Pred. No. 0.012; Indels 0; Gaps 0;  
Matches 122; Conservative 24; Mismatches 127

Qy 23 GCGAGGAGGAGGCGGCGCTTGTAGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 82  
Db 1021 GCGGCGGCGCGCGGCGGCG 962  
Qy 83 GCGGCGGCGCGCGGCGGCG 142

Db 961 GSCCCCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 902  
Qy 143 TTCCAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 202  
Db 901 CSCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 842  
Qy 203 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 262  
Db 841 CCCCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 782  
Qy 263 GAGCGCTTGTAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 295  
Db 781 CCCCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 749

RESULT 15  
BX415926 1144 bp mRNA linear EST 13-MAY-2003  
LOCUS BX415926 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP008YH01  
DEFINITION 5-PRIME, mRNA sequence.  
ACCESSION BX415926  
VERSION BX415926.1 GI:30650131  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polyes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished  
COMMENT Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 9016.f For  
more information about this cluster, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CS0CAP008YH01&cluster=9016.f. Contact :  
Feng Liang Email : filiang@lifetech.com URL :  
http://fulllength.invitrogen.com/Invitrogen Corporation 1600  
Faraday Avenue Genoscope sequence ID : CS0CAP008YH01.

FEATURES  
source  
Location/Qualifiers  
1..1144  
/organism="Homo sapiens"  
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/db\_xref="taxon:9606"  
/clone="CS0CAP008YH01"  
/issue\_type="THYMUS"  
/clone\_id="Homo sapiens THYMUS"  
/note="Vector: pCMVSPORT 6, 1st strand cDNA was primed  
with a NotI-oligo(dT) primer. Five prime end enriched,  
double-strand cDNA was digested with Not I and EcoRV sites of the  
pCMVSPORT 6 vector. Library was not normalized."  
BASE COUNT 230 a 297 c 389 g 123 t 105 others  
ORIGIN

Query Match 18.5%; Score 59.8; DB 13; Length 1144;  
Best Local Similarity 35.6%; Pred. No. 0.015; Indels 0; Gaps 0;  
Matches 115; Conservative 58; Mismatches 150

Qy 1 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 60  
Db 794 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 853  
Qy 61 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120  
Db 854 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 913  
Qy 121 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180



Oy	122	GCGAGGAAAGGGGCACGGCTTCCAGAGGCCGGCCGACACAGAATTGGTCGA	181
Db	551	SSSSSSSSSVSVSSVBSSSSSSSSRASSSSSSSVRVVVAAAVALVAIVSGGS	610
Oy	182	GCACGGCCCTTAGCGCAGCGAGGCTTTCTCAGACGGCGCAAGCCCGCCTGG	241
Db	611	GSSGAAACGCGSSGCGSSSSSSSSSSSGSSSSSGCGSIVSGSSSAAGGG	670
Oy	242	AGGGCGCAGACCCTGG	257
Db	671	GGGGGGRGRRGGGGG	686

RESULT 18	CNS0052P	LOCUS	CNS0052P	DEFINITION
ACCESSION	CNS00052P	844 bp	DNA	linear
VERSION	Drosophila melanogaster genome survey sequence TTT3 end of BAC # BACR1P16 of RP11-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.			GSS 03-JUN-1999
KEYWORDS	AL056652			
SOURCE	AL056652.1	GI:4932342		
ORGANISM	GSS.			
REFERENCE	Drosophila melanogaster (fruit fly)			
TITLE	Drosophila melanogaster			
AUTHORS	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.			
JOURNAL	1 (bases 1 to 844)			
	genoscope.			
	Direct Submission			
	Submitted (02-JUN-1999)			
	Genoscope - Centre National de Sequencage			

**COMMENT**

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the *Drosophila melanogaster* genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP *Drosophila* melanogaster BAC library was prepared by Kazutoyo Oosagawa and Aaron Mammoser. In Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPC1-98 and was constructed by partial EcoRI digestion of *Drosophila* DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

source	1..844			
	/organism="Drosophila melanogaster"			
	/mol_type="genomic DNA"			
	/db_xref="taxon:7227"			
	/clone="BACR11p16"			
	/clone_1lb="RRC1.98"			
	/note="end : TE13"			
BASE COUNT	261 a	112 c	92 g	35 t 344 others
ORIGIN				

[illegible]

Db 537 GGGGGSVSSGVYSSSSSVGMGCAACASASVYSCBSSVAASSVSSGBVSRGGCRVGGG 596

Qy 181 GGCACGGCCGTATGACCGGACGGGACAGGCTTTCACAGAGCGCGCGAGACCGCGCT 240

Db 597 GGSRVSCSSGSSSSSSSCGSSVSRSGANGVYRGSGRRGGCGGGRGAGNAPAD 658

Qy 241 GAGGGCGAGACCGGCTTAAGAACTCTG 271

Db 657 AABRABKAPANSNADAPAAVSSVSSBG 687

RESULT	19
CNSO17SY	
LOCUS	1101 bp DNA linear GSS 26-JUL-1998
DEFINITION	Drosophila melanogaster genome survey sequence S66 end of BAC BACN37J08 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION	AL108460
VERSION	ALI08460.1 GI:5628764
KEYWORDS	GSS.
SOURCE	Drosophila melanogaster (fruit fly)
ORGANISM	Drosophila melanogaster
REFERENCE	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephyroidae; Drosophilidae; Drosophila. 1 (bases 1 to 1101) Genoscope. Direct Submission Submitted (23-JUN-1999) Genoscope - Centre National de Sequencage
AUTHORS	
TITLE	
JOURNAL	

COMMENT  
determination of this BAC and sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP) - <http://www.edgp.ebi.ac.uk> - . This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaut at CEPH (centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBeloBAC11.

```

FEATURES
  source
    location/Qualifiers
      1..1101
        /organism="Drosophila melanogaster"
        /mol_type="genomic DNA"
        /db_xref="taxon:7227"
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        /clone_11b="DrosBAC"
        /plasmid="pBeloBAC11"
        /note="end : SP6"
BASE COUNT
  254 a 176 c 160 g 152 t 359 others
ORIGIN

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[illegible]

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Db          916 VSSSSSCSSSSASVVSASVAASASVSSSSSSSVSTSSASVSVSAAVMSAVSSS 974

RESULT 20
LOCUS      AG054687              703 bp    DNA             linear   GSS 02-NOV-2001
DEFINITION Pan troglodytes DNA, clone: PTB-040H03.F, genomic survey sequence.
ACCESSION  AG054687
VERSION     AG054687.1 GI:16592130
KEYWORDS   GSS.
SOURCE      Pan troglodytes (chimpanzee)
ORGANISM   Pan troglodytes
AUTHORS     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
REFERENCE   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
1           Tokoki,Y., Watanabe,H. and Sakaki,Y.
            BAC end sequences of library PTB
            Unpublished
2           (bases 1 to 703)
3           Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Tokoki,Y., Watanabe,H. and Sakaki,Y.
            Direct Submission
            Submitted (02-AUG-2001) Asso Fujiyama, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
            1-7-22 Suhrtschu-chou Tsunumi-hu, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:chihirosegcc@riken.go.jp URL:http://hsp.sec.riken.go.jp/,
            Tel:+81-45-503-9111, Fax:+81-45-503-9170)
            Clones are derived from the chimpanzee BAC library PTB This BAC end
            was generated during the Rad process and may have higher chance of
            clone tracking errors.
COMMENTARY PRIMERs
            Sequencing: -21M13
LIBRARY     Vector : pKS145
            R.site 1 : SacI
            R.site 2 : SacI.
FEATURES
source      Location/Qualifiers
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               /db_xref="taxon:9598"
               /clone="PTB-040H03.F"
               /sex="male"
               /cell_type="Tymphoblast"
               /clone_1lb="PTB Chimpanzee Male BAC Library"
BASE COUNT  51 a                369 g                16 t                13 others
ORIGIN
Query Match      18.3%; Score 59; DB 29; Length 703;
Best Local Similarity 52.6%; Pred.No.0.022;
Matches 154; Conservative 0; Mismatches 135; Indels 4; Gaps 14.
Dy      31 GCCGGCGCGGAGGTGGGCTTGCGCGAGAACAAGGCCGGCCTTCCTTCAGAGGGCCCA 90
Db       269 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 328
Qy      91 GCGCCTGCGCAAGAGGAATGCTCTGAGCGCCCGGCGAGGGAAGGGGGCACGGGCTTCCCAAG 150
Db      329 GGCCCCCCCACACCGCCCCCGCGCGCGCGCCCCCGCGGGGGGGGGGGCGCGCGCGCGCG 388
Qy     151 GCCCGCGCGCGCGAGAGGAATTGGCGCAGGGGCACGGCCGTGAG-----CGAAGCGGGCAG 206
Db     389 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCAAGCGCGGGGGCCGGGAGCCCCCGCAAGCCCG 448
Qy     207 GGGTTTCTCAGAGAGCGCGGGCGAGGCGCGGCTGAGAGGGGCGAGAACCGGATTAAGAG 266
Db     449 GGGGGGGCGCGCGCGCGCGCAAGCGCGCGCGCGCTCGCGCGCGCGCGCGCGCGCGAGCAGAG 508
Qy     267 CCTCGTAGCTTTCGCCGGCAGCGCAGATTTCCCGCGCGCGCGCGAGCGCCCG 319
Db     509 CGCCCCCGCGCGCGCGCGCGCGCGCGGATCGAGCGCGCGCGCGCGCGCGCGCGCGCG 561

```

[illegible]



KEYWORDS	EST.	Homo sapiens (human)
SOURCE	Homo sapiens	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
REFERENCE	1 (bases 1 to 515)	
AUTHORS	L. W. B. Gruber, C. J. Jassie, J. and Polayes, D.	
TITLE	Full-length cDNA libraries and normalization	
JOURNAL	unpublished	
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex France Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 6304.f. For more information about this cluster, see http://www.genoscope.cns.fr/ cgi-bin/cluster.cgi?seq=CL0BA005ZH04.f&lib=6304.f. Contact : Feng liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Farday Avenue Genoscope sequence ID : CL0BA005ZH04.fpl. location/Qualifiers 1. 515	
FEATURES		
source	/organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CL0BA005ZH04" /tissue_type="PLACENTA" /clone_lib="Homo sapiens PLACENTA" /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."	
BASE COUNT	44 a 22 c 56 g 173 t 220 others	
ORIGIN		
Query Match	18.0%; Score 58; DB 13; Length 515;	
Best Local Similarity	8.3%; Pred. No. 0.034;	
Matches	17; Conservative 116; Mismatches 59; Indels 0; Gaps 0;	
OY	131 GGGGCGACGGGCTTCCAGAGGCGCCGCGCGACAGAAATTGGCCAGGCGACGCGCC 190	
DB	323 GGGGCGSS 382	
OY	191 TGACGCGAGCGGCGAGGGCTTTCTTCAGAGCGCGCGCGCGCGCGCGCGCGCGCGAG 250	
DB	383 AAAAASS 442	
OY	251 GACCGGATATAGAAGACCTCGTGCAGCTTGCAGCCGCGGACCGCAGAGTTCCCGCGCGCCC 310	
DB	443 NANNNNANNNNNSGNNSS 502	
OY	311 GAGCCCGCGCGC 322	
DB	503 SSSSSSSSSSSSSS 514	
RESULT 25		
CNS015Z3		
LOCUS		
DEFINITION	CNS015Z3 1201 bp DNA linear GSS 26-JUL-1999	
ACCESSION		
VERSION		
KEYWORDS		
SOURCE		
ORGANISM		
REFERENCE		
AUTHORS		
TITLE		
JOURNAL		
COMMENT		

AUTHORS	Genoscope.
TITLE	Direct Submission
JOURNAL	Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr)
COMMENT	- Web : www.genoscope.cns.fr Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (BDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billard at CERN (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelOBAC11.
FEATURES	Location/Qualifiers
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	/mol_type="genomic DNA"
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	/clone_11b="BACN15106"
	/clone_11b="DrosBAC"
	/plasmid="pBelOBAC11"
	/note="end : Sp6"
BASE COUNT	177 a 221 c 322 g 279 t 202 others
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Query Match	18.0% ; Score 58; DB 29; Length 1201;
Best Local Similarity	36.0%; Pred.No. 0.035;
Matches 116; Conservative 58; Mismatches 148; Indels 0; Gaps 0;	
Oy	2 CGCGTGGGCTCAGACCAGCAAGATGTCCGGGTCGGGCTTCGCGAGACAAG 61
Db	840 CVGAAAGGGGRAGGGGMWAMGAMGGGGGGGGGGSGSCCS CRMCAAAAAMVWG 899
Oy	62 GCCGGCCCTGCCTCTCAGAGGGGCCCAAGCCCTGCAGAAGAACCTCTGAGACCCG 121
Db	900 VGGMWSMCRAACCGGGGGGGGASCCCTCCVASGMRGVYVSVRGGSSGSSSCC 959
Oy	122 GCGAGGAAGAGGGGAGACGGCTTCCAGAGGCCCGCGCGCGACAGAAATTGGCCAG 181
Db	960 GCTCCSCGCCCCSCSSCGGCRGSVMKRGCCGCSGCGGGGGGGGGGGCGGG 1019
Oy	182 GCACGCGCCGTAGCCGACCGGCGAGGCTTTCTCAGAGCGCGGCGAGCCGCGCTG 241
Db	1020 GGSGGGGCGCGGGGGGGGGGGGSGGSGGSGGSGGSCAACGGGCGCGCCGG 1079
Oy	242 AGGGCGAGACCGCGGTATAAGACTCTGTGCTTGCCCGGCGAGCGCAGATTCCC 301
Db	1080 GGGGGGGGGGGCGCCGSSASCGCCCGCGSGGSGGSGGSCCGCGVSGSCACCGSGCG 1139
Oy	302 GCGCGCCCGCAGACCCCGCGCGC 323
Db	1140 GGSGCACGSGGGSGCGGGGGGCG 1161
RESULT 26	
EX381320/c	693 bp mRNA linear EST 08-MAY-2003
LOCUS	EX381320 Homo sapiens PLACENPA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION	Clone GS01064Y109 5-PRIME, mRNA sequence.
ACCESSION	EX381320
VERSION	EX381320.1 GI:30458947
KEYWORDS	EST
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eskayaeva, Metazova; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 693) L.I., W.B., Gruber,C., Jessee,J. and Polymer,D. Full-length cDNA libraries and normalization Unpublished Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France







http://fulllength.invitrogen.com/Invitrogen Corporation 1600  
Paradise Avenue Genoscope sequence ID : CS0BAE0212A02\_AE01930\_1.  
Location/Qualifiers  
1. .881

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/issue\_type="PLACENTA COT 25-NORMALIZED"  
/note="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with NotI and cloned into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library was normalized."  
BASE COUNT  
37 a 147 c 355 g 65 t 277 others  
ORIGIN

Query Match 17.8%; Score 57.8; DB 13; Length 881;  
Best Local Similarity 48.8%; Pred. No. 0.038;  
Matches 143; Conservative 0; Mismatches 150; Indels 0; Gaps 0;  
QY 31 GCGGGCGGGGCTGCGCTCGGAGACAAAGCGCGGCTGCTCTCGAGAGGCCCA 90  
DB 552 GGG 611  
QY 91 GCGGCTCCAGAGAGAGTCTCTGAGCGCGGCGAGGAGGAGGAGCGGCTTCCACG 150  
DB 612 GGG 671  
QY 151 GCGGCGCGCGCGAGAGAGTGGCGAGGCGAGCGCGCTGAGCGGAGCGGCGAGGCT 210  
DB 672 GGG 731  
QY 211 TTCTCAGAGAGCGCGGAGAGCGCGCGCTGAGGAGGAGGAGCGGCTTAAGAGACCTC 270  
DB 732 TTGG 791  
QY 271 GTGGCTTGGCGCGCGCGAGCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCG 323  
DB 792 GCG 844

RESULT 29  
CNS0060N/c 910 bp DNA linear GSS 03-JUN-1999  
LOCUS  
DEFINITION  
Drosophila melanogaster genome survey sequence T7 end of BAC #  
BACR14J21 of RPCI-98 library from Drosophila melanogaster (fruit  
fly), genomic survey sequence.  
ACCESSION  
AL065629 GI:4944698  
VERSION  
KEYWORDS  
Drosophila melanogaster (fruit fly)  
SOURCE  
ORGANISM  
Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.  
1 (bases 1 to 910)  
Genoscope.  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Direct Submission  
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :  
BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
Determination of this BAC-end sequence was carried out as part of a  
collaboration with the Berkeley Drosophila Genome Project (BDGP).  
The BDGP is constructing a physical map of the Drosophila  
melanogaster genome using these BACs. For further information  
please see <http://www.fruitfly.org> the BDGP Drosophila  
melanogaster BAC library was prepared by Kazuo Ogoe and  
Aron Mammerer in Peter de Jong's laboratory in the Department of  
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,  
NY. The library is named RPCI-98 and was constructed by partial  
EcoRI digestion of Drosophila DNA provided by the BDGP from the  
isogenic strain Y2; cn bw sp, the same strain used for the BDGP s

P1 and EST libraries. A more detailed description of the library  
and how to order individual BAC clones, the entire library, or  
filters for hybridization from the BACPAC Resource Center can be  
found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).  
Location/Qualifiers  
1. .910

FEATURES  
source  
/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7227"  
/clone="BACR14J21"  
/note="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with NotI and cloned into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library was normalized."  
BASE COUNT  
202 a 112 g 198 t 335 others  
ORIGIN

Query Match 17.8%; Score 57.6; DB 29; Length 910;  
Best Local Similarity 15.6%; Pred. No. 0.042;  
Matches 48; Conservative 148; Mismatches 112; Indels 0; Gaps 0;  
QY 16 CCGCAAGCGAGGTGCGGCGCGGCTGCGCTCGGAGACAAAGCGGCTGCTC 75  
DB 819 VSRSSASVSVSVGSASRSASVSSSSAGSAVSAVMAVSAVSAVSAVSAVSA 760  
QY 76 TCTCAGAGGCGCGCGCGCTGCGAGAGAGTCTCTGAGCGCGCGCGAGGAGGAG 135  
DB 759 ARAAKAAASWAAVAAVAAVAAVAAVAAVAAVAAVAAVAAVAAVAAVAAVAA 700  
QY 136 CACGAGCTCCAGAGGCGCGCGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAG 195  
DB 699 SSSSSASASSAS 640  
QY 196 GAGCGGCGAGGCTTCTCAGAGAGCGCGCGAGAGAGAGAGAGAGAGAGAGAG 255  
DB 639 SSSSSVSVSVSVGSASRSASVSSSSAGSAVSAVMAVSAVSAVSAVSAVSA 580  
QY 256 GGTATAGAGAGCTTCTGAGAGCGCGCTTCCCGGAGAGAGAGAGAGAGAGAG 315  
DB 579 SSVGCVSSCGSS 520  
QY 316 CCGCGCGC 323  
DB 519 CCGCGCGC 512

RESULT 30  
B2046906/c 723 bp DNA linear GSS 09-OCT-2002  
LOCUS  
DEFINITION  
Brassica oleracea 002 Brassica oleracea genomic, genomic survey  
sequence.  
ACCESSION  
B2046906 GI:23642870  
VERSION  
KEYWORDS  
Brassica oleracea  
SOURCE  
ORGANISM  
Brassica oleracea  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids  
; eurosids II; Brassicales; Brassicaceae; Brassica.  
1 (bases 1 to 723)  
W. Rahmowicz, P.D. and Wilson, R.K.  
Whole genome shotgun reads from Brassica oleracea  
unpublished  
Contact: Richard K. Wilson  
Genome Sequencing Center  
Washington University School of Medicine  
Email: [rahmowicz@wustl.edu](mailto:rahmowicz@wustl.edu)  
Phone: 314.772.1000  
Fax: 314.772.1000  
Web: <http://www.genome.wustl.edu>  
Class: shotgun  
Seq primer: -210bp forward  
High quality sequence start: 38  
High quality sequence stop: 159.  
Location/Qualifiers  
1. .723

```
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/db_xref="taxon:3712"
/clone_lib="B.oleracea02"
/notes="Vector: pOTW13; Whole genome shotgun library from
flowering buds. DNA was purified from a crude nuclear
prep using Brassica oleracea T01000D3 buds provided by
Thomas Osborn at the University of Wisconsin. Genomic
DNA was provided by Pablo Rabinowicz (CSHL) and the
shotgun library prepared at Washington University Genome
Sequencing Center."

BASE COUNT      64 a      360 c      211 g      79 t      9 others
ORIGIN

Query Match      17.8%; Score 57.4; DB 28; Length 723;
Best Local Similarity 48.6%; Pred. No. 0.046;
Matches 157; Conservative 0; Mismatches 166; Indels 0; Gaps 0;

QY      1 GCGCGTGGGCTCAACCGCAAGAGTGCGGGCTGGGCTCGCGAGCAAA 60
      |||||
DB      635 GGGCGGGGGGGGGCGCGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCG 576
QY      61 GCGCGGCTGCTCTCTCTCAAGAGGCGCCCAAGCGCTTCCAGAGAGAA 120
      |||||
DB      575 GCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 516
QY      121 GGGGAGGAAAGGGGGGCAAGGCTTCCAGAGCGCGCGCGAGAGAGATTG 180
      |||||
DB      515 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 456
QY      181 GGCACGCGCGTGAACGCGAGCGGCGCTTCTCAAGAGCGCGCGAGCGCGCTG 240
      |||||
DB      455 GCGCGCGCGCGCGCGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 396
QY      241 GAGGGGCGAGAGCGGGTATTAAGAGCTGTGGCTTGGCGGAGCGCGAGTTCC 300
      |||||
DB      395 GGGGGCGCGCGCGCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 336
QY      301 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 323
      |||||
DB      335 GGGGGCTCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 313

RESULT 31
CNS010RY/C      776 bp      DNA      linear      GSS 26-JUL-1999
LOCUS      Drosophila melanogaster genome survey sequence SP6 end of BAC
DEFINITION      BACN04P24 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION      AL093932
VERSION      AL093932.1 GI:5610963
KEYWORDS      GSS.
SOURCE      Drosophila melanogaster (fruit fly)
ORGANISM      Drosophila melanogaster
AUTHORS      Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE      1 (bases 1 to 1776)
GENOSCOPE.
DIRECT SUBMISSION
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billand at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelobAC11.

FEATURES
source      1..776
Location/Qualifiers
```

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/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone_lib="BACN04P24"
/clone_lib="DrosBAC"
/plasmid="pBelobAC11"
/notes="end : SP6"

BASE COUNT      110 a      439 c      135 g      0 t      92 others
ORIGIN

Query Match      17.8%; Score 57.4; DB 29; Length 776;
Best Local Similarity 38.6%; Pred. No. 0.046;
Matches 124; Conservative 43; Mismatches 154; Indels 0; Gaps 0;

QY      1 GCGGTGGGCTCAACCGCAAGAGTGCGGGCTGGGCTCGCGAGCAAA 60
      |||||
DB      356 GGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 297
QY      61 GCGCGGCTGCTCTCTCTCAAGAGGCGCCCAAGCGCTTCCAGAGAGAA 120
      |||||
DB      296 GGGGAGGAGGGGGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 237
QY      121 GGGGAGGAAAGGGGGGCAAGGCTTCCAGAGCGCGCGCGCGAGAGAGATTG 180
      |||||
DB      236 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 177
QY      181 GGCACGCGCGTGAACGCGAGCGGCGCTTCTCAAGAGCGCGCGAGCGCGCTG 240
      |||||
DB      176 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 117
QY      241 GAGGGGCGAGAGCGGGTATTAAGAGCTGTGGCTTGGCGGAGCGCGAGTTCC 300
      |||||
DB      116 GCGGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 57
QY      301 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 321
      |||||
DB      56 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 36

RESULT 32
B0957113/C      1019 bp      mRNA      linear      EST 21-ANG-2002
LOCUS      AGENCOURT 8779542 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:6371648
DEFINITION      5' UTR mRNA sequence.
ACCESSION      B0957113
VERSION      B0957113.1 GI:22372591
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
AUTHORS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 1019)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph. D.
Email: sgabbs-remail.nih.gov
Tissue Procurement: DCTD/DRP/Gazdar
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHCW546 row: C column: 09
High quality sequence start: 25
High quality sequence stop: 300.
Location/Qualifiers
1..1019
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6371648"
```

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/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_1lb="NIH MG C 18"
/notes="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGGACGAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MG C library."
BASE COUNT      50 a 506 c 311 g 99 t 53 others
ORIGIN
Query Match      17.8%; Score 57.4; DB 13; Length 1019;
Best Local Similarity 48.3%; Pred. No. 0.046;
Matches 157; Conservative 0; Mismatches 166; Indels 2; Gaps 1;
QY 1 GCGGCTGGGTCAACCGGCAAGGTCGGGCGGGGTGGGCTTCGGGAGCAAA 60
DB 769 GCGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 710
QY 61 GCGCGGCGCTGCTCTCTCAAGGCGCCCAAGCGCTTGCAGAGGAATCTTGAAGCC 120
DB 709 GGGGCGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 650
QY 121 GGGCAGGAAAGGGGCGACGGGCTTCCAGGGCCCGCGCGCGAGAGAAATTGGCCAG 180
DB 649 GCGCGAGGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 590
QY 181 GGCACGCGCGTGAAGCGGA--GCGGCGAGGCTTTCTTCAAGAGCGCGGCGAGCGCGCC 238
DB 589 GAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 530
QY 239 TGAAGGCGGAGAGACCGGGTATTAAGAGCTCTGTGGCTTGCCTGGGCGAGCGAGTTTC 298
DB 529 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 470
QY 299 CCGGCGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 323
DB 469 GGGGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 445

RESULT 33
LOCUS      BG844318      873 bp      mRNA      linear      EST 29-MAY-2001
DEFINITION Chlamydomonas reinhardtii CC-1690, normalized, lambda Zap II
ACCESSION  BG844318
VERSION     BG844318.1 GI:14225502
SOURCE      EST.
ORGANISM    Chlamydomonas reinhardtii
            Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
            Chlamydomonadaceae; Chlamydomonas.
REFERENCE   1 (bases 1 to 873)
AUTHORS    Grossman,A., Davies,J., Federstepiel,N., Harris,E., Lefebvre,P.,
            McDermott,J.P., Sillflow,C., Stern,D. and Surzycki,R.
TITLE       Analyses of the Chlamydomonas reinhardtii Genome: A Model,
            Unicellular System for Analyzing Gene Function and Regulation in
            Vascular Plants; project phase 2
JOURNAL     Unpublished
CONTACT     Charles Hauser
            DCMB Box 91000
            Duke University
            Durham, NC 27708-1000
            Tel: 919 613 8159
            Fax: 919 613 8177
            Email: chauser@duke.edu
FEATURES
SOURCE      1..873
            location/Qualifiers
            /mol_type="mRNA"

```

```

/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_1lb="C. reinhardtii CC-1690, normalized, lambda Zap
II"
/notes="Vector: pBluescript II SK-; Site 1: EcoRI; Site 2:
XhoI; This library, constructed by John Davies and Jeffrey
McDermott, combines cDNAs from CC-1690 cells grown to
mid-log phase in YAP (acetate-containing) medium in the
light, YAP medium in the dark, HS (nutrient) medium in
ambient levels of CO2 and HS medium bubbled with 5% CO2.
PolyA mRNA was purified from each sample, pooled and cDNA
synthesized. The cDNA was directionally cloned into lambda
ZAP II (Stratagene) in the EcoRI (5') and XhoI (3') sites.
pBluescript II SK- plasmids were excised from the lambda
phage. The library was normalized using method A described
in Bonaldo et al (1996) Genome Research 6: 791-806."
BASE COUNT      17 a 334 c 471 g 22 t 29 others
ORIGIN
Query Match      17.7%; Score 57.2; DB 12; Length 873;
Best Local Similarity 50.5%; Pred. No. 0.05;
Matches 163; Conservative 0; Mismatches 159; Indels 1; Gaps 1;
QY 1 GCGCTGGGTCAACCGGCAAGGTCGGGCGGGGTGGGCTTCGGGAGCAAA 60
DB 398 GGGGCGGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 457
QY 61 GCGCGGCGCTGCTCTCTCAAGGCGCCCAAGCGCTTGCAGAGGAATCTTGAAGCC 120
DB 458 GGGGCGGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 517
QY 121 GGGCAGGAAAGGGGCGACGGGCTTCCAGGGCCCGCGCGCGAGAGAAATTGGCCAG 180
DB 518 GGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 577
QY 181 GGCACGCGCGTGAAGCGGA--GCGGCGAGGCTTTCTTCAAGAGCGGCGGCGAGCGCGCG 240
DB 578 GGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 636
QY 241 GAGGCGGAGAGACCGGGTATTAAGAGCTCTGTGGCTTGCCTGGGCGAGCGAGTTTC 300
DB 637 CCGGCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 696
QY 301 CCGGCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 323
DB 697 GCGGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 719

RESULT 34
LOCUS      AG136798      828 bp      DNA      linear      GSS 04-NOV-2001
DEFINITION Pan troglodytes DNA, clone: PTB-150H19.R, genomic survey sequence.
ACCESSION  AG136798
VERSION     AG136798.1 GI:16666476
SOURCE      GSS.
ORGANISM    Pan troglodytes (chimpanzee)
            Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
REFERENCE   1
AUTHORS    Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Torok,Y., Watanabe,H. and Sakaki,Y.
TITLE       BAC end sequences of library PTB
JOURNAL     Unpublished
CONTACT     Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Torok,Y., Watanabe,H. and Sakaki,Y.
AUTHORS     2 (bases 1 to 828)
            Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Torok,Y., Watanabe,H. and Sakaki,Y.
TITLE       Direct Submission
JOURNAL     Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
            1-7-22 Suenhiro-cho,Tsukumi-Ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,

```

## COMMENT

Tel:81-45-503-9111, Fax:81-45-503-9170)  
Clones are derived from the chimpanzee BAC library PTB. This BAC end  
was generated during the R&D process and may have higher chance of  
clone tracking errors.

## PRIMERS

Sequencing: M13Rev  
Library Vector : pKS145  
R.Site 1 : SacI  
R.Site 2 : SacI

## FEATURES

Location/Qualifiers  
1 828f  
/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
/clone="PTB-150H19.R"  
/sex="male"  
/cell\_type="lymphoblast"  
/clone\_lib="PTB Chimpanzee Male BAC Library"

BASE COUNT 22 a 147 c 479 g 27 t 153 others  
ORIGIN

Query Match 17.6%; Score 57; DB 29; Length 828;  
Best Local Similarity 50.7%; Pred. No. 0.055;  
Matches 152; Conservative 0; Mismatches 147; Indels 1; Gaps 1;

23 GCGAAGTGGCGGCGCGGGTGGCGCTTCGCGAGACAAAGCCGGGCTCTCTTCACG 82  
Db GNNNGGGGGGGGGCGCTGTGGGGGCGCCCAANNAAGAGGGGGGGGCGCCCGGG 494  
Qy GGGCCCGAGCGCTCTCGAAGAGAGTCTCTGAGCGCCGGGCGAGGAGGGGCGACGGGC 142  
Db GGGCGGCGGGCGCGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 554  
Qy 143 TTCCAGAGGCGCGCGCGCGCGAGAGATTGGCCAGGCGCACGGCGCTGAGCGGACGG 202  
Db GCGGGGGGGGGCGCGGGGCGCGGGCGCGGGCGGGGGGGGGGGGGGGGGGGGGGG 614  
Qy 203 GCAGAGGCTTTCTCAGAGAGCGCGGCGAGCGCGC-GCTGAGGGGGCGAGACCGGGTATA 261  
Db 615 CCGGGGGCGGGCGCGGGCGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 674  
Qy 262 AGAAGCGCTGCGCTTGGCGCGGGCGAGCGCGAGGTTCCCGCGCGCGCGCGCGCGCG 321  
Db 675 CCGGGGGCGGGCGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 734

## RESULT 35

BO678466/c 971 bp mRNA linear EST 15-JUL-2002  
LOCUS AGENCOURT 8208927 NIH\_MGC\_112 Homo sapiens cDNA clone IMAGE:5260268  
DEFINITION 5', mRNA sequence.

ACCESSION BO678466

VERSION BO678466.1 GI:21791145

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE NIH-MGC http://mgi.nci.nih.gov/

1 (bases 1 to 971)  
National Institutes of Health, Mammalian Gene Collection (MGC)

AUTHORS Unpublished

JOURNAL Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov

COMMENT Tissue Procurement: DCTD/DTF

CDNA Library Preparation: Rubin Laboratory

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LINL at:

http://image.llnl.gov

Plate: LNCM2419 row: b column: 13

## FEATURES

source

High quality sequence stop: 536.  
Location/Qualifiers  
1..971  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6260268"  
/issue\_type="melanotic melanoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC 112"  
/note="Organ: skin; Vector: pORF7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally cloned  
into EcoRI/XhoI sites using the following 5' adaptor:  
GGCAGGAG(G). Library constructed by Ling Hong in the  
laboratory of Gerald M. Rubin (University of California,  
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and  
Superscript II RT (Life Technologies). Note: this is a  
NIH MGC Library."

BASE COUNT 143 a 366 c 267 g 107 t 88 others  
ORIGIN

Query Match 17.6%; Score 56.8; DB 13; Length 971;  
Best Local Similarity 41.3%; Pred. No. 0.061;  
Matches 124; Conservative 0; Mismatches 176; Indels 0; Gaps 0;

23 GCGAAGTGGCGGCGCGGGTGGCGCTTCGCGAGACAAAGCCGGGCTCTCTTCACG 82  
Db GGGGGGGGGGGGGGCGNNNGGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 898  
Qy 957 GGGCCCGAGCGCTCTCGAAGAGAGTCTCTGAGCGCCGGGCGAGGAGGGGCGACGGGC 142  
Db GGGCGGNNNGGNNNGGNNCGCGGGGNNCGGGGGNNNGGGGGGGGGGGGGGGGGGG 838  
Qy 143 TTCCAGAGGCGCGCGCGCGCGAGAGATTGGCCAGGCGACGCGCTGAGCGGACGG 202  
Db 837 GNNCGCGCGGNNNNCCNNNNNGGGGGGGGGGGCGCCGNNNNNGNNNNCGGGGGCGG 778  
Qy 203 GCAGAGGCTTTCTCAGAGAGCGCGGCGAGCGCGCGCTGAGGGGGCGAGACCGGGTATA 262  
Db 777 GGCNCGCGGGGGGGGGCGNNNGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 718  
Qy 263 GAAGCTCTGCGCTTGGCGCGGGCGAGCGCGAGGTTCCCGCGCGCGCGCGCGCGCGCG 322  
Db 717 GNNCCCCCGGGGGCGCGGGCGGGGGGNNNGGCGNNNNNGGGCGCGCGCGCGCGGGG 658

## RESULT 36

BU185501 1126 bp mRNA linear EST 04-SEP-2002  
LOCUS AGENCOURT 8108662 NIH\_MGC\_112 Homo sapiens cDNA clone IMAGE:6253571  
DEFINITION 5', mRNA sequence.

ACCESSION BU185501

VERSION BU185501.1 GI:22699485

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE NIH-MGC http://mgi.nci.nih.gov/

1 (bases 1 to 1126)  
National Institutes of Health, Mammalian Gene Collection (MGC)

AUTHORS Unpublished

JOURNAL Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov

COMMENT Tissue Procurement: DCTD/DTF

CDNA Library Preparation: Rubin Laboratory

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LINL at:

http://image.llnl.gov

Plate: LNCM2401 row: k column: 12

High quality sequence start: 70

High quality sequence stop: 292.  
Location/Qualifiers

1. 1126  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6253571"  
/issue\_type="melanotic melanoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_id="NIH MGC 112"  
/note="Organ: SKIN; Vector: pORF7; Site\_1: XhoI; Site\_2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCGACAGAG(G). Library constructed by Ling Hong in the Laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA distribution information can be found through the I.M.A.G.E. Consortium/UMIN at: http://image.11n1.gov  
NIH MGC Library."

BASE COUNT 57 a 57A 625 G 89 C 24 others.

ORIGIN

Query Match 17.5%; Score 56.4; DB 13; Length 1126;  
Best Local Similarity 48.8%; Pred. No. 0.073;  
Matches 144; Conservative 0; Mismatches 151; Indels 0; Gaps 0;

OY 28 GGTGCGGGCCGGGGGTGGGCTCTGCGGGAACAAAGGCCCGGGCTGCTCTCAAGAGGCC 87  
DB 548 GTGGGGGGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCG 607  
OY 88 CCAGGCGCGCTGCCAAGAGAGATCTTCGAGGCCCGGGGCGAGGAGGGGGCGAGGGCTTCCC 147  
DB 608 GGGGCGGGCGGGGGGGGGGGGGGGGGGGGGCGAGCGGGCGGGGCGGGCGGGCGGGCG 667  
OY 148 AGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGG 207  
DB 668 CGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGG 727  
OY 208 GCTTTCTCAAGAGCGCGGGCGAGGCTTCCCGCTCGAGGGGGCGAGAGCGGGATTAAGAGC 267  
DB 728 GGGGGCGGG 787  
OY 268 CTCTGTGCTTGGCCCGGCGAGCGCGAGCTTCCCGCGCGCGCCCGGAGGCCCGGGCG 322  
DB 788 GCGGCGGGCGGG 842

RESULT 37  
B0892481/c 1150 bp mRNA linear EST 16-AUG-2002  
LOCUS B0892481/c 8296666 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6249766  
DEFINITION AGENCOURT 8296666 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6249766  
5', mRNA sequence.  
ACCESSION B0892481  
VERSION B0892481.1 GI:22284495  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 1150)  
NIH-MGC http://mgi.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: rgs@bbs-remail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (UMIN)  
DNA sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/UMIN at:  
http://image.11n1.gov  
Plate: L12CM231 row: 1 column: 23  
High quality sequence start: 20

FEATURES	High quality sequence stop: 171.
SOURCE	Location/Qualifiers
1	1150
/organism="Homo sapiens"	
/mol_type="mRNA"	
/db_xref="taxon.9606"	
/clone="IMAGE:6249766"	
/label_type="ductal carcinoma, cell line"	
/id_host="DH108 (phage-resistant)"	
/clone_id="NIH_MGC_110"	
/note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Specially cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Hong Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."	
BASE COUNT	39 a 550 c 358 g 70 t 133 others
ORIGIN	
Query Match	17.5%; Score 56.4; DB 13; Length 1150;
Best Local Similarity	48.1%; Pred. No. 0.073;
Matches 156; Conservative	0; Mismatches 166; Indels 2; Gaps 1;
Oy	2 CGCGTGGGGTTCAGACCGCCAGAGAGATGCGGGCGGGGGGCTTCGCGAGACAAG 61
Db	658 CGCGCGGGGNCGGGGGGCGCGGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 599
Oy	62 GCGGGGGCTCTCTCTCAGAGGGGCCCGCCAGCGCTGCGAGAGAGATCTCGAGCGCG 121
Db	598 CCGGGGGCGGG 539
Oy	122 GGCAGGGAAGGGGGGCAAGGGCTTCCAGAGGGCGCGCGCGCGCGCGCGCGCGCG 179
Db	538 GGGGGGGGGGNCGG 479
Oy	180 GGGGACCGCGGTGACCGGAGCGGGGCGAGGCGCTTCTCAGAGCGCGGGCGAGCGCGCGCT 239
Db	478 CGGG 419
Oy	240 GAGGGGCGAGGACCGGGTATTAAGAAAGCTCTGTGGCTTGTCCCGGCGAGCGCGGACGTTC 289
Db	418 GCGGG 359
Oy	300 CCGGCGCGCGCGCGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 323
Db	358 NCCCCCCCCCGGG 335
RESULT 38	
AG060267	810 bp DNA linear GSS 03-NOV-2001
LOCUS	
DEFINITION	Pan troglodytes DNA, clone: PTB-047L09.R, genomic survey sequence.
ACCESSION	AG060267
VERSION	AG060267.1 GI:16611499
KEYWORDS	GSS.
SOURCE	Pan troglodytes (chimpanzee)
ORGANISM	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euteleia; Primates; Catarrhini; Homnidae; Pan.
REFERENCE	Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,
AUTHORS	Tsokaki, Y., Watanabe, H., and Sakaki, Y.
TITLE	BAC end sequences of library F1B
JOURNAL	2 (bases 1 to 810)
REFERENCE	Unpublished
AUTHORS	Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,
TITLE	Tsokaki, Y., Watanabe, H., and Sakaki, Y.
JOURNAL	Submitted
REFERENCE	Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
AUTHORS	and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
TITLE	1-7-22 Suehiro-Chou, Tsukuba, Ibaraki, 305-8565, Japan

(E-mail:chimpbes@gsic.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,  
Tel:81-45-503-9111, Fax:81-45-503-9170)  
Clones are derived from the chimpanzee BAC library PTB this BAC end  
was generated during the R&D process and may have higher chance of  
clone tracking errors.

## PRIMERS

Sequencing: M13Rev

## LIBRARY

Vector : pKS145

R.Site 1 : SacI

R.Site 2 : SacI

Location/Qualifiers

1. .810

/organism="Pan troglodytes"

/mol\_type="genomic DNA"

/db\_xref="taxon:9598"

/clone="PTB-047109.R"

/sex="male"

/cell\_type="lymphoblast"

/clone\_lib="PTB Chimpanzee Male BAC library"

/origin

BASE COUNT

20 a 202 c 511 g 26 t 51 others

Query Match

Best Local Similarity 48.6%; Pred. No. 0.08;

Matches 142; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

1 GCGCGTGGGCTCAAGCCGCAAGCGAGTCCGCGCGCGCGCTCGCGCAACAA 60

451 GCG 510

61 GCG 120

511 GCG 570

121 GCG 180

571 GCG 630

181 GCG 240

631 GCG 690

241 GCG 292

691 GCG 742

RESULT 39  
BG809572/c 888 bp mRNA linear EST 22-MAY-2001  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

888 bp mRNA linear EST 22-MAY-2001  
mgct001x14f Magnaporthe grisea Appressorium Stage cDNA Magnaporthe  
grisea cDNA clone mgct001x14f 5', mRNA sequence.

EST

Magnaporthe grisea (anamorph: Pyricularia grisea)

Magnaporthe grisea

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Sordariomycetes; Incertae sedis; Magnaporthaceae; Magnaporthe.

1 (bases 1 to 888)

Choi, W. and Dean, R.A.

Library in the Rice Blast Fungus, Magnaporthe grisea

Unpublished

Contact: Ralph A. Dean

Fungal Genomics Laboratory

North Carolina State University

Campus Box 7251, Raleigh, NC 27695, USA

Tel: 919-513-0020

Fax: 919-513-0024

Email: ralph.dean@ncsu.edu

Seq primer: T3 primer (AATTAACCTCACTAAGG).

## FEATURES

Source

1. .888

/organism="Magnaporthe grisea"

/mol\_type="mRNA"

/strain="70-15"

/db\_xref="taxon:148305"

/dev\_stage="germinated conidia on appressorium-inductive  
surface"

/clone\_lib="Magnaporthe grisea Appressorium Stage cDNA"

/note="Vector: pBluescript SK(+) Vector; Site 1: EcoRI;  
Site 2: XhoI; The appressorium formation-specific cDNA  
library was constructed from conidia germinated for 5-8 hr  
on an inductive surface. The library contains over 55,000  
clones with average insert size of 1.5 kbp."

BASE COUNT

22 a 431 c 397 g 4 t 34 others

Query Match

Best Local Similarity 50.5%; Pred. No. 0.08;

Matches 162; Conservative 0; Mismatches 158; Indels 1; Gaps 1;

3 GCGTGGGCTCAAGCCGCAAGCGAGTCCGCGCGCGCGCTCGCGCAACAA 62

721 GCG 662

63 GCG 122

661 GCG 602

123 GCG 181

601 GCG 542

182 GCG 241

541 GCG 482

242 GCG 301

481 GCG 422

302 GCG 322

421 GCG 401

RESULT 40  
AG042900 978 bp DNA linear GSS 01-NOV-2001  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

978 bp DNA linear GSS 01-NOV-2001  
Pan troglodytes DNA, clone: PTB-021A20.R, genomic survey sequence.

GSS

Pan troglodytes (chimpanzee)

Pan troglodytes

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Pan.

1 (bases 1 to 978)

Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,  
Toki, Y., Watanabe, H., and Sakaki, Y.

BAC end sequences of library PTB

Unpublished

Submitted (02-AUG-2001) Aao Fujiyama, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC), Japan

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

(E-mail:chimpbes@gsic.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,  
Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the chimpanzee BAC library PTB this BAC end

was generated during the R&D process and may have higher chance of  
clone tracking errors.

## PRIMERS

Sequencing: M13Rev

## LIBRARY

Vector : PKS145

R.Site 1 : SacI

R.Site 2 : SacI

Location/Qualifiers

1. 978

/organism="Pan troglodytes"

/mol\_type="genomic DNA"

/db\_xref="taxon:9598"

/clone="PTB-021A20.R"

/sex="male"

/cell\_type="lymphoblast"

/clone\_lib="PTB Chimpanzee Male BAC Library"

## BASE COUNT

66 a 321 c 528 g 24 t 39 others

## ORIGIN

## Query Match

Best Local Similarity 49.3%; Score 56; DB 29; Length 978;  
Matches 140; Conservative 0; Mismatches 144; Indels 0; Gaps 0;

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QY 38 GGGGTGGGCTCGCGAGACAAAGCCGGGCTCTCTCTCAAGAGGCCCCCAAGCCCTG 97
DB 577 GCGGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 636
QY 98 CCAAGAGGAAGTCTCTGAGGCTCCCGGCAAGAGGGGCAAGGGCTTCCAGGGCCGCC 157
DB 637 CGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 696
QY 158 GGGCGGAGCAAGAAATTGCGCGAGGAGCGGCGCGTGTAGCGAGCGGGCGAGGGCTTCTCAG 217
DB 697 GCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 756
QY 218 GAGCGCGCGCGAGGCGCGCGCGCTGTGAAGGAGCGAGACCGGAGTATTAAGAGCTTGAGGCT 277
DB 757 CGGGGGGCGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 816
QY 278 TGCCCGGAGCGCGAGGTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 321
DB 817 CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 860
```

Search completed: November 6, 2003, 09:03:39  
Job time : 1866.61 secs

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